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            ESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVV
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                                                                                                                   The sequence encoding the P195 protein of Plasmodium falciparum (AAN50530) and a peptide comprising at least one of its epitopes (see AAP50777) are claimed. Also claimed is a vaccine for inducing immunity to malaria comprising the novel peptide or P195 or a peptide comprising at least one epitope when derived from the new DNA sequence, together with a carrier.
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                                                                sequence encoding plasmodium expressing the protein for us
                  Odink K, Lockyer
                                                                                                   Claim 6; Fig 1; 51pp; English.
(WELL ) WELLCOME FOUNDATION
                  Sandhu J,
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N-PSDB; AAN50530.
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1264 AVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRE 1323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a 42 kDa C-terminal portion of malaria merozoite surface protein MSP-1 (i.e. MSP-1-42), an important target for the development of a vaccine against plasmodium falciparum. The nucleic acid sequence encoding MSP-1-42 has been modified (see AAX25586) compared to the native sequence (see AAX25587) such that 306 nucleotide positions have been replaced to lower the AT content (from 76 to 49.7%) and to eliminate 10 mRNA instability motifs while maintaining the same protein amino acid sequence. These alterations allow MSP-1-42 to be expressed in mammalian cell culture and in transgenic mice. The invention provides modified recombinant nucleic acid sequences and methods for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New modified recombinant nucleic acid sequences useful for producing malarial DNA vaccine
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100.0%; Pred. No. 4.4e-75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a 42 kDa C-terminal portion of malaria merozotte surface protein MSP-1 (i.e. MSP-142), an important target for the development of a vaccine against Plasmodium falciparum. The nucleic acid sequence encoding MSP-1-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCS 1618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified malarial protein for use in anti-malarial vaccines
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protein engineering; protein expression; codon usage;
                     Merozoite surface protein MSP-1-42
                                                                                                                                                                                                                                                                                                                                                                                                            (GENZ ) GENZYME TRANSGENICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example, Fig 1; 35pp; English
                                                                                                                                                                                                                                                                                              98WO-US22226.
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97US-0062592.
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Matches 355; Conservative
                                                                                                                                                      Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1999-288313/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Meade H;
                                                                                                                transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           355 AA;
                                                              MSP-1; merozoite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAX56008
                                                                                                                                                                                                      WO9920774-A2
                                                                                                                                                                                                                                                                                              20-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen LH,
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1444 LNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLSTDYNHNNLLTKFLSTGM 1503
                                 NFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVL 1383
                                                                                                                         This present sequence comprises a 42 kDa C-terminal portion of malaria merozoite surface protein MSP-1 (i.e. MSP-1-42), an important target for the development of a vaccine against Plasmodium falciparum. The C-terminal end of the sequence is modified to include a 6xHis tag. Nucleic acids (see AAX25586 and AAX25593) encoding MSP-1-42 have been modified according to a method of the invention in order to improve expression in mammalian cells and in transgenic animals. The invention provides modified recombinant nucleic acid sequences and methods for increasing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New modified recombinant nucleic acid sequences useful for producing
                                                                                                                                                                                                                                                                       LNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLSTDYNHNNLLTKFLSTGM
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                                                                                                                                                                             GYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLFVIHLEAKV
                                                                                                                                                                                                                                                                                                                                                                                            DKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCS 1618
                                                                                                                                                                                                                                                                                                                                                                                                             MSP-1; merozoite surface protein; malaria; vaccine; protein engineering; protein expression; codon usage;
Mismatches
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355; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transgenic animal
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                                                                                                                                                          240
                                                                                                                                                                                                                                   300
This present sequence comprises a 42 kDa C-terminal portion of malaria merozoite surface protein MSP-1 (i.e. MSP-1-42), an important target for the development of a vaccine against.

Plasmodium falciparum. The C-terminal end of the sequence is modified to include a 6xHis tag. A nucleic acid (see AAX56008) encoding MSP-1-42 has been modified according to a method of the invention in order to improve expression in mammalian cells and in transgenic animals by reducing the AT content and removing mRNA instability motifs. The invention allows expression of MSP-1-42 in the milk of transgenic animals, and also provides a DNA vaccine comprising a vector containing the altered MSP-1-42 nucleic
                                                                     GYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLFVIHLEAKV
                                                                                                                                                                                              VFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEG
                                                                                                                                                                                                                                                                   DKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCS 1618
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                                                                                                                                                                                                                                                                                      protein for use in anti-malarial vaccines
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protein engineering; protein expression; codon usage;
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Pred. No. 4.5e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Merozoite surface protein MSP-1-42.
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100.0%;
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Query Match

98WO-US22226

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20-OCT-1998;
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                                                                                                                                                                                                                                                                                            GYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLFVIHLEAKV 1443
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                                                                                                                                                                                                                                                                                                                                                                                                241 VFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQNSGCFRLDEREECKCLLNYKQEG 300
                                                                                                                                                                                                            Gaps
          to express in cell culture systems, especially mammalian cell culture systems or in transgenic animals. The preferred difficult protein candidates for expression are those derived from lower corganisms such as parasites, bacteria and viruses that have DNA coding sequences of high AT content or which have mRNA instability motifs or rare codons relative to the recombinant expression system to be used. The invention allows expression of MSP-1 in the milk of transgenic animals, and also provides a DNA vaccine comprising a vector containing the altered MSP-1-42 nucleic acid.
'mRNA levels and protein expression of proteins that are difficult
                                                                                                                                                                                                                                                                                                                                                                                                                                DKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCS 1618
                                                                                                                                                                                                                                                                                                                                                                                                                                             278
/note= "Asn in native MSP-1-42 (N262Q mutation)"
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                                                                                                                                                      Length 361;
                                                                                                                                                                             Indels
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100.0%; Pred. No. 4.5e-75;
ive 0; Mismatches 0;
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1264 AVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRE 1323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEG 1563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LQYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLSTDYNHNNLLTKFLSTGM 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 AVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRE 75
                                                                                                                                                                                                                                                                                                                    The present sequence represents a 42 kDa C-terminal portion of manalaria merozoite surface protein MSP-1 (i.e. MSP-1-42), an important target for the development of a vaccine against plasmodium falciparum. The sequence has been modified to include an N-terminal beta-casein signal peptide and an N-terminal office and an N-terminal office and introduced eliminate 2 N-glycosylation sites. These modifications allow the MSP-1-42 protein to be expressed in the milk of transgenic mice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 VFENLAKTVLSNLLDGNLQGMLQISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 376;
                                                                                                                                                                                                                                   Modified malarial protein for use in anti-malarial vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSP-1; merozoite surface protein; malaria; vaccine;
protein engineering; protein expression; codon usage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   malaria; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1869; DB 20;
Pred. No. 1.6e-74;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified merozoite surface protein MSP-1-42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Æ
                                                                     (GENZ ) GENZYME TRANSGENICS CORP.
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                                                                                                                                                                                                                                                                              Example; Fig 11; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.28;
98US-0085649.
97US-0062592.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-AUG-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transgenic animal; mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 99.4
Matches 353; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum
                                                                                                                                                              WPI; 1999-288313/24.
P-PSDB; AAX56008.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376 AA;
                                                                                                                  Chen LH, Meade H;
15-MAY-1998;
                       20-OCT-1997;
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256 VFENLAKTVLSNLLDGNLQGMLQISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEG 315
                                                                                                                                                                                                                                                 Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-015762/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAC68978
                                                                                                                                                                                                                                                                        WO200063245-A2
                                                                                                                                                                                                                                                                                                                           20-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                               25-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                      20-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                   13-MAY-1999;
                                                                                                                                                                    27-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                   Holder A,
                                                                                                                                           AAB37610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                  316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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                                                                                        RESULT 9
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0
                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a 42 kDa C-terminal portion of malaria merozoite surface protein MSP-1 (i.e. MSP-1-42), an important target for the development of a vaccine against plasmodium falciparum. The sequence has been modified to include plasmodium falciparum. The sequence has been modified to include on N-terminal beta-casein signal peptide and an N-terminal 6xHis tag. In addition, N1810 and N2620 mutations have been introduced to eliminate 2 N-glycosylation sites. These modifications allow the MSP-1-42 protein to be expressed in the milk of transgenic mice. The invention generally relates to modified recombinant nucleic acid sequences and methods for increasing the mRNA levels and cell culture systems, mammalian cell culture systems or in transgenic animals. The preferred difficult protein candidates for transgenic animals. The preferred difficult protein candidates for transgenic animals. The preferred difficult systems such as parasites, bacteria and viruses that have DNA coding sequences of high AT content or which have mRNA instability motifs or rare codons relative to the recombinant expression system to be used.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEG 1563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1264 AVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKOLENNVMTFNVNVKDILNSRFNKRE 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVL 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLFVIHLEAKV 1443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 NFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVL 135
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                                                                                                                                                                                                                                                                                                                                        New modified recombinant nucleic acid sequences useful for producing malarial DNA vaccine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (N1810 mutation)"
                                                                                                    (N262Q mutation)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                         signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1869; DB 20;
Pred. No. 1.6e-74;
                                                                          'note= "Asn in native MSP-1-42
                                                                                                    /note= "Asn in native MSP-1-42
                       note= "beta-casein
Location/Qualifiers
                                    371..376
/note= "6xHis tag"
                                                                                                                                                                                                                                              (GENZ ) GENZYME TRANSGENICS CORP.
                                                                                                                                                                                                                                                                                                                                                                              Example; Fig 11; 43pp; English.
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99.4%;
                                                                                                                                                                                                        98US-0085649
97US-0062592
                                                                                                                                                                                 98WO-US22225
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                                                                                                                                                                                                                                                                                               WPI; 1999-302742/25.
                                                                                                                                                                                                                                                                        Chen LH, Meade H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                      Misc-difference 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           376 AA;
                                                                                                                                                                                                                                                                                                              N-PSDB; AAX25593
                                                              Misc-difference
                                                                                                                              WO9920766-A2
                                                                                                                                                                                20-OCT-1998;
                                                                                                                                                                                                        15-MAY-1998;
                                                                                                                                                                                                                       20-OCT-1997;
                                                                                                                                                      29-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
 Key
Peptide
                                      Peptide
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The present invention relates to non-natural variants of a C-terminal fragment of a Plasmodium merozoite surface protein-1 (MSP-1). The mon-natural variants have reduced affinity for at least 1 antibody capable of blocking a second antibody that inhibits the proteolytic cleavage of Plasmodium MSP-1_4_2, and has the same affinity for at least one third antibody that inhibits the proteolytic cleavage of plasmodium MSP-1_4_2, and has the same affinity for at least MSP-1_2, compared to natural MSP-1_1_9. The non-natural variants of the present invention are useful for immunising a mammal against malaria, and can be used to treat malaria. The present sequence is MSP-133 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Uthaipibull C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel variants of the C-terminal fragment of Plasmodium merozoite surface protein-1, useful as vaccines for treating or preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRE
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surface protein; protazoacide; vaccine; malaria
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                                                                                                                                                                                                                                            Ä.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 5; Fig 15; 126pp; English.
                                                                                                                                                                                                                                         AAB37610 standard; Protein; 262
                                                                                                                                                                                                                                                                                                                                                                                                                                              Merozoite surface protein-133
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99US-0311817.
99CA-2271451.
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                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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DKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLSTDY 1489
           chromatography.
                                                                                                                                                                                                                                                                                                                                                                08-MAR-1988;
                                                                                                                                                                                                                                                                                                                                                                                  19-MAR-1987;
                                                                                                                                                                                                           11-NOV-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                     Ulrich C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                         AAP80547;
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                                                                                                                                                                                                                                                                                          Region
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                                                                                                                                                                                                                                                                                                                                                                                 Producing malaria vaccine, useful for treatment or prevention of all forms of malaria in humans, by expressing immunogenic merozoite protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1270 IDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFKNVL 1329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYYKIL 1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                β
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                             Major merozoite surface protein-1; MSP1-42; melittin signal peptide; malaria vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a major merozoite surface protein-1 C-terminal fragment of 42kDa (MSP1-42). This fragment is linked to amelittin signal peptide, and then expressed in a in a silkworm/baculovirus system. The protein is used to prepare a malaria vaccine, which is used to treat or prevent malaria, caused hany of the four species of Plasmodium that infect humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.8%; Score 1165.5; DB 22; Length 375; 59.2%; Pred. No. 1.1e-43; ive 54; Mismatches 76; Indels 21;
                                                                                                                                             A major merozoite surface protein-1 fragment of 42kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Page 87-88; 95pp; English.
                                                                                        AAB83926 standard; Protein; 375 AA
                                                                                                                                                                                                                                                                                                                                                                                                  fragment in a baculovirus system
                            VFENLAKTVLSNLLDGNLQGML 1525
                                   VFENLAKTVLSNLLDGNLQGML 262
                                                                                                                                                                                                                                                                                                 (UYHA-) UNIV HAWAII.
(UYCH-) UNIV CHINESE HONG KONG
(QUEE-) QUEEN EMMA FOUND.
                                                                                                                                                                                                                                                                                                                                      HO WKK;
                                                                                                                                                                                                                                                             12-NOV-1999; 99US-0165178.
01-DEC-1999; 99US-0168327.
22-AUG-2000; 2000US-0226861.
                                                                                                                                                                                                                                             2000WO-US31064
                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                         Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                      Lap-Yin P,
                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-335879/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  375 AA;
                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAF89840.
                                                                                                                                                                                                         WO200134188-A1
                                                                                                                                                                                                                                            09-NOV-2000;
                                                                                                                           23-JUL-2001
                                                                                                                                                                                                                            17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219;
                                                                                                          AAB83926;
                                                                                                                                                                                                                                                                                                                                      Hui GSN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                            1504
                                            241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                        RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The polypeptide contains at least one epitope of the 190 kD precursor of the major merozoite surface antigen of P.falciparum. The polypeptide is immunogenic and can be used in vaccines to protect against malaria. Presence of the affinity peptide allows the polypeptide to be purified by affinity chromatography resins. Antibodies raised against the polypeptide are useful for diagnosis and for purificn. by affinity
                                                                                      REECKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSY 1609
                                                                                                                                    365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGNSRRTNPSDNSSDSAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHML----TLCD 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                   247 TKKDMLGKLLSTGLV-QNFPNTIISKLIEGKFQDMLNISQHQCVKKQCPENSGCFRHLDE
                                                                                                                 NHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQNSGCFRHLDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptide p190-3; P.falciparum; merozoite; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 913; DB 9;
Pred. No. 1.2e-32;
); Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1..7
/label=affinity peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          AAP80547 standard; protein; 355 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HOFF ) F. HOFFMANN-LA ROCHE &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.8%;
80.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87GB-0006599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takacs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88EP-0103564
                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144..355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum
                                                                                                                                                                                PLFDGIFCSS 1619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gentz H,
                                                                                                                                                                                                            PLFDGIFCSS 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1988-272339/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptide p190-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAN81151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106
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New immunogenic polypeptides - derived from Plasmodium falciparum 190 kD surface antigen precursor useful in vaccines, and encoding DNA sequences
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                                         81 ELFDLTHHHHHLTLCDNIHGFKYLIDGYEEINELLYKLNFYYDLLRAKLNDRCANSYCQIPF 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 VLKKLVFGYRRPLDNIKDNVGKMEDYIKKNKTIENINELIEESKRTIDKNKNATKEEEK 128
                                                                                                  NLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMEDYIKKNKKTIENINELIEESKKTID 264
--- TNPSDNSSDSDAKSYADLKHRVQNYLFTIKELKYP
                            146 QLFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQIPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 TLCDNIHGFKYLIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 TLCDNIHGFKYLIDGYEEINELLYKLNFYFDLLRAKLNNVCANDYCQIPFNLKIRANELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 VLKKLVFGYRKPLDNIKDNVGKMEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          276 KKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLDKINEIKNPPPA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 905; DB 9; Lengtn Lengtn Lengtn Lengtn No. 1.5e-32;
                                                                                                                                                                                                                                                                                                        Polypeptide p190-1; P.falciparum; merozoite; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  1..8
/label=affinity peptide
184..219
                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                           A
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                                                                                                                                                                                         AAP80544 standard; protein; 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HOFF ) F. HOFFMANN-LA ROCHE &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 26; 45pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88EP-0103564
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                                                                                                                                                                                                                                                   entry)
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Matches 174; Conservative
                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum.
                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gentz H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1988-272339/39.
                                                                                                                                                                                                                                                                              Polypeptide p190-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-MAR-1987;
                                                                                                                                                                                                                                                 11-NOV-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                           EP283829-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ulrich C,
                                                                                                                                                                                                                      AAP80544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                               Region
46
                                                                                     902
                                                                                                                                                              RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 GSVASGGSVASGGSGNSRRTNPSDNSSDSDAKSYADLKHRVRNYLLTIKELKYP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 QELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGTAVTTSTPGSKGSVASGGSGGSVASG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----- 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence encodes a polypeptide which contains the unique sequence of the surface antigen of P. falciparum, but lacks the immunodominant repeat sequences which may allow the parasite to evade and decoy the immune system. The DNA for the stage-specific late schizoint-merozoite antigen 31-1 in p31-1 (W08503725) was modified to delete the entire sequence coding for the repitope. The expression plasmid, 31-1 Repeated Delete, was introduced into E.coli K12 to produce the modified peptide. The transformant has been deposited in the Deutsche Sammlung von Microorganismen as B.coli K12 (956936cl) (p31-1 Repeat Delete). The peptide was used in compsns. to treat and prevent protozoan parasitic infections.
                            LVFGYRKPLDNIKDNVGKMEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLY
                                                                                      109 LVFGYRKPLDNIKDNVGKMEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLY
               NIHGFKYLIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigen 31-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprising
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 910.5; DB 9;
Pred. No. 8.6e-33;
1; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                      schizont-merozoite repitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide(s) for prodn. of antiprotozoal vaccines surface antigen sequence with deleted repitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 QELWKKLEALEDAVLTGYSLFQKEKMVLNEGTSGTAVTTS-
                                                                                                                                                                                                                                    AAP82523 standard; protein; 219 AA.
                                                                                                                                                                                                                                                                                                                                                      stage-specific late
protozoan parasite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.8%;
76.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87EP-0108867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86US-0879076
                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BEHW ) BEHRINGWERKE AG.
                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                      31-1 Repeated Delete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1988-030152/05.
N-PSDB; AAN82176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Humbert Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219 AA;
                                                                                                                                                                                                                                                                                             12-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUN-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-FEB-1988.
                                                                                                                                                                                                                                                                                                                                                                                                                          EP254862-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3est Local Sir
Matches 182;
                                                                                                                                                                                                                                                               AAP82523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                      Malaria;
                                                                                                                                                                                                                                                                                                                                                                   vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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             160
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                                                                                                                                                                                                       RESULT 12
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Gaps

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chromatography
                                                                                         08-MAR-1988;
                                                                                                       19-MAR-1987;
                                                                          28-SEP-1988
                                                                                                                                                                                                                                                                                                   Matches 136;
                                                           EP283829-A.
                                                                                                                                   Ulrich C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW36103;
                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Region
                        Key
Region
                                             Region
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                                                                                                                                                                                                                                                                                                                                                                                                          61 AVTTSTPGSKGSVASGGSGGSVASGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDS 120
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                    1 MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFOKEKMVLNEGTSGT 60
                                                                                                                                                                                                                                                                                          The sequence encodes a Plasmodium falciparum, Plasmodium vivax, Plasmodium malariae and Plasmodium ovale antigen which may be used in the diagnosis of malaria and as a vaccine against malaria.
                                                                                                                                                                                                                                                 - by
DAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEI 174
                                                                                                                                                                                                                                                                                                                                                       ;
9
                                                                                                                                                                                                                                                falciparum
protecting
                                                                                                                                                                                                                                                                                                                                      Length 244;
                                                                                       Storage-specific, late schizont merozoite malaria antigen.
                                                                                                                                                                                                                                                                                                                              Score 794; DB 6; Length 27.
Pred. No. 1.2e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptide p190-2b; P.falciparum; merozoite; vaccine.
                                                                                                                                                                                                            Shaw A;
                                                                                                                                                                                                                                              Prodn. of antigens of Plasmodium species, esp. of recombinant DNA methods giving polypeptide(s) for against malaria or for diagnosis.
                                                                                                                                                                                                           Cheung A,
                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                           AAP50304 standard; Protein; 244 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP80546 standard; protein; 151 AA
                                                                                                                                                                                                                                                                             Disclosure; Fig 6; 49pp; English.
                                                                                                                                                                                                            McGarvey M,
                                                                                                                                                                                                                                                                                                                                      9.4%;
                                                                                                                                                                85WO-GB00072.
                                                                                                                                                                               84GB-0004378
                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                      160; Conservative
                                                                                                                                                                                                                         WPI; 1985-223371/36.
N-PSDB; AAN50355.
                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity
Matches 160; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polypeptide p190-2b
                                                                                                                                                                                                           Perrin L,
                                                                                                                                                                                                                                                                                                                        244 AA;
                                                                                                                                                                                             (BIOJ ) BIOGEN NV
                                                                                                     Malaria; vaccine.
                                                                                                                   Plasmodium spp
                                                                                                                                                                20-FEB-1985;
                                                                                                                                                                              20-FEB-1984;
                                                                         22-OCT-1991
                                                                                                                                 WO8503725-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-NOV-1990
                                                                                                                                                 29-AUG-1985
                                                           AAP50304;
                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                           Mach B,
                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                            189
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                              RESULT 14
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                                     AAP50304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptides - derived from Plasmodium falciparum 190 kD precursor, useful in vaccines, and encoding DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The polypeptide contains at least one epitope of the 190 kD precursor of the major merozoite surface antigen of P.falciparum. The polypeptide is immunogenic and can be used in vaccines to protect against malaria. Presence of the affinity peptide allows the polypeptide to be purified by affinity chromatography reasins. Antibodies raised against the polypeptide are useful for diagnosis and for purificn. by affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1069 AEIAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKL 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1129 EGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKF 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 AEIAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium vivax; merozoite surface protein; MSP1; p19;
Plasmodium falciparum; malaria; vaccine; immunity; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 677; DB 9; Le
Pred. No. 9.5e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                             /label=affinity peptide
                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1..95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 27; 45pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                 'n
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                                                                                                                                                                                                                                                                                                                                                                            (HOFF ) F. HOFFMANN-LA ROCHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New immunogenic polypeptides
surface antigen precursor, us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.0%;
95.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88EP-0103564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 95.8
nes 136; Conservative
Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gentz H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1988-272339/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 AA;
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/note= "glycosylphosphatidylinositol anchoring sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                      This is the amino acid sequence of a recombinant protein comprising amino acids 1613-1705 of the Plasmodium falciparum merozoite surface protein 1 (MSP1) 19 kD C-terminal fragment (p19), linked to a glycosylphosphatidylinositol membrane anchoring sequence. p19 is the C-terminal fragment of the 42 kD MSP1 from Plasmodium species. The recombinant protein can be used for the production of anti-malarial vaccines, where the p19 fragment provides a high level of protective immunity since it includes epitopes not presented in the p42 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1526 NISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADA 1585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
                                                                                                                                                                                                                                                                                                                         Recombinant protein containing Plasmodium merozoite surface protein-1 p42 fragment - useful in antimalarial vaccines, also new antibodies for diagnosis and protein purification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Merozoite surface antigen 1; MSP-1; pl15MSP-1; antigen; immunogen; malaria; vaccine; Venezuela equine encephalitis virus; DVEE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 NISQHQCVKKQCPENSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1586 KCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSSNFLGISFLLILMLILYSFI 1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 116;
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                                                                                                                                                                                                                        <u>г</u>,
                                                                                                                                                                                                                        Nato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 637; DB 18;
Pred. No. 3.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum MSP-1 peptide p115MSP-1.
                                                                                                                                                                                                                        Mendis K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.
                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 1B; 85pp; French.
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                                                                                                                                                                                                                        Longacre-Andre S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.6%;
ilarity 99.1%;
Conservative
                                                                                                      97WO-FR00291
                                                                                                                                     96FR-0001821
                                                                                                                                                                       PASTEUR.
NEW YORK STATE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vector; immunisation.
                                                                                                                                                                                                                                                                        WPI; 1997-425034/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 113; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 AA;
                                                                                                                                                                                                                                                                                           P-PSDB; AAW22592
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                                                                                                                                                                     (INSP ) INST
(UYNY ) UNIV
                                                                                                                                                                                                                        Barnwell JW,
                                    WO9730159-A2
                                                                                                    14-FEB-1997;
                                                                                                                                     14-FEB-1996;
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                                                                    21-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                          Roth C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
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0
                                                   /note= "glycosylphosphatidylinositol anchoring sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the amino acid sequence of a recombinant protein comprising amino acids 1613-1705 of the Plasmodium falciparum merozoite surface protein 1 (MSP1) 19 KD C-terminal fragment (p19), linked to a glycosylphosphatidylinositol membrane anchoring sequence. p19 is the C-terminal fragment of the 42 kD MSP1 from Plasmodium species. The recombinant protein can be used for the production of anti-malarial vaccines, where the p19 fragment provides a high level of protective immunity since it includes epitopes not presented in the p42 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..95
/note= "amino acids derived from P. falciparum MSP1 p19
fragment"
   p_{19}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDK¢VENPNPTCNENNGGCDADA 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 NISQHQCVKKQCPENSGCFRHLDEREECKCLLNYKQEGDKCVENPNTCNENNGGCDADA 62
   P. falciparum MSP1
                                                                                                                                                                                                                                                                                                                                                                        Recombinant protein containing the merozoite surface protein-1 p19 fragment - useful in anti-malarial vaccines, diagnosis and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium vivax; merozoite surface protein; MSP1; p19;
Plasmodium falciparum; malaria; vaccine; immuņity; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                         Nato F;
   /note= "amino acids derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 637; DB 18;
Pred. No. 3.9e-21;
1; Mismatches 0;
                                                                                                                                                                                                                                                                         Mendis K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA.
                 fragment"
                                                                                                                                                                                                                                                                         Longacre-Andre S,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1B; 85pp; French
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.68;
                                                                                                                                                                                     96FR-0001822
                                                                                                                                                                                                                      PASTEUR.
NEW YORK STATE
                                                                                                                                                     97WO-FR00290
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                                   96..116
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                                                                                                                                                                                                                                                                                                                         WPI; 1997-425033/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 AA;
                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT94550
                                                                                                                                                                                                                                                                        Barnwell JW,
                                                                                                                                                                                                                      (INSP ) INST
(UYNY ) UNIV
                                                                                    WO9730158-A2
                                                                                                                                                                                                                                                                                                                                                                                                        purification
                                                                                                                                                     14-FEB-1997;
                                                                                                                                                                                       14-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-1998
                                                                                                                    21-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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Region
                                                                                                                                                                                                                                                                                           Roth C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1526
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us-09-269-874a-3.rag

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Plasmodium falciparum
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                                                                                                                                                                                                                                  Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HOFF/) HOFFMAN S.
(CARU/) CARUCCI D.
(GARD/) GARDNER M.
                                                                                                                                                                                                  108 AA;
   N-PSDB; AAC68977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200025728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                               AAB18171;
                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                    67
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                                                                                                                                                                                                                                                                                                                                                                              AAB1817.
   δλ
                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                              δλ
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                                                                                                                                                                                                                                                                                                                                                                                         1002 QLSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVLQNFSV 1061
                                                                Novel vaccine for immunizing mammals against Plasmodium falciparum infection, comprises a viral vector system expressing protein corresponding to specific domain of major merozoite surface protein 1 of Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Uthaipibull C;
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    1 QLSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVLQNFSV 60
                                                                                                                                                                                  invention relates to a malaria vaccine comprising an expression vector, preferably a defective Venezuela equine encephalitis (DVEE) fragment after administration to a patient. The pli5MSP-1 protein or fragment raises a humoral and/or cell-mediated response to the erythrocytic merozoite malaria antigen, protecting the patient from continues to express antigen in the patient for a subsequent malaria infection. The DVEE viral vector system continues to express antigen in the patient for a period of days, months or even years. The pl15MSP-1 antigen may also include and/or an anchor peptide sequence, which enhances the immunogenic response of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                   1062 FFNKKKEAEIAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNY 1116
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0
                                                                                                                                           The present sequence is that of immunogenic protein p115MSP-1,
                                                                                                                                                   specific domain (amino acids 1002-1116) of the major merozoite surface protein 1 (MSP-1) of the erythrocyte stage of the West African Wellcome strain of Plasmodium falciparum. The
                                                                                                                                                                                                                                                                                                                                            DB 23; Length 115;
8.1e-19;
hes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Merozoite surface protein; protazoacide; vaccine; malaria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Morgan W,
                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                             6.9%; Score 584;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB37609 standard; Protein; 108 AA
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                                                                                                                       Disclosure; Page 4; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Merozoite surface protein-119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                  Matches 115; Conservative
(GEOU ) UNIV GEORGETOWN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum
                        Nikodem
                                            WPI; 2002-049444/06
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                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                       115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200063245-A2
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                                                                                                                                                                                                                                                                                                                         Sequence
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                      Davidson
                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB37609
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                                                                                                                                                                                                                                 The present invention relates to non-natural variants of a C-terminal fragment of a Plasmodium merozoite surface protein-1 (MSP-1). The non-natural variants have reduced affinity for at least 1 antibody capable of blocking a second antibody that inhibits the proteolytic cleavage of Plasmodium MSP-1_4_2, and has the same affinity for at least one third antibody that inhibits the proteolytic cleavage of Plasmodium MSP-1_4_2. The non-natural variants of the present invention are useful for immunising a mammal against malaria, and can be used to treat malaria. The present sequence is MSP-119 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1520 NLQGMLNISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNG 1579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel variants of the C-terminal fragment of Plasmodium merozoite surface protein-1, useful as vaccines for treating or preventing malaria -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum chromosome 2 related protein SEQ ID NO:28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1580 GCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSSN 1621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSSN 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.6%; Score 560; DB 22; 94.1%; Pred. No. 8.5e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gardner M, Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 70-75; 577pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB18171 standard; Protein; 1979 AA
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                                                                                                                                                              Example 5; Fig 15; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US26796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis of P.falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96; Conservative
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vaccines against P. falciparum infection compitising (I) or (II).

(I) and (II) are useful for the development of vaccines against

P. falciparum infection. (I) and polyclonal antitisera or a monoclonal

antibody raised to immunogens comprising the sequences of (I), are

useful in the detection of infection with P. falciparum. Furthermore,

(I) (especially when they are rifins or secreted or membrane proteins)

can aid the identification of farugs to treat or prevent P. falciparum.

CC an idection, or they can be used to identify drug resistance in

infection, or they can be used to identify drug resistance in

CC P. falciparum. Sequencing of the Plasmodium chromosome 2 and the

c subsequent identification of proteins encoded by it will help to expand

cour understanding of parasite biology, a process hampered by the

couplexity of the parasite infectode, and provide new targets for

vaccine and drug development. Parasite resistance to drugs and mosquito

resistance to insecticides have led to a resurgence of malaria in many

cracine and drug development and there is a pressing need for vaccines and new

cracines. AAA70078 to AAA70287 and AAB18135 represent nucleotide

and protein sequences given in the present inventon, but which are not

conspecticially mentioned within the specification. Also described are: (1) nucleotide sequences (II) encoding (I); and (2)

1979 AA; Sequence

82; 333 321 427 492 551 535 595 595 648 702 759 751 RTNPSDNSSDSDAKSYADLKHRVRNYLLTIKELKYPQLFDL'TNHMLTLCDNIHGFKYLID 169 322 KNKOIDLLNKOEKEKEKEKEKEKEKEKEKEKEKEKEYEYTLIKELKDEKISILEKVHSIKVRE 381 Gaps GYEEINELLYKLNFY---FDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRK 213 KINEKEKNIIKKEETFHNIEKEYLEKNKER-ETISIEIIDIKKHLEKLKIEIKEKKE---382 MDIEKREH------NFLHMEDQLKDLKNSFVKNNNQLKVYKCEIKNLKTELE KITKDENKP---DEKILEVS-DIVKVQVQKVLLMNKIDEL-KKTQLILKNVELKHN--IH PLDNIKDNVGKME-----DYIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKL 279 YQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLDKINEIKN-----PPPANS GNTPNTLLDKNKKIEEHEKE - - - IKEIAKTIKFNIDSLFTDPLELEYYLREKNKNIDI - S AKVETKESTEPNEY PNGVTY PLSYNDINNALNEL - NSFGDLINPFDYTKEPSKNIYTDNE -----KFINEIKEKIKIEKKKIESDKKSYEDRSKSLNDITKEYEKLL NEIYDSKFNNNIDLINFE-KMMGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYME 483 TKIETQELQEMVDIKQKELDQLQEKYNAQIESI-----SIELSKKEKEYNQYKNTYIE DYSLRNIVVEKELKYYKNL-----ISKIENEIETLVENIK------KDEEQLFEK 649 VPNSYKQE-----NKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSE PSTEGEITGQATTKPGQQAGSALE - - - GDSVQAQAQEQKQAQPPVPVPVPEAKAQVPTPP 174 DYE--NKLKEKEDFVKQKIDMLNEKEN-----EK QIDKLINNEKGTLINSKISELNVQIMDLKEEKDFLINQIVDLSNQIDLLTRKMEEKENKMLE QENKYKQEMELLRGNIKSSENILNNDEEVCDLK----RKLSLKESEMKMMKEEHDKKLAE Indels 373; Length 1979; DB '21; 6.6%; Score 559.5; DB 21; llarity 22.2%; Pred. No. 2.9e-16; Conservative 314; Mismatches 609; 712 LKDDCDVRIREMNEKNEDKINMLKEEYEDKINTLKEONED Similarity RK----Matches 370; Query Match 969 703 110 126 227 334 536 596 170 269 390 449 493 552 g g õ g ŝ 엄 ò g ò a δ 셤 ò g ö g ò g ò g ô à ò

(first entry)

27-FEB-2001 AAB37608;

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1287 INNLKKKNEDMCIKYNEMNIKYGDICVKYEEMSLTYKETSLKYEQIKVKYDEKCSOY--- 1343 1019 FDKKKTVGKYKMQIKKLTLL----KEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAE 1073 VEVKIKELNYLKTIQDKLADFKKNNN-----FVGIADLSTDYNHNNLLTKFLSTGMV 1504 998 961 811 MKEEYEDKMNTLN------EQNEDKMNSLKEEYENKINQINSNNEIKIKDVV-NEY-I EEVDKLKVTLDEKKKQFDKEINYAHIKAHEKEQILLITEME--ELKCQRDNKYSDLYEKYI 962 FYNESFTNFVKSKADDINSLNDE---SKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERL 1074 TENTLENTKILLKHYKGLVKY----YNGESSPLKTLSEESIQTEDNYASLENFKVLSKLE VNNALESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEV DDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIEN-EYEVLY----LKPLAGV DEIRFOYDEKCFOYDEINKKYGALLNINITNKMVDSKVDRNNN----EIISVDNK--VE SIKKYINDKQGENEKYLPF - - - LNNIETLYKT - VNDK - - IDLFVIHLEAKVLNYTYEKSN FENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQNSGCFRHLDEREECKC-----LLN -----LGKNKNIYQELIGQKSSENFYEKILKDSDT LKKDVEKQKKEIEKLNKQLTKCNKQIDELNEEVEKLNNENIELITYSNDL----NNKFDMK 1293 YRSLKKQLENNVMTFN-VNVK--DILNSRFNKRENFKNV-LESDLIPYK-DLTSSNYVVK DPYKFLNKEKRDKF------LSSYNYIKDSIDTDINFANDVLGYYKILSEKYKSDLD TKEE-ESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFM--EIYEKEMVCNLYKL KDNDKIKNLLEEAKK - - - VSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSL YKQ----EGDKC-----VENPNPTCNENNGGCDA-DAKCT 1588 1130 GKLKD---NLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENN-760 APVNN-KTENVSKLDYLEKLYEF-LNT--SYICHKYILVSH-Ä AAB37608 standard; protein; 96 KLFENILS----1082 1188 1348 1344 1399 1505 1178 1238 1559 RESULT 21 AAB37608 1245 861 752 310 867 924 В 원 QΥ qq δy qq δλ g δ g δ q δ qq δ qq δ g ŏ g ò g ŏ g pp δλ g Q ŏ g QY

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sedneuce nsed

p19

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This is the amino acid sequence of a chimeric protein comprising amino acids 1-32 of the plasmodium vivax merozoite surface protein 1 (MSP1) linked to amino acids Asn1613-Ser1705 which correspond to the 19 KD C-terminal fragment (pl9) of MSP-1 from Plasmodium falciparum. ppl is the C-terminal fragment of the 42 kD MSP1 from Plasmodium species. The recombinant protein can be used for the production of anti-malarial vaccines, where the p19 fragment provides a high level of protective immunity since it includes epitopes not presented in the p42 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1526 NISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADA 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant protein containing Plasmodium merozoite surface protein-1 p42 fragment - useful in antimalarial vaccines, also new antibodies for diagnosis and protein purification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric; Plasmodium vivax; merozoite surface protein; MSP1; p19; Plasmodium falciparum; malaria; vaccine; immunity; epitope.
                                                                                                                                            /note= "derived from P. falciparum C-terminal fragment of MSP1"
                                                                                                   'encoded by restriction enzyme create the chimeric sequence"
                                                                        "derived from P. vivax MSP1"
                                                                                                                                                                                                                                                                                                                                               Nato F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.4%; Score 539; DB 18;
98.9%; Pred. No. 8.6e-17;
tive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mendis K,
                 'note= "signal peptide"
                                            /note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW36102 standard; Protein; 127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 1C; 85pp; French.
                                                                                                                                                                                                                                                                                                                                               Barnwell JW, Longacre-Andre S,
                                                                                                 /note= "encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PfMSP1(p19)S protein sequence.
                                                                                                                                                                                                                                                                          96FR-0001821.
                                                                                                                                                                                                                                              97WO-FR00291
                                                                                                                                                                                                                                                                                                    PASTEUR.
NEW YORK STATE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 98.9
Matches 92; Conservative
                                                                                                                             35..127
                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-425034/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 AA;
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                                                                                                                                                                                                                                                                                                   (INSP ) INST
(UYNY ) UNIV
                                                                                                                                                                                     W09730159-A2
                                                                                                                                                                                                                                                                        14-FEB-1996;
                                                                                                                                                                                                                 21-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Peptide
                               Protein
                                                                                                                                                                                                                                                                                                                                                              Roth C;
                                                           Region
                                                                                       Region
                                                                                                                                Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to non-natural variants of a C-terminal fragment of a plasmodium merczoite surface protein-1 (MSP-1). The non-natural variants have reduced affinity for at least 1 antibody capable of blocking a second antibody that inhibits the proteolytic cleavage of Plasmodium MSP-1.4.2, and has the same affinity for at least one third antibody that inhibits the proteolytic cleavage of plasmodium MSP-1.4.2, compared to natural MSP-1.1.9. The present sequence is the wild-type MSP-1 protein. This sequence was used to generate the variants of the present thuvention. The non-natural variants of the present unvention are useful for immunising a mammal against malaria, and can be used to treat malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADA 1585
                                                                                                                                                                                                                                                                        Syed S, Uthaipibull C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NISOHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENPNFTCNENNGGCDADA 60
                                                                                                                                                                                                                                                                                                                            Novel variants of the C-terminal fragment of Plasmodium merozoite surface protein-1, useful as vaccines for treating or preventing malaria -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric; Plasmodium vivax; merozoite surface protein; MSP1; p19; Plasmodium falciparum; malaria; vaccine; immunity; epitope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 96;
                                         Merozoite surface protein; protazoacide; vaccine; malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 556; DB 22;
Pred. No. 1.1e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1586 KCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSSN 1621
                                                                                                                                                                                                                                                                     Holder A, Birdsall B, Feeney J, Morgan W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 48; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW22593 standard; Protein; 127 AA.
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Chimeric - Plasmodium falciparum.
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              Merozoite surface protein-1.
                                                                                                                                                                                                99US-0311817.
99CA-2271451.
                                                                                                                                                      20-APR-2000; 2000WO-GB01558
                                                                                                                                                                                  99GB-0009072
                                                                                                                                                                                                                                           (MEDI-) MEDICAL RES COUNCIL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                     Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
es 96; Conservat
                                                                                                                                                                                                                                                                                                 WPI; 2001-015762/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 AA;
                                                                                                WO200063245-A2.
                                                                                                                                                                                                 13-MAY-1999;
25-MAY-1999;
                                                                                                                                                                                  20-APR-1999;
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                                                                                                                            26-OCT-2000
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Gaps

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Length 127; Indels

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157 LC-DNIHGFKYLIDGYE----EINELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRA 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266 NKNATKE-----EEKKKLYQAQYDLSIYNKQ----LEEAHNLISVLEKRIDTLKKNENIK 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
                                                                                                                                                                                                                                                                                                                                                                                                                                        A MAEP compound having a binding affinity for a Duffy blood group antigen of primate red blood cells, is antigenic for the complete protein, and may be used in diagnosis, treatment and vaccination against invasion by P. vivax and P. knowlesi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 DISFDEKKKSIEKAYEKMGN---TLKELEKMDDEKNIEKEVEEAQIQYKRIF--IDHDVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 NELDVLKKLVFGYRKPLDNIKDNVGKMEDYI-----KKNKKTIENINELIEESKKTIDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | : :: : |:|| | |::|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELLDKINEIKNPPPANSGNTPNTLLDKN - - - - KKIEEHEKEIKEIAKTIKFNIDSL - - F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      272 KDKCTTEISNSKRGKD----KIEFLEKFKPNEESNS-----NKVN--INEINE--NI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELLORVAAMIEEAKAHKNNIDIALEDAQIDTEVSKIEQINREIMNKKDEIKSYLSEIKEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     370 TDPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSFGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------EIKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLTNFEKMMGKRYSYKVE----KLTHHNT-------FASYEN-----
                                                                                                                                                                                                                                                                                                                                           Malarial apical end merozoite proteins and peptide(s) - used for developing cpds. for treating, preventing and diagnosing malarial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 1254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 IMNDEVEKSKIVMEKIELYKKEIDEIKQKTNEY-----KQGDT-SNFY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IKIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.4%; Score 455.5; DB 11; Best Local Similarity 20.5%; Pred. No. 6.1e-12; Matches 319; Conservative 221; Mismatches 469;
                                                                                                                                                                                                                                                               Wertheimer SP;
                  Duffy blood group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 DNSSDSDAKSYADLKHRVRNYLLTIKEL-
                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Fig la; 66pp; English.
                                                                                                                                                 90WO-US01849
                                                                                                                                                                               89US-0334270.
89US-0334041.
                                                                                                                                                                                                                                                               MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      430 INPFDYTKE-----
                                                                                                                                                                                                                                                               Galinski
                                                                                                                                                                                                                               (UYNY-) NEW YORK UNIV.
                                                                                                                                                                                                                                                                                             WPI; 1990-334616/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1254 AA;
                    Malaria; vaccine;
                                                  Plasmodium vivax.
                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ06328
                                                                                                                                                 03-APR-1990;
                                                                                                                                                                                                                                                               Barnwell JW,
                                                                                                                                                                                 06-APR-1989;
                                                                                                                                                                                               05-APR-1989;
                                                                                 W09011772-A
                                                                                                                 18-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                             infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105
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     qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is the amino acid sequence of a chimeric protein comprising amino acids 1-32 of the Plasmodium vivax merozoite surface protein 1 (MSP1) linked to amino acids Asn1613-Ser1705 which correspond to the 19 kD c-terminal fragment (P19) of MSP-1 from Plasmodium falciparum. P19 is the C-terminal fragment of the 42 kD MSP1 from Plasmodium species. The recombinant protein can be used for the production of anti-malarial vaccines, where the P19 fragment provides a high level of protective immunity since it includes epitopes not presented in the P42 fragment.
                                                                                                                                                                                 Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1526 NISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENPPTCNENNGGCDADA 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       merozoite surface protein-1 p19 vaccines, diagnosis and protein
                                                                                                                                                                                                                           "derived from P. falciparum C-terminal p19 fragment of MSP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Merozite apical-end-localised protein (MAEP) insert 5.3.
                                                                                                                                               MSP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
щ
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 539; DB 18;
Pred. No. 8.6e-17;
; Mismatches 0;
                                                                                                                                             'note= "derived from P. vivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mendis K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1586 KCTEEDSGSNGKKITCECTKPDSYPLFDGIFCS 1618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "mature protein"
                                                                               'note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; 1254 AA.
                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant protein containing the fragment - useful in anti-malarial

    Plasmodium vivax.
    Plasmodium falciparum.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 1C; 85pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Longacre-Andre S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.4%;
98.9%;
                                                                                                                                                                                                                                                                                                                                                                                                         (INSP ) INST PASTEUR.
(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                             97WO-FR00290
                                                                                                                                                                                                                                                                                                                                                                           96FR-0001822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                            35..127
                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-425033/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR07503 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT94549
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barnwell JW,
                                                                                                                                                                                                                                                                              WO9730158-A2
                                                                                                                                                                                                                                                                                                                                           14-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                           14-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       purification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-FEB-1991
                                                                                                                                                                                                                                                                                                            21-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
Chimeric
               Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR07503
                                                              Peptide
                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roth C;
                                                                                                                              Region
                                                                                                                                                              Region
                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95
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qq οy g

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EXAXXX

71;

(first entry)

10-NOV-1997

AAW24575;

οχ	536	TKALKSKHNDEKLTKALK	548
QQ	495	TEKNRLNGIDSTITNIEGALKESKGNYEIGELEKLEEIGKNRKLKVDITKKSINSTVGNF	554
οy	549	YMEDYSLRNIVVEKELKYYKNLISKIENEIBTLVENIKKDEQLFEKKITKDEN ::	602
QQ	555	SSLFNNFDLNQYDFNKNINDYENKMGE1YNEFEGSLNKISENLRNASENTSDYN	809
ΟY	603	SDIVKVQVQKVLLMNKIDELKKTQLILKNVELKHNIHVPN : : :	662
Q	609	SAKTLRLESFRSFR	645
Qy	663	YLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGGSDNS :: : : : :	701 705
οy	702	EPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQAQPVPV	746
qq	106		758
ΟŊ	747	DYLEKL	803
qq	759	ESKNNVVLETENMSKNTNELDVHKNI	784
ογ	804	SKLSSCDPLDLLFNIQNNIPVM	863
qq	785	HSDE	827
Qy	864	YKLKDNDKIKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSL	923
QQ	828	YKNKISSIKSKEEAVSVKIGNVSKKHSELSKITCSDKS	. 598
ογ	924	KLFENILSLGKNKNIYQELIGQKSSENFYEKILKDSDTFYNESFTNFVKSKADDINS :: ::	086
Ωp	998	YDNIIALEKQTELQNLRNSFTQEKTNTNSDSKLEKIKTDFESLKNALKTLEGEVNA	921
δy	981	LNDESKRKKLEBDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGKYKMQIK	1033
g	922	LKASSDNHEHVOSK-SEPVNPALSEIEKEETDIDSLNTALDELLKKGRTCEVSRYK	926
οy	1034	LTLLKEQLESKLNSLNNPKHVLQNFSVFF : ::::	1092
g	977	LIKDTVTKEISDDTELINTIEKNVKAYLAYIK	1008
δ _λ	1093	IQTEDNYASL	1152
QΩ	1009	KNYEDTVQDVLTLNEHFNTKQVSNHEPTNFDKSNKSSEELTKAVTDSKT	1057
oy.	1153	GNSPSENNTDVNNALESYKKFLPEG	1212
g	1058	IISKLKGVIIEVNENTEM-NTIESSAKEIEALYNELKN	1094
Qy	1213	KKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSV	1269
ag	1095	KKTSLNEIYQTSNEVKLOEMKSNADKYID	1123
Οy	1270	KRE	1329
qq	1124	VSKIFNTVLDTQKSNIVTNQHSIN-NVKDKLKGKLQELI	1161
٥y	1330	KDLTSSNYVVKDPYKFLNK	1389
Dp	1162	SSFTLESIKKFNEIX	1192
Qy Dp	1390	SEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTV-NDKIDLFVIHLEAKVLN 1445 : : : :	20 02
}	1	NEAL VELLIARY ESLINGUVANADDULLANASELAN	7

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AAW24575 and AAW24576 represent the merozoite apical end proteins (MAEP) isolated from two different Plasmodium vivax strains. These proteins are the antigens of the invention, and immunoreact with antibodies against a native MAEP sequence. P. vivax is one of the four malarial species that infects humans, and is difficult to target for a vaccine, as it cannot be cultured in vitro. The preinvasion orientation of malarial merozoites indicates that the apical end plays an important role in the invasion process. The MAEP protein binds to the surface of susceptible crythrocytes from P. vivax susceptible humans and primates, and also binds to rabbit erythrocytes. The antigen can be used for the production of antimalarial vaccines. The antigen can be used for the production of antimalarial oparticularly P. vivax) blood stage parasites. Synthetic apints malaria (particularly P. vivax) blood stage parasites. Synthetic process, and are immunochemically reactive with antibodies raised antigens can be used similarly. As the antigens specifically bind to a configuration of red blood cells), and are necessary in the process of invasion of red blood cells by a malarial organism. The antigens can also be used in a method for inhibiting the propagation of a malarial organism in susceptible red confining the propagation of a malarial organism in susceptible red
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71;
                                                                                                              Merozoite apical-end protein; MAEP; Plasmodium vivax; antigen; malaria; human; erythrocyte; antimalarial vaccine; antibody; blood stage parasite; Duffy blood group antigen; red blood cell; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------KYPQLFDLTNHMLT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LC-DNIHGFKYLIDGYE----EINELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium merozoite apical end protein - useful as antigen for production of anti-malarial vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 18; Length 1254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.4%; Score 455.5; DB ]
20.5%; Pred. No. 6.1e-12;
ive 221; Mismatches 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 DNSSDSDAKSYADLKHRVRNYLLTIKEL------
                                                                                  Merozoite apical-end protein clone 5.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Column 29-38; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative 221;
                                                                                                                                                                                                                                                                                                                       91US-0792865.
89US-0334041.
89US-0334270.
90WO-US01849.
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                                                                                                                                                                                                                                                                                                                                                                                            900S-0608639
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Galinski MR;
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N-PSDB; AAT80072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1254 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                      Plasmodium vivax.
                                                                                                                                                                                                                                                                                                                       04-OCT-1991;
05-APR-1989;
06-APR-1989;
03-APR-1990;
02-NOV-1990;
                                                                                                                                                                                                                                                                                        05-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barnwell JW,
                                                                                                                                                                                                                      US5646247-A.
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Matches 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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AAW24575 standard; Protein; 1254 AA.

RESULT 25 AAW24575 ID AAW2

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DD 63 LMNDEVEKSKIVMEKIELYKKEIDEIKQKĪNEYKQGDŢ-SNFY 104	QY 212 NELDVLKKLVFGYRKPLDNIKDNVGKMEDYIKKNKKTIENINELIEESKKTIDK 265 Db 105YTEQYNSATQSKAKIEQFINIATTKKGTSDTSQDINEL-ESIKEEVHK 151	QY 266 NKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISYLEKRIDTLKKNENIK 316 	QY 317 ELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLF 369 	OY 370 IDPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSFGDL 429 DD 272 KDKCTTEISNSKRGKDKIEFLEKFKPNEESNSNKVNINEINENI 315	OY 430 INPFDYTKE	OY 460 IKIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNI- 504 :	QY 505 DLTNFEKMMGKRYSYKVEKLTHHNT	OY 536	OY 549YMEDYSLRNIVVEKELKYYKNLISKIENBIETLVENIKKDEEQLFEKKITKDEN 602 1:	OY 603 KPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPY 662 	OY 663 YLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGOSDNS 701 :: : ::: ::: ::: ::: ::: ::: ::	OY 702 EPSTEGEITGOATTKPGQQAGSA	OY 747 PVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSXICHKYILVSHSTMNEKI 803	QY 804 LKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNL 863	QY 864 YKLKDNDKIKNLLEEBAKKVSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSL 923	QY 924 KLFENILSLGKNKNIYQELJGQKSSENFYEKILKDSDTFYNESFTNFVKSKADDINS 980 :: :: : : : : : : : : : : :	OY 981 LNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGKYKMOIK 1033	QY 1034 KLTLLKEQLESKLNSLNNPKHVLQNFSVFRNKKEAEIAETENTLE-NTKILLKHYKGLV 1092 Db 977LIKDTVTKEISDDTELINTIEKNVKAYLAYIK 1008
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encoded The present invention describes proteins and their fragments (1) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (1) nucleotide sequences (II) encoding (1); and (2) vaccines against P. falciparum infection comprising (I) or (II). (1) and (II) are useful for the development of vaccines against antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Purthermore, useful in the detection of infection with P. falciparum. Purthermore, (I) (especially when they are rifins or secreted or membrane proteins) 1153 LIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSESGSDTLEQSQP 1212 1213 KKPASTHVGAESNTITTSQ---NVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSV 1269 1270 IDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFKNVL 1329 1124 ----VSKIFNT------VLDTQKSNIVTNQHSIN-NVKDKLKGK-----LQELI 1161 1330 ESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYYKIL 1389 ::| |::| ::| |::| 1162 DAD-------GSFTL------ESIKKFNEIYSHIKTNI------GELEQL 1192 1093 KYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHH 1152 1009 KNYEDTVQDVLTLNEHF-----NTKQVSNHEPTNFDKSNKSSEELTKAVTDSKT 1057 Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide. 1390 SEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTV-NDKIDLFVIHLEAKVLN 1445 Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection Plasmodium falciparum chromosome 2 related protein SEQ ID NO:29 Venter JC; Disclosure; Page 75-82; 577pp; English. AAB18172 standard; Protein; 2485 AA Gardner M, 99WO-US26796 98US-0107131 (first entry) Hoffman S, Carucci D, Plasmodium falciparum. WPI; 2000-365347/31 (VENT/) VENTER J C (HOFF/) HOFFMAN S. (CARU/) CARUCCI D. (GARD/) GARDNER M. WO200025728-A2. 05-NOV-1999; 07-NOV-2000 05-NOV-1998; 11-MAY-2000. AAB18172;

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can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in subsequent identification of the Plasmodium chromsome 2 and the complexity of the parasite biology, a process hampered by the complexity of the parasite lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insectiodes have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70078 and AAB18144 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification.
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iive 257; Mismatches 579
                                                                                                                                                                                                                                                                            SNSNNNNNNNNISSSSSSSKKNHVIINKKISSY-----
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1084 LLKHY-----KGLVKYYNGESSPLKTL----SEESIQTEDNYASLENFKVLSKLEGKL 1132
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(I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the used to produce the used to produce hosts cells which express the polypeptides. (II) (and/or nucleic acids) may then be polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AH55091 to AAH55098 represent oligonucleotide sequences and primers which are used in the present invention of the present present specification, N. B. The present invention specifically claims all the polynucleotide sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4455 to 4472, no sequences are present for SEQ ID NO:4455 to 4472,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
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Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis.
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                                                                                         Staphylococcus epidermidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                         || | : | | | | : | | | : | 309
                                                                                                     NKALKEAKGVLNKNSGTNVN----INDIQHLLTQIDNAKDQLNGERRLKEHQQKSEVFII 4365
                                                                                                                                              ---DVTN-----KVNSANTLTE----L 4264
                          KDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSI---DTDINFANDVLGYYKILSEKY 1393
                                                                            ----KIDLFVI 1437
                                                                                                                                1438 HLEAKVLNYTYE-----KSNVEVKI-----KELN-YLKTIQDKLADF----KKNN 1477
                                                                                                                                                                               1478 NFVGI-ADLSTDYNH----NNLLTKFLSTGMVFENLAKTVLSNLLDGN--LQGMLNISQ 1529
                                                                                                                                                                                                                                   1530 HQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCV-ENPNPTCNENNGGCDADAKCT 1588
                                                                                                                                                                                                                                                          4484 AQ-TKAHNDIKDTLKRQLDEIEHANATSNSKAQAKQMVNEEARKAFSNINHATSNDLVNQ 4542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3159
                                                                           1394 KSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVND--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID 3159; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                              ABP38314 standard; Protein; 10182 AA
LATE-KSKDLKLIKGLKDLNKAQLE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epidermidis;
gene therapy.
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                                                                                    Indels 498;
                                                                                                                                107 NSRRTNPSDNSSDSDAKSYADLKHRVRNYLLTIKELKYPQLF--DLTNHMLTLCDN-
                                         Length 10182;
                                                                                                                                                                                                                                                                8014 TMSHDEIENAINNIKHAINALDGEHKLQQAKENAN----LLINSLND-
                                         5.3%; Score 448; DB 23;
ilarity 20.6%; Pred. No. 1.6e-10;
Conservative 250; Mismatches 651;
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                                                                                                                                                                             NSLNNPKHVLQNFSVFFNKKKEAEIAETENTLENT-KILLKHYKGLVKYYNGESSPLKTL 1105
                                                                                                                                                                                                                                           SEESIQ-----TEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEV 1160
                                                                                                                                                                                                                                                                                                           1161 IKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSESGSDTLEQSOPKKPASTHV 1220
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                                                ENFYEKILKDSDTFYNESFTNFVKSKADDINSLN----DESKRKKLEEDINKLKKTLQLS
                                                                               8861 INYI-----NADNLRKDNFTQAINNARDALNKTQGQNLDFNAIDTFKDDIFKTKDALN-G
                                                                                                                                                                                                 -----AENNIHNSDDLSSLANTLSKASDLDNAMKDL-RDTIESN----STSV
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                                                                                                                                           8915 IERLTAAKSKAEKLIDSLKFINKAQFTHANDEIMNTNSIAQLSRIVNQAFDLNDAMKSLR
                                                                                                                                                                                                                                                                -----LKRQFNKALKEAKGVLNKNSGTNVN----INDIQHLLTQIDNAKDQLNGERRL
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes; colymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The cand gene also used in diagnostics as expressed sequence tags correlated for interesting and in gene therapy techniques contention of (II) is useful for generating antibodies against it, detecting or canditating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical calsorders involving abereant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other trails to assess biodiversity and to produce other types of data and products dependent on DNA and and conding sequences. ABGOO010-ABG30377 represent novel human of adagnostic mainto acid sequences of the invention.

Specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -- LCDNIHGFKY 166
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4.3e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 19.0%; Pred. No. 4.3e Matches 334; Conservative 327; Mismatches
                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID No 36864; 103pp; English.
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19.0%; Pred. No. 4
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                                  2001WO-US08631
                                                                     2000US-0540217
2000US-0649167
                                                                                                                                                                 Tang
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                                                                                                                                                                 Liu C,
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                                                                                                                            (HYSE-) HYSEQ INC
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                                  30-MAR-2001;
                                                                       31-MAR-2000;
                                                                                      23-AUG-2000;
                                                                                                                                                                 Drmanac RT,
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	ELHIITSEKDKLFSEVVHKESRVQGLLEE	413 YNDINNALNELNSFGDLINPFDY-TKEPSKNIYTDNERKKF	829 FEQKYKMVLEENERMNQEIVNLSKEAQKFDSSLGALKTELSYKTQELQEKTREVQERLNE	453 INEIKEKIKIESKKIESDKKSYEDRSKSLNDITKEYEKL	889 MEQLKEQLENRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESLQIERDQL	-	:: : :	536SKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEIETL	TGETKDEFQQKMVGIDKKQDLEAKNTQTLTADVKDN		: ::	637 ILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEK	1115 LSRTCDRLAEVEEKLKEKSQQLQEKQQQLLNVQEEMSEMQKKINEIENLKNEKK	690KNIKTESQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQ	1172 LTLEHMETERLELAQKLNENYEEVKSITKERKVLKELQKSFETERDHLRGYIREIEATGL	736 EQKQAQPPVPVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVS	1232 QTKEELKIAHIHLKEHQETIDELRRSVSEKTAQIINTQDLEKS	796 HSTMNEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNS	1275 HTKLQEEIPVLHEEGELLPNVKKVSETQETMNELELLTEGSTTKDSTTLARIEMER		1331 LRLNEKFQESQEEIKSLTKERDNLKTIKEALEVKHDQLKEHIRETLAKIQESQ	SMQPLSLTPQDKPEVSAN	SKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLGLSKRL		QESHDEMKSVAKEKD	990 LEEDINKLKKTLQLSFDLYN-KYKLKLERLFDKKKTVGKYKMQIK		1034 ALIADARA LALANDARA LALANDARA LALANDARA SAFERANA LALANDARA SAFERANA LALANDARA LALANDARA SAFERANA LALANDARA SAFERANA LALANDARA LALANDARA SAFERANA LALANDARA LALANDA	1077 TLENTKILLKHYKGLVKYYNGESSPLKTLSEESI-OTEDNYASLENFKVLSKLEGKLKDN	1609 LKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCELEHLKEQFETQKLNLEN	LNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSEN : : : : :	1663 IETENIRLTQILHENLEEMRSVTKERDDLRSVEETLKVERDQL	ATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPI	1/06 KENLRETITRDLEKQEELKIVHMHLKEHQETIDKLRGIVSEKTNEISNMQKDLEH 1760
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85 LSTDY--NHNNLLTKFLSTGMVFENLAKTVLSNLL---DGNLQGMLNISQHQCVKKQCPQ 1539
61 SNDALKAODL------KIQEELRIAHM------HLKEQQE----TID-KLRGIV 1797
                                                                                NSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTD 1375
                                                                                                                                                                                                                        :| ::| |:: :|| |:: :|| |:: :|| |:| :|| 39 VN-------ETQKKVSEMEQLKKQIKDQSLTLSKLEIENLNLAQELHENLEEMKSV 1887
                                                                                                                                                                                                                                                                                                                            uman; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; ripheral nervous system; neuropathy; central nervous system; CNS; zhelmer's; Parkinson's disease; Huntington's disease; haemostatic; vyotrophic lateral sclerosis; Shy Drager Syndrome; chemotactic; emokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                    76 INFANDVLGYYKILSEKYKSDLDSIKKYINDK-----QGENEKYLPFLN-NIETLYKT 1427
                                                                                                                                                                                                                                                                                              28 VNDKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNY---LKTIQDKLADFKKNNNFVGIAD 1484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        wel nucleic acids and polypeptides, useful for treating disorders ich as central nervous system injuries -
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Zhang J;
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Yang Y,
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13
M40883 standard; Protein; 2688 AA.
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55-APR-2000; 2000US-0552317.

99-JUL-2000; 2000US-0598042.

99-JUL-2000; 2000US-0620312.

JANG-2000; 2000US-0653450.

4-SEP-2000; 2000US-0653191.

99-0CT-2000; 2000US-069391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -DEC-2000; 2000WO-US34263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 NSGCFRHLDEREECKCL 1556
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PSDB; AAI60039.
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immunosuppressant and cytostatics activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to tread diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as Alzheimer's, parkinson's disease, amyotrophic lateral sclerosis, and disease, Huttington's disease, such as Alzheimer's, parkinson's disease, Huttington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/Inhibin activity, chemotectic/chemokinetic activity, mannestatic and thrombolytic activity, arthritis and inflammation, leukaemias and C.N. S disorders.

Note: The sequence data for this patent did not form part of the printed specification. 82; AKRKRRVTWCLGKINKMKNSNYADQFNIPTNITTKTHKLSINLLREIDESVCSESDVFSN 498 557 --KEIKEIAKTIK--- 362 491 913 MEQLKEQLENRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESLQIERDQL 972 --LKKLVFG---YRKPLDN-----IKDNVGK 237 LDEFEALERKTKKDQEMQLIHEISNIKNIVKHREVYNQDLENELSSKVELLREKEDQIKK 617 LIDGYEEI-----PFNLKINFYFDL--LRAKLNDVCANDŸCQI-----PFNLKIR-ANE -TID-KNKNATKEEEKKKL YQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKN--ENIKELLDKINEIKNPPPANSGNT -----FNIDSLFTDPLELEY ----YLREKNKNIDISAKVËTKESTEPNEYPNGVTYPLS ELHIITSEKDKLFSEVVHKESRVQGLLEEIGKTKDDLATTQSNYKSTDQEFQNFKTLHMD FEQKYKMVLEENERMNQEIVNLSKEAQKFDSSLGALKTELSYKTQELQEKTREVQERLNE INEIKEKIK -----IEKKK -----IESKK SYEDRSKSLNDITKEYEKL LESVIAEKEQL - - - KTDLKENIEMTIENQEELRLLGDELKKQ - QEIVAQEKNHAIKKEGE -----NSFGDLINPFDY-TKEPSKNIYTDNERKKF LNEIYDSKFNNNIDLTNFEXMMGKRYSYKVEKLTHH----NTFAS----YEN ---SKHNLEKLTKALKYMEDYSLRNI------VVEKELKYYKNLISKIENEIETL VENIKKDEEQLFEKKITKDEN-----KPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQL Length 2688; Indels 559; encoded polypeptides (AAM38642-AAM42213) with nootropic DB 22; 616; Query Match 5.3%; Score 444.5; DB Best Local Similarity 18.4%; Pred. No. 4.6e-114atches 345; Conservative 350; Mismatches 61 MEDYIKKNKKTIENIN-----ELIEESKK--------DKNKKIEEHE----126 ADLKHRVRNYLLTIKELK---YPQLFDLTNHMLT-YN-----DINNALNEL-----2688 AA; PNTLL----Seguence Query Match 439 558 337 733 363 793 413 853 453 492 167 214 238 618 279 536 582 \$ ð q ò q Dp 셤 g ò 셤 ò g δy g ò g ò g ò 임 ò à ò g ò

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ILKN----VELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEK---

----KCLLNY-- 1559 1354 1196 LTLEHMETERLELAOKLNENYEEVKSITKERKVLKELOKSFETERDHLRGYIREIEATGL 1255 1408 SKQEQSLNMKEK-----DNETTKIVSEMEQFKPKDSALLRIEIEMLGLSKRL---- 1454 1299 HTKLQEEI----PVLHEEQELLPNVKKVSETQETMNELELLTEQSTTKDSTTLARIEMER 990 LEEDINKLK-----KTLQLSFDLYN-KYKLKLERLFDKK-----KTVGKYKMQIK ELKOFKEHRKAKDSALOSIESKMLELTNRLQESQEEIQIMIKEKEEMKRVQEALQIERDQ 1633 LKENTKEI-----VAKMKESQEKEYQFLKMTAVNETQEKMCEIEHLKEQFETQKLNLEN INLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDV 1790 KAQDLKIQEELRIAHMHLKEQQETIDKLRGIVSEKTDKLSNMOKDLENSNAKLQEKIQEL 1850 KANEHQLITLKKDVNETQKKVSEMEQLKKQIKDQSLTLSKLEIENLNLAQKLHENLEEMK ----LKLERDQLKES---LQETKARDL : | ::|| ::|| :| :|| :| ::| : | ::|| EIQQE-LKTARMLSKEHKETVDKLREKISEKTIQ-----ISDIQKDLDKSKDELQKKI -------ELSTGMVFENLAKTVLSN------LLDGNLQGM EEIRIVAKERDELRRIKESLKMERDQFIAT -- LREMIARDRONHOVKPEKRLLSDGQQHL EQKQAQPPVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVS --LSQLFMEIYEKEMVCNLYKLKDN-------DKIKNLLEEAKKVSTSVKTLSSS 1355 LRLNEKFQE--SQEEIKSLTKERDNLKTIKEALEVKHDQLKEHIRE-----TLAKIQESQ SMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFE-----NILSLGKNKNIYQELI GOKSSENFYEKILKDSDTFYN-----ESFTNFVKSKADDINSLNDESKR------KK 1077 TLENTKILLKHYKGLVKYYNGESSPLKTLSEESI-QTEDNYASLENFKVLSKLEGKLKDN -VGAESNTITTSONVDDEVDDV-1730 KENLRETITRDLEKQEELKIVHMHLKEHQETIDKLRGIVSEKTNEISNMOKDLEHSNDAL ---IIVPIFGESEEDYDDLGQVVTGEAVTPS----VIDNILSKIE----SRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDI NFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLFV IHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKN------NNFVGIADLSTDY HSTMNEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNS-----1279 --NEYEVLYLK-----PLAGVYRSLKKQLENNVMTF-----NVNVKDILN------QLESKLNSLNNPKHVLQNFSVFFNKKK-------GQSDNSEPSTEGEITGQATTKPGQQAGSALEGD QTKEELKIAHIHLKEHQETIDELRRSVSEKTAQIINTQDLEK-LNISQHQC--VKKQCPQNSGCFRHLDEREEC-----ATVVSESGSDTLEQSQPKKPASTH-----SVMKERDNLRRVEET - - ----KNIKTE-KLTLLKE--1256 1196 1377 1945 1034 1687 1317 1910 1437 2054 2112 1573 1136 069 196 847 893 1241 qq pp g g qq g g g g Db q a Qγ g ò q δy g ò g ò δ òγ ŏ ò ò q ò ò g δ ó δ ζ δ

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     273 SQSNIKSYLHIFLTFPKLSLSNTYMNEDIITSTLQQKEYSVIF----FICSLCN----- 322
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                                                                                   --IITYEDIHKYVNCCLSINLFKLFFF----KKNYHTNDNRNYYEHNIKMLSGSLHYF
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                                                     YLIDGYEEINEL-----LYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANE----
                                                                                                                                                  LDVLKKLVFGYRKPLDNIKDNVGKMEDYIKKNKKTIENI--NELIEESKKTID-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes proteins and their fragments (1) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (1) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

(I) and (II) are useful for the development of vaccines against P. falciparum infection. (1) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of the plasmodium chromosome 2 and the complexity of the parasite blology, a process hampered by the complexity of the parasite ilfecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94;
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                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
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and in the
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CARUCCI D.
GARDNER M.
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                                                 SYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIV 1243
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM8642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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Yang Y,
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6.5e-11;
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18.8%; Pred. No. 6
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Xu C,
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Wehrman T, Xu
Goodrich R,
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2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0663450.
2000WO-US34263
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Wang Z, W
Zhou P,
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Best Local Similarity
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Wang
                                                                     25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
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                                                                                                                                                                                                                           YN-----DINNALNEL--------NSFGDLINPFDY-TKEPSKNIYTDNERKKF
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The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (I) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

(I) and (II) are useful for the development of vaccines against p. falciparum infection. (I) and polyclonal antisers or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the Plasmodium chromosome 2 and the
                                                     1826 KANEHQLITLKKDVNETQKKVSEMEQLKKQIKDQSLTLSKLEIENLNLAQELHENLEEMK 1885
                                                                                                                                                                                                                                                             1706 KENLRETITRDLEKQEELKIVHMHLKEHQETIDKLRGIVSEKTNEISNMQKDLEHSNDAL 1765
                                                                                                                                                                                                     SVMKERDNLRRVEET-------1920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
                                                                                                                                                                     SRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum chromosome 2 related protein SEQ ID NO:152.
                                                                                                   --NEYEVLYLK------PLAGVYRSLKKQLENNVMTF-----NVNVKDILN---
                                   --IIVPIFGESEEDYDDLGQVVTGEAVTPS----VIDNILSKIE--
                                                                                                                                                                                                                                                                                                         1437 IHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKN 1476
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(CARU/) CARUCCI D.
(GARD/) GARDNER M.
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52; parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification. subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasite lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many 396 628 685 121 KELINNLNDISDELKNCIEQVNSVSRNMANVEKEKENIINĖLQILRMKNDTMRKRISKFV 180 286 -----KLNEEIKRRNSF---IKNKDRKIDLLTNIENELLKKKEINNIKLMEKQNVIKN 336 KKKCIENLKDELINIKKKMEDKMHMTNEMDLL----SNKVEELNRIN--KTYEKNIVELN 450 NELDVIKKKLNDEEFLKEEEKKKNIDMVYKIKEYEIQIKEKENEIDSLKKNEONLHVLKN 510 647 803 861 --KEEMGL 729 862 NLYKLKDNDKIKNLL---EEAKKVSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTN 918 ELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDN----I 231 232 KD-----NVGKMEDYIKKNKKTIENINEL---IEESKKTIDKN---KNATKEEEKKKL 278 ----DILKKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHE 351 KEIKEIAKTIKFNIDSLFTDPLELEYYLREK--NKNIDISÄKVETKES--TEPNEYPNGV 407 457 ----KKKIËSDKKSYEDRSKSLNDITKE 487 Gaps ELILKKKNY-EELRLKLNHL----ECVERDSVKIN-SEKEKGEKVIYELKEKLDNDEKII 60 -----EEAHNLISVLE------KRI----337 NEQLLKDIKDENEKMNEHVNKLQNELIKRELQNKCISKDIĘFCKKEKEDKIKNLEDDLLE HNLEKLTKALK----YMEDYSLRNIVVEKELKYYKNLISKIENEIETLVEN----IKKD EBNKKELKREKRVCDMNLQSQILIKENEKHMQEKVEEYKNLLKQKDQELKNIIQEYDERI 686 NEEKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQAQPPVP -DIVNDCEEKLKQAK----746 VPVPEAKAQVPTPPAPVNN--KTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKI -----NDLMKDME EQEKVLKFKLYTLNNDIFSKNEKLNDMQKKLNDV-NEKYKNIVECLNNYKTEHK--EQIE 488 YEKLLNEIYD-----SKFNNNIDLINFEKMMGKRYSYKVEKLTHHNTFASYENS----K EEQLFEKKITKDENKPDEKILEVSDIV----KVQVQKVLLMNKI------DELKKTQLILKNV---ELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLI LKQYKITK - - EEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVC Indels 354; ; Length 980; TYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIK-Query Match 5.1%; Score 431; DB 21; Best Local Similarity 23.1%; Pred. No. 5.4e-11; Matches 263; Conservative 177; Mismatches 343; 687 KKKEEINKLVEEKSKLEHSH-----VKIQNEMSLLVEQNEKL 648 --INNKKLTTATNMANNNMLMDENLKEKD--KKI----279 YQAQYDLSIYNKQL------EIQNKEME----980 AA; Sequence 176 7 61 408 397 307 181 352 238 287 458 538 451 589 511 629 999 979 q . **අ** ò g qq δ ò qq ò g g ōλ Ω ò g δ ò g à ò g ò δ q ò q ò qq ŏ

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity 1028 Y-KMQIKKLTLLKEQLESKLNSL----NNPKHVLQNFSVFFNKKKEAE-IAETENTLEN 1080 979 NSLNDESKRK-----KLEEDINKLKKTLQLSFDLY--NKYKLKLERLFDKKKTVGK 1027 ------KKKNEEE----KERNEET LINNSLKLFENILSLGKNKNIYQELIGQKSSENFYEKILKDSDTFYNESFTNFVKSKADDI New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess 814 EHOKEDRKRKDKKKKGHSSDKEEKYNKKEKTKEKSSNILFDEEYIIQLEELRDTGENCFI i; chromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder. STIAIKDMEEIKKDMEKYEEEKKKNEEERKK-----KNEERKKNEEE---1081 TKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDN-----YASLENFKVLSKLEGK Claim 20; SEQ ID No 36660; 103pp; English. Novel human diagnostic protein #6292. AA. ABG06301 standard; Protein; 2017 YT; 2001WO-US08631 2000US-0540217 2000US-0649167 (first entry) Tang Liu C, WPI; 2001-639362/73. (HYSE-) HYSEQ INC N-PSDB; AAS70488 WO200175067-A2. GNI Homo sapiens. 30-MAR-2001; 31-MAR-2000; 23-AUG-2000; biodiversity 13-FEB-2002 Drmanac RT, 11-OCT-2001 ABG06301; 730 food 874 919 779 RESULT 34 ABG06301 δ g qq ŏ g g QY

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----PKTLDSVTELASEVSQLNTIKEHLEEEIKHHQKIIEDQNQSKMQLLQSLQEQKK 1006
                                                                                                                                                                                                                                     | ::|| | | : : ::: | | | :|| | FRETIQUEAGGVNSNQFEELLQERDK 1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLS 1147
                                                                                                 ----VSHSTMN----- 826
                                                                                                                                                                                                                                                                                                      SVKTLSSSSMOPLSLTPQDKP-EVSA----NDDTSHSTNLNNSLKLFENILSLGKNKNI 938
                                                                                                                                                                                                                                                                                                                                                                                                               QELIGQKSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDI---N 995
                                                                                                                                                                                                     --FNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKDNDKIKNLLEEAKKVS
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Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 YQELVKKLEALEDALLIGSSLEQKEKMVLNEGTSGTAVTTSTPGSGGSVTSGGSGSVA- 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 YQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGTAVTTSTPGSKGSVASGGSGGSVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum chromosome 2 related protein SEQ ID NO:75
                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence encodes a Plasmodium falciparum, Plasmodium vivax, Plasmodium malariae and Plasmodium ovale antigen which may be u in the diagnosis of malaria and as a vaccine against malaria.
                                                                                                                                                                                                                                                                                                                                                   Prodn. of antigens of Plasmodium species, esp. of falciparum recombinant DNA methods giving polypeptide(s) for protecting against malaria or for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 424; DB 6; LE
Pred. No. 7.3e-12;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 GGSVASGGSVASGGSGNSRRTNPSDNSSDSDAKS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cheung A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB18218 standard; Protein; 2010 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 5; 49pp; English.
                                                                                                                                                                                                                                                                  McGarvey M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.0%;
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                                                                                                                                                            .85WO-GB00072
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nes 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum.
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N-PSDB; AAN50354.
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CARUCCI D.
GARDNER M.
VENTER J C.
                                                                                                                                                                                                                                                               Mach B, Perrin L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 AA;
                                                                                                                                                                                                                                (BIOJ ) BIOGEN NV
                    Malaria; vaccine.
                                                     Plasmodium spp.
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                                                                                      WO8503725-A.
                                                                                                                         29-AUG-1985.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                          New gene encoding merozoite surface protein of Plasmodium vivax, useful for producing protein for diagnosis of malaria and for vaccination -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1425 YKTVNDKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIAD 1484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1485 LSTDYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQNSGCF 1544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RHLDEREECKCLINYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECT 1604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S KKNEVKSSGLLEKLAMKSKLIKENESKEILSQLLNVQTQLLTMSSEHTCIDTNVPDNAACY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Merozoite surface protein; malaria; blood; serum; diagnosis; vaccine; antigen-antibody composite; Enzyme Linked Immunosorbent Assay; ELISA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 206;
Plasmodium vivax merozoite surface protein C-terminal region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Storage-specific, late schizont merozoite malaria antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 424.5; DB 2
Pred. No. 1.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1605 KPDSYPLFDGIFCSSSNFLGISFLLILMLIL 1635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 KEGSEPLFEGVFCSSSFLSLSFLLLMLLFL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP50303 standard; Protein; 102 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Page 24; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.0%;
                                                                                                                                                                                                                                            15-NOV-1999; 99KR-0050616.
25-APR-2000; 2000KR-0022041.
20-MAY-2000; 2000KR-0027305.
                                                                                                                                                                                                             15-NOV-2000; 2000WO-KR01302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-1991 (first entry)
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                                                                                                        Plasmodium vivax.
                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAS00655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and selectivity.
                                                                                                                                         WO200136587-A2.
                                                                                                                                                                          25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80;
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1545

AAP50303

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Matches

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Gaps 84

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Length 102; Indels

nseq

- by

Shaw A;

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The fractions are accounted by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (1) nuclectide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

(1) and (II) are useful for the development of vaccines against antibody raised to immunogens comprising the sequences of (I).

(2) antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, and the identification of fungs to treat or prevent P. falciparum infection, or they are rifins or secreted or membrane proteins) and the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many drugs. Ana/10078 to Ana/10287 and Analasis represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification.
                                                                                                                                                                                                                                                                          The present invention describes proteins and their fragments (I) encoded
                                                                                                          Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection -
        Venter JC;
                                                                                                                                                                                                                  Disclosure; Page 177-182; 577pp; English.
     Gardner M,
Hoffman S, Carucci D,
                                                        WPI; 2000-365347/31
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2010 AA; Sequence

87; : | ::|: | ::| | ::| | 1000 ENCMNTTDILYNDVKKNTKIDDLENIDIPIITNDKEEYHVNNSIISVLKKHNSSVYKLKK 1059 60 TAVITISTPGSKGSVASGGSGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSD 119 854 334 394 TKES-----TEPNEYPNGVTYPLSYN-DINNALNELNSFGD-LINPFDYTKEPSKNIYT 445 D---NERKKFINEIKEKIKIEKKK-----IESDKKSYEDRS-----KSLNDITKEYE 489 Gaps SDAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHG-----FKYLIDGYE 172 EINELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFG----YRKPL 228 229 DNIKDNVGKMEDYIKKNKKTIEN------INELIEESKKTIDKNKNATKEEEK 275 335 NTPNTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKNKNIDIS-AKVE 393 2 KIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGY--SLFQKEKMVLNEGTSG 59 LNEFSKFFKLFKFLNKNVENIDNTFNSITNIYNKYYIN-MVVHRKDCFEKKQIHSKEHMM ERNSLMLKTLKTKKNHYIKKLRNHIIHNSDVYKILN--NYYKDEIFIVYDITK-----WT 276 KKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLDKINEIK-NPPPANSG Query Match
4.9%; Score 414; DB 21; Length 2010;
Best Local Similarity 20.0%; Pred. No. 7e-10;
Matches 347; Conservative 283; Mismatches 588; Indels 516; KKIH-----KIXX 899 173 964 855 446 Op ò g ò g ŏ qq ò ρp ò g οy g ò g ò

Qy	490	KLLNEIYDSKFNNNIDLTNFEKMGKRYSYKVEKLTHHNTFASYENSKHNL 540
Qy Db	541	EKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEIETLVE-NIKKD 588
Qy	589	EEQ
λο á	638	KLKVEMPKVESLINEEKKNIK 693
S &	69	AGSA
- qa	1285	:
oy .	75	s 795
8 8	796	TUDGTNDGTN-DKIKKFYRNIYTCYKLMCKNEYSNKYLSMLCSGMSLIDVVI 1355 HSTMNEKILKOXKITKEEESKLSSCDPLDLLFNIONNIPVMYSMFDSLNNSLS-OLEMEI 854
· 6	1356	FQSCVGI 1
δy	855	DNDKIKNLLEEAKKVSTSVKTLSSSSMQPLS
g	1401	RKKDMKIPPFASFISLELIHIK-KKKIKNLSNKLCNVSNNEKSYCYSNKYNI-MKGEKKK 1458
ço ç	906	EVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQELIGQKSSENFYEKIL 956
3 8	າ ໄດ	SONGYPRINGLERLEVENSETITING ANTECCADDCVWA-VREIENERNEERICK IST SOUFFYNESFINEVESKADDINGLINDESKRKLERDINKLKKHLOLSFDLYN 100
g G		
ΟŊ	1010	KYKLKLERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNK 1065
QQ	1566	NKKYESYLPKCLNKIHDFK-NLFYLLCYKNNNIQDLIQLYDICLNNNY 1612
οy	1066	KKEAEIAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIOTEDNYA 111
qq	1613	THIKKNMQLKEGKKHGKRNFYGYFVKFTFNNSVPLKLKKNKLIKKYN 1659
oy y	1118	LSSGLHHLIAELKEVIKNKNYTGNSPSENNTD
an i	1990	NNSNNNN 170
oy og	1710	VNALESYKKELPEGITOVATVVSESGSDTEESOPKRASTHVGAESYRITTSONVDDEV 1237 N. 1: 1
δy	1238	DDVIIVPIEGESEEDYDDLGQVVTGEAVTPSVIDNILSKIENEYEVLYLK 1287
QQ	1757	KSNIHNNSSKYIFNTVRFFKMKDIAKINTNKKCDBNSISCINNMRE 1802
δy	1288	PLAGVYRSLKKQLENNVMTFNVNVKD-ILNSRFNKRENFKNVLESDLIPYKDLTS 1341
qq	1803	KRNIFKNLNRNILLNFNNSNNDKYMNYIYNSTNVTYGKNYKRINKKDVH 1850
δy	1342	SNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYYKILSEKYKSDLDSIK 1401
QQ	1851	SSDNNNNNNNAEDDISSRKLK
٥٧	1402	INDROGENEKYLPFLNNIETLYKTVNDKIDLFVIHLEAKVLNYTYEKSNVEVKI 145
qq	1902	OKYINDH1NINSYDNNINNGLINEHKNVLHNECK1935

92;

Indels

559;

Mismatches

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363; Conservative 262;
 Matches
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C vaccines against P. falciparum infection or monoclonal infection. (I) and polyclonal aprilsers or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of farugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in infection, or they can be used to identify drug resistance in complexity of the parasite biology, a process hampered by the complexity of the parasitic lifecycle, and process hampered by the complexity of the parasitic lifecycle, and process hampered by the complexity of the parasitic lifecycle, and process hampered by the complexity of the world, and there is a pressing need for vaccines and new concent and drug development. Parasite resistance to drugs and new concent and protein sequences given in the present invention, but which are not specifically mentioned within the specification.
                         1966
1458 KELNYLKTIQDKLADFKKNNNFVGIADLSTDYNHNNLLTKFLSTGMYFENLAKTVLSNLL 1517
                                                                                                                                                                                                                                             Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
                         --- VVSENSCSDVITSLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 malarial parasite, vaccines and in the
                                                 DGNLQGMLNISQHQCVKKQCPQNSGCFRHLDEREEC-KCLLNYKQEGDKCVENP 1570
                                                                 Plasmodium falciparum chromosome 2 related protein SEQ ID NO:52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 411.5; DB 21; Length 1516; Pred. No. 6.5e-10;
                        ---NKNNOIIG---YSIKYDKN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proteins encoded by chromosome 2 of the human Plasmodium falciparum, useful as antimalarial
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diagnosis of P.falciparum infection -
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CARUCCI D.
GARDNER M.
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Best Local Similarity
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ELKYP-QLFDLTNHMLTLCDNIHGFKYL-IDGYEEIN----ELLYKLNFYFDLLRAKLN 193
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                                                                                                                                              -NLKIRANELDVLK---KLVFGY--RKPLD
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                                                     GVKE--NKVDKTNVEYDKKGDDGVIEISFE--DSHKLE-ESKFDDNNNIYDNDDELEK-N 1050
                                                                                                                                                                                                                                     1096 NGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIA 1155
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                                                                                                                    LLKEQL-ESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENTLENTKILLKHYKGLVKYY
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CARUCCI D.
GARDNER M.
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the present inverticul usersities proteins and utelf iragments (1) encoded are confirme present inverticul usersities, plasmodium falciparum.

Also described are: (1) nucleotide sequences (11) encoding (1); and (2) of accines against P. falciparum infection comprising (1) or (II).

(I) and (II) are useful for the development of vaccines against C. (1) and (II) are useful for the development of vaccines against consistent in the detection. (1) and plyclonal antisera or a monochonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in falciparum. Sequencing of the plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand to our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for resistance to insecticides have led to a resurgence of malaria in many contine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many carbones of the world, and there is a pressing need for vaccines and new carbones and many carbones of the world, and there is a pressing need for vaccines and new carbones and many carbones and ma
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and in the
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                                                                                                                                                                                                            Proteins encoded by chromosome 2 of the human malarial Plasmodium falciparum, useful as antimalarial vaccines
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                                     Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 126-133; 577pp; English.
                                                                                                                                                                                                                                                                                                        diagnosis of P.falciparum infection -
                                     Gardner M,
                                     ۵
                                     Carucci
                                                                                                                             WPI; 2000-365347/31.
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                                     Hoffman S,
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falciparum and Candida albicans are used to detect infections of these
                                                                                                           The invention relates to identification and use of telomerase reverse transcriptase (TERT) genes and proteins isolated from Plasmodium falciparum, Candida albicans and rice. TERT gene is also called as ever shorter telomere (EST) gene. TERT genes are used to detect P. falciparum and C. albicans infection in mammals. They are also used to diagnose the state of an infection in a patient and the relative amount of the pathogen in a cell, tissue, organ or organism. The potential binding partners and modulators of the activity of TERT genes and proteins are used to inhibit or promote growth of the pathogens and hence are used to treat e.g. stomach cancer, malaria and vaginal candidiasis in
                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is Plasmodium falciparum TERT full length
                                                                      Page 104-111; 138pp; English
                              pathogens in mammals
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                                                                        Claim 10;
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94; YEEINELLYKLNFYFDLLR------AKLNDVCANDYCQIPFNLKIRANELDVLKK 219 615 SDNSSDS--DAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHG-FKYLIDG 170 LVFGYRKPLDNI------KDNVGKMEDYIKKNKKT--IENINELIEESKKTIDK----- 265 DFFSEDRKEKSSSVGYDXKKKNXSNIKRFHNKINRTKEEKKKK-------WNKIIIN 362 295 AHNLIS------VLEKRI--DTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLD 342 343 KNKKIEEHEKEI-KEI-AKTIKFNIDSLFTDPLELEYY----LREKNKNIDISAKVETKE 396 415 HNNFIDEYKQKICKQIKCSTKKNDISHIITSRKENHLFHVQKLENNYKHPNINKQL---R 471 STEPNEYPNGVTYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEI 456 472 KTKILKY----VYNYFKEFINNVIN--TKFGKIYRKF------FPRKHILNKI 512 KEKIKIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKR 516 620 -----KVLLMNKI----DELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIV 666 LKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALE 726 YSYKVEKLTHHNTFASYE-----NSKHNLEKLTKALK-----YMEDYSLRNIVVEKE 563 DNLNNSFKIKTTLFNKLRRKYFNKIKKINIAIQKRHLMNRL----IYFLFN----YFIMP 722 Query Match 4.8%; Score 402.5; DB.22; Length 2184; Best Local Similarity 20.4%; Pred. No. 2.5e-09; Matches 362; Conservative 268; Mismatches 585; Indels 557; Gaps LK-YYKNLISKIENEIETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQ--171 671 148 254 313 363 220 997 919 198 557 397 621 qq ò g δ g ò Ω ò g ò qq ò Ω δý q ò g g ò a ò ŏ

LIRRF----FFLTKSEQTLH---KTIFFDRKIWNH------FTK-----IS 755

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oy d	727	GDSVQAQAQEQKQAQPPVPVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYE 780	0 -
oy o	00	SHSTMNEKILKQYKITKEEESKLSSCDPLDLLFNION 83	
qa	792	::::	7
QY	832	NIPVWYSMFDSLMNSLSQLFMEIYEKEMVCNLYKLKDNDKIKNLLEEAKKVS 883	
q	838	NIFIKKDMEKKSKTNNLINKSIDNLYKLKEINKKSVRPYIKKFYKIKKY 888	
Οŷ	884	TSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLN 920	
qq	889	FALKKMYIHMRMAKEEKSNIKLERAFKHFFIFAQEKEHILKYFSSHFFQNRKINYGKRFN 948	
QY	921	NSLKLFENILSLGKNKN-IYQELIGQKSSENFYEKILKDSDTFYNESFTNFVKSK 974	4
qa	949	KLIHRIKKNIIIKQNSGIVKNKDKTFLHLIKNKSNKNNNNK-KKNKNNYNNNNINNNNN 100	05
οy	975	NDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKK 102	23
qa	1006	NUNNINNNNKCKLSNSKRYNIRNNNNKKAKNNEKNNIDDSNLEKKKK 10	57
Qy	1024	108	83
qq	1058	KIYIYKIKNIIEKRNFMLKLNSINH	91
QY	1084	S	34
qa	1092	SSEFYFHNILNNLEREKKOK 114	46
ογ	1135	NENLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALE-SYKKFLPE 119	91
qq	1147	120	04
ογ	1192	DDVIIVPIFGESEE 125	51
qq	1205	N 124	42
δλ	1252	EAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMT-FNVN 131	10
qq	1243	CYEHINHNYLFK-ILKNFFDNINNFEFIYLFKRSFRLYNKNLNNSFLSYYPVN 129.	
οy	1311	135	52
qq	1295	VKSFGLHYIRNLRELIIKSHLNDNHHFLLNQMFKTKSKSDLYIFADSYKS 134	44
Qy	1353	KDSIDTDINFANDVLGYYKILSEKYK 139	94
QQ	1345	LQVDKRDIFWTIITVIRYYYLNIYFSIKEFKLNRKNIFYFQIFQENQMKGVYLSVRDK 140	02
Qy	1395	TLYKTVNDKIDLFVIHLEAKVLNYTYEKSN 145	52
qq	1403	HDEILESLKNSSININNKNFMICTNHEQDTEEKGN 145	
Oy	1453	VEVKIKELNYLKTIQDKLADFKKNNNFVG-IADLSTDYNHNNLLTKFLSTGMVFEN 1507	07
qq	1456		90
QY	1508	YKQEGDKCV 156	
qq	1507	::	21
ογ	1568	PLFDGIFCSSS 162	20
qq	1522	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	16
Qy	1621	NFLGISFLLILMLILYSFI 1639	
QΩ	1577	NELDKKIISNIYGLPQGFSLSNILCSLYYAYL 1608	

2013 AA.	do yo	133 LNTNFVKTFKGKIKSMACTNNNIFVLIKKKKKIINKNKNNQMKS 277 KLYQAQYDLSIYNKQLEBAHNLISVLEKRIDTLKKNENIKEL
chromosome 2 related protein SEQ ID NO:122. chromosome 2; human malaria parasite; vaccine; protozoacide; infection; insecticide.	o da o da	
iparum.	o d o d	379 LREKNKNIDISAKVETKESTEPNBYPNGVTYPLSYNDINNALNELNSFGDLINPFD 273 NEBKNEKTNEEKNEDTNKDPYEEKENDNIPLGDHHSVQYNIFTFSILNK 435 YTKEPS-KNIYTDNERKKFINEIKEKIKIEKKIESDKKSYEDRSKSLNDITKEYE 436 YTKEPS-KNIYTDNERKKFINEIKEKIKIEKKIESDKKSYEDRSKSLNDITKEYE 437 LI
dner M, Venter JC;		
Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection . Disclosure: Page 285-291; 577pp; English. The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (I) nucleocitde sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II). (I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polycional antitisera or a monoclonal antibody raised to imminocens comprising the sequences of (I) are	0 A A A A A A A A A A A A A A A A A A A	S66 KKDEEQLFEKKITKDENKPDEKILEVSDIVKOVQKVLLMNKIDELKKTQLILKNVEL. S55 SNNDYNIFYEDGEINKDELKN
useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the Plasmodium chromosome 2 and the Subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasite lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito parts of the world, and there is a pressing need for vaccines and new farges have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new and protein sequences given in the present invention, but which are not specifically mentioned within the specification.	6 6 6 6 6 6	746 VPVPEAKAQVPTPPAPAVNNKTENVSKLDYL
tch 4.7%; Score 399; DB 21; Length 2013; al Similarity 19.5%; Pred. No. 3.2e-09; 366; Conservative 235; Mismatches 593; Indels 684; Gaps 85; LCDNIHGFRYLIDGYEEINELL	60 60 60	918 NLNNSLKLFENILSLGKNKNIYQELIGQKSSENFYEKILKDSDT 965

98WO-US19231.

10-SEP-1998;

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: : || :|| :| | | 1416 KNFFEDIVCMEKKYLENNKNNNEKMNIKVDININMNMPTHYNILKNKILLLNDVEKTKCI 1475
 ---KLER----LFDKKKTVGKYKMQIKKLTLLKEQLESKL--NS 1048
                                  1073 FNNYYMSSGETPSSFFVSHKLEEPCVYKMKKKKEKQKYTCN-----MKEESESKIDYST 1126
                                                                                                                                                                                                                                                                                                                               1306 KKNFLLLRNNIKEDEEAIIKQKEKDHSTICNPKLIQNQQNDQTYNTKCVEENVFNVTINS 1365
                                                                                                                                                                                                                                                                                                                                                                     DDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDN---ILSKIENEYEVLYL-KPL, 1289
                                                                                                                                                                                                                                                                                                                                                                                                       1366 NEHISFYLSKWIIEDNNTSY-----YINDSLIKNMNIVFLKIKNDISQNYTNRKR 1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----YKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSS----Y 1365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|||: :|| : :|
1532 TFIKDNSSQNISLKKCL----KIYQNKYYLQ----EKY--EKKKLEKKITYLRKQLNDL 1581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IETLYKTVNDKIDLFVIHLEAKVLN----YTYEKSNVEVKIK-----ELNYLKTIQDK-- 1469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1642 ILNKIDFLSAFKKNLYVVNFYNNQTGYKFCNYISYPSNKSNHLSNEKSNFSSYNNLSSY- 1700
                                                                      1049 LNNPKHVLQNFSVFFNKKKEAEIAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEE 1108
                                                                                                                                            SIQTEDNYASLENFKVLSKLEGKLKDN----LNLEKKKLSYLSSGLHHLIAELKEVIKNK 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1476 EPONNNHNINNKEIEFKQISNMD----KLNEEKTYILKDKNYIIHNKNTNYFFDNETIIF 1531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plus end-directed microtubule motor activity; chromosome congression; microtubule binding activity; chromosome movement; mitosis; cell proliferation; tumor; metastasis; vascular malfunction; inflammatory disease; immune disease; anglogenesis; hypertension; restenosis; fungal infection; selective herbicide; fungicide; insecticide; plant growth regulator; activator; cancer cell marker.
                                                                                                                                                                                                                                                                                             ------DVATVVSESGSD-----TLEQSQPKKPASTHVGAESNTITTSQNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1366 NYIKDSIDTDINFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of centromere-associated protein-E (CENP-E)
                                                                                                                                                                                                                                                                                                                                                                                                                                           1290 AGVYRSL----KKQLENN-----VMTFNVNVK-----DILNSRF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         centromere-associated protein-E; ATPase activity;
                                                                                                                                                                                                                     N----YTGNS---PSENNTDV-----NNALESYKKFLPEGT-----
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1008 YNKYKL---
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87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --KKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKE 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLELEY 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 ADLKHRVRNYLLTIKELKYPQLFDLTNHM---LTLCDNIHGFKYLIDGYEEINELLYKLN 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   804 AELRKRADNLOKKVRN-----FDLSVSMGDSEKICEEIFOLKOSLSDAEAVTRDAQKEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 FYFDL----LRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFLRSENLELKEKMEDT-SNWY-----NQKEKAASL-----FEKQLETEKSNYKKM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2954;
                                                                                                                                                                                                                                         Centromere-associated protein-E and related nucleic acid
                                                                                                                                        Wood KW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
4.7%; Score 393; DB 20;
Best Local Similarity 19.3%; Pred. No. 9.3e-09;
Matches 341; Conservative 325; Mismatches 583;
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                                                                                                                                        Sakowicz R,
                                                                                                                                                                                                                                                                                  Claim 5; Page 66-67; 77pp; English
                                                                                                                                        Cleveland DW, Goldstein LSB,
                                                         97US-0058645.
                                                                                               (REGC ) UNIV CALIFORNIA
                                                                                                                                                                            WPI; 1999-229233/19.
N-PSDB; AAX26819.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer cells.
                                                         11-SEP-1997;
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ογ	999	YYKNLISKIENEIETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIV 615
qq	1264	DSLKQDLSENIEQSIET-QDELRAAQEELREGKQLVDSFFQQLLDCSVGISSPNHDAV 1320
οy	616	KVQVQKVLLMNKIDELKKT-QLILKNVELKHNIHVPNSYKQENKQEPYYL 664
QQ	1321	
δò	665	
g D	1379	NGLEKEILGKSEESEVLKSMLENL-KEDNNKLKEQAEEYSSKENQFSLEEVFSGSQK 1434
οy	721	OPPVPVPVPEAKAOVPTPPA,PVNNKT
QQ	1435	LVDEIEVLKAQLKAABERL
δy	781	FLNTSYICHKYILVSHSTWNEKILKQYKITKEEESKLSSCDP 822
qq	1466	TANTNLVEGKLETPLQADHEEDSIDRRSEEMEIKVLGEKLERNQYLLERLQEEKL 1520
οχ	823	LDLLFNIQNNIPVMYSMFDSLNNSLSQLFWEIYEKEMVCNLYKLKDNDKIKNLLEE 878
QQ	1521	ELSNKLELLQKEMETSVL-LKDDLQQKLESLLSENI 1555
δ	879	AKKVSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFE 927
QQ	1556	ILKENIDITLKHHSDTQAQ-LQKTQQELQLAKNLAIAASDNCPITQEKETSADCVHPLEE 1614
δý	928	GOKSSENF
qq	1615	KILLLTEELHQKTNEQEKLLHEKNELEQAQVELKCEVEHLMKSMIESKS-S 1664
Óλ	978	NKLKKTL
qq	1665	LESLQHEKHDTEQQLLALKQQMQVVTQEKKELQQTHEHLTAEVDHLKENIELGLNFKNEA 1724
δ	1012	KLKLERLEDKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFN 1064
QQ	1725	QQKTTKEQCLLMENKELEQSQHRLQCEIEELMKSLKDKESALETLKESEQKVINLN 1780
οy	1065	KYYNG
qq	1781	OEMEMVMLEMEELKNSGRTVIAERDQLQDDLRESVEMSIETQDDLRKAQEA 1831
ογ	1125	LSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNN- 1180
g	1832	LENOMLYN
ογ	1181	ALESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAE 1223
Ωp	1892	SLSLKEKEFALEQAEKDKADAARKTIDITEKISNIEEQLLQQATNLKETLYERESLIQCK 1951
ζ	1224	VDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDNILS
QQ	1952	EQLALNTEHLRETLKSKDLALGKMEQERDEAANKVIALTEKMSSLEEQINENVTTLKE 2009
ογ	1277	-KPLAGVYRSLKKQLENN
qq	2010	GEGEKETFYLORPSKOOSSOMEELRESLKTKDLOLEEAEKEISEATNEIKNLTAKISSL 2069
οy	1314	ILNSRFNKRENFKNVLESDLIPYK-DLTSSNYV1345
qq	2070	EEEILQNASILNEAVSERENLRHSKQQLVSELEQLSLTLKSRDHAFAQSKREKDEAVNKI 2129
ζŏ	1346	VKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYYKILSEKYKSDLDSIKKY 1403
qq .	2130	ASLAEEIKILTKE-MDEFRDSKESLQEQSSHLSEELCTYKTELQMLKQQKEDINNK 2184
č	1404	INDKQGENEKYLPFLNNIETLYKTVNDKIDLFVIHL-EAKVLNYTY-EKSNVEVKIKELN 1461
Op	2185	LAEKVKEVDELLQHLSSLKEQLDQIQMELRNEKLRNYELCEKMDIMEKEIS 2235

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The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Chromosome 2 of the human malarial parasite, Plasmodium falciparum. Chromosome 2 of the human malarial parasite, Plasmodium falciparum. Chromosome 2 of II) and (II) and (II) are useful for the development of vaccines against (I) and (II) are useful for the development of vaccines against (II) and infection. (I) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in conspectanding of the Plasmodium chromosome 2 and the subsequent identification of proteins ancoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasite biology, a process hampered by the resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new cruger. Ash/7078 to AAA/70287 and AABIB352 represent nucleotide and protein sequences given in the present invention, but which are not second consecutions and the present invention.
1462 YLKTIQ-----DKLAD----FKKNNNFVG--IADLSTDYNHNNLLTKFLSTGMVFE-- 1506
                                                                                                              2296 AHKHCMINIKESLSSTLSRSFGSLQTEHVKLNTQLQTLLNKFKVVYRTAAVKEDHSLIKD 2355
                                            2236 VLRLMQNEPQQEEDDVAERMDILESRNQEIQELMEKISAVYSEQHTLLSSLSSELQKETE 2295
                                                                                   -----ILSQHQCVKKQ 1536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum chromosome 2 related protein SEQ ID NO:37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gardner M, Venter JC;
                                                                                                                                                                     1537 CPQNSGC--FRHLDEREECKCLLNYKQEGDK 1565
                                                                                                                                                                                               :: | | : | | | : | | 2356 YEKDLAAEQKRHDELKLQLQCL---EQHGRK 2383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 92-98; 577pp; English.
                                                                                                                                                                                                                                                                                                                      AAB18180 standard; Protein; 2295 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US26796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0107131
                                                                                                                                                                                                                                                                                                                                                                                                          07-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoffman S, Carucci D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HOFF/) HOFFMAN S.
(CARU/) CARUCCI D.
(GARD/) GARDNER M.
(VENT/) VENTER J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-365347/31.
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                                                                                                                                                                                                                                                                               RESULT 43
AAB18180
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QY 1062 FFNKKKEABIAETENTLENTKILLKHYKGLVKYYNGESSPLKT-LSBESIQTEDN 1115	1127 KLEGKLKDNLNLEKKKLSYLSGCLHHLIAELKE	Qy 1160YIKNKN	Db 1111 ERDEIKAFEFWKKAADQGDTTSALSTGYAYLDEYKKFLKKEELVKNMDREDILTMIHLEN 1170Qy 1204 SDTLEQSQPKKPASTHVGAESNTITTSQNVD-DEVDDVIIVPIFGESEEDYDDL 1256	1257 GQVVTGEAVTPS-VIDNILSKIENEYEVLYLKPLAGVYRSLKKQLEN : : : :	NVMTFNVNVKDILNSRFNKRENFKNVLESDLIPYKDLTSS :	1343 NYVYKDPYKFLNKEKRDKFLSSYNYIKDSI-DTDINFAND	1382VLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNI 14.08 DENDEMIKKYMKDLNDDLNKSLKNAEEYFHKAIRNNDDSLENILAKYNIHKFGLGTEKNI	ETLY KTVNNKIDLEVIHLEAKVLNYTYEKSNVEVKI	1463	1498 FLSTGMVFENLANIVLANLIDGMLQGMLMISGHQCVKUCVQ	QY 1541 SGCFRHLDDRFEECKCLLNYKOEGDKCVENPNPTCNENGGCDADAKCTFEDSGSNGKK 1598 QY 1541 SI	RESULT 44 AAY31946 ID AAY31946 standard; Protein; 4134 AA.	AA AAV31946; XX XX 21-DEC-1999 (first entry)	Plasmodium falciparum cytoadherence gene protein GLAG9 par CLAG9; paralogue; cytoadherence linked asexual gene; CLAG	<pre>XW erythorogte; red blood cell; malaria; infection; therapy; vaccine. XX OS Plasmodium falciparum. XX</pre>
SQ * Sequence 2295 AA; Query Match 4.6%; Score 388.5; DB 21; Length 2295; Best Local Similarity 19.9%; Pred. No. 1.1e-08; Best Local Similarity 19.9%; Pred. No. 1.1e-08; Matches 370; Conservative 282; Mismatches 591; Indels 615; Gaps 98; At 178 LYKLNFYFD-**LLRAKLNDVGANDVGANDYGDIFFILKIRANELDVLKKLYFGYRKPLDNIKDNV 235 QY 178 LYKLNFYFD-**LLRAKLNDVGANDVGANDYGDIF**:	Db 5 VFYLNFIFSFFLLIIKCDESVSNGRKEIYFDDDEKLKLSSFFDRSTNINLDV 56 QY 236 GKMEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQ 282 Db 57 GENDELSSYVPREVDEKKKKNKKDIDSKENSKSGNNIYNKDNTKNNEDVN 106	283 YDLSIYNKQLEBAHNLISVLEKRIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLD ::::::	TDPLELEYYLREK-NKNIDISAKVETKE	Db 208YDSLNYLIRLMNNKNSRKFISFSNNEKKRIIKNDNN 244 Qy 458 EKIKIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKF 500 Db 245 ENIVIER	501 NNIDLTNEEKMMCKRYSYKVEKLTH	Qy 538 HNLEKLIKALKYMEDYSLRNIVVEKELKYYKNLISKIENEIETLVENIKKDEEQL 592	Qy 593 FEKKITKDENKPDEKILEVSDIVKVQVQKVLLAMKIDELKKTQLILKNVELKHNIHVPNS 652	Qy 653 YKQENKQEPYYLIVLKKEID-KLK-VFMP-KVESLINEEKKNIKTEGQSD 699	Qy 700NSEPSTEGEITGQATTKPGQAGSALEGDSVQAQAQAGGQQ 741	Qy 742 PPVPVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICH 789	OY 790 KYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVWYSMFDSLNNSL 847 1	QY 848 SQL-FMEIYEKEMVCNLYKLKDNDKIKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQDKPE 906 :: : :	OY 907 VSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQELIGQKSSENFYEKIL- 956	OY 957 -KDSDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKL 1015	QY 1016ERLFDKKTYGKYKMQIKKLTLKEQLESKINSLNNPKHYLQNFSV 1061 DD 814 FTPAAIKMKDKIYDQLKLLRSNFVEKLKNESICVLSFLYLIGINDDNGKLHFPYGFPRNI 873

604 PDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYY	Db 673 INTEDGEYCIRPYDPSVYTHEKSCYKICDLGNSLWIDESRYABIQTRQYRABEVIL- 728 Qy 748 VPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTW-NEKILKQ 806	Z X X	QY 1024 TVGKYKMOIKKITLLKEQLESKLNSLNNPKHVLQNFSVFENKKE 1068 L032DTYRKQIIKNIPAHQISKLKDGKNFKAYNESIQYEMHDFQQYNEHDFEXKFNKFEHA 1089 QY 1069	QY 1128 LEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSEN 1174	QY 1275 SKIENEYEVLKKELAGGVRÄSLÄKÖLENNVMTFNVNVKDILNSRFNKRENFÄNVLES 1331
Holt DC, Cowman AF;	lasmodium infections in humans, ih. roduct of a clag9 paralogue 3 of Plasmodium falciparum. ied cytoadherence linked v31945) encoded by the clag9 arum. CLAG9 facilitates sed with Plasmodium to other	clag genetic species, and the bles a range of therapeutic agents to didentified that are useful for the disease conditions caused or Plasmodium spp., e.g. malaria, score 387.5; DB 20; Length 4134; Pred. No. 2.4e-08; Pred. No. 2.4e-08; Indels 567; Gaps 93;	KLNH : HICH LLKKI LVSE		
PN W09949048-A1. XX PD 30-SEP-1999. XP 25-MAR-1999; 99WO-AU00213. XX XX XX XX XX XX XX XX XX YX XX YX XX YX Y	9-591099/50. eins useful for treatment ly malaria - re; Page 90-115; 150pp; E. uence represents the protte also AAZ20056) on chrom paralogue of the newly ind gene 9 (CLAG9) protein (ss fromosome 9 gene of erythrocytes par	Due Bes	(VNSFDSSWVELK (VNSFDSSWVELK (VNSFDSSWVELK (LINDVCAN-DYCO 1 : : I 1 : : I 1 : : I 1 : : I 1 : : I	270 270 285 330 320 371	429 424 488 477 544 532

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2464 AVQN--INAVQVEVIKK-
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                                                                                                                                                                                                                     epidermidis; open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis lifection.

NB. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site.
1428 UNDKIDLFVIHLEAKVLNYTYEKSN-VEVKIKELNYLKTIQDKLADFKKNNNFVGIADLS 1486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2404 ALAALASEAKNKNAIIDQTPNATAEEKEEANNKVDRLQEEADANILKAHTTDEVNNIKNQ 2463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMEDYIKKNKKTIENINELIEESKKT 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDNSSDSDAKSYA----YPQLFDLTN 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                  ---IKLMLIPLN-----SYKQNNDLKSALEELNNVFTNKEA----QKESSPIG----
                                                                                                                                                                                               Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 314; Conservative 231; Mismatches 592; Indels 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 387; DB 23;
Pred. No. 2.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID 5080; 267pp; English
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                                                                                                                            ABP40235 standard; Protein; 3696
                                                                                                                                                                                                                                                                                                                                                                              (GENO-) GENOME THERAPEUTICS CORP.
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97US-064964P.
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                                                                                                                                                                                                                                                     Staphylococcus epidermidis
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---DHGTFFRKLLT 1567
                                                 1487 TDYNHNNLLTKFLS 1500
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                                                                                                                                                                                                                   Staphylococcus
antibacterial;
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-QLNQFIDNQKKI 2495
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|ENTPDATLEEKAEA-----NRLLQ---NVLTSTSDEIANVDHNNEVDQALDKA
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                                                                              263 IDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLD--
                                                                                                                                                                                                                                        --KINEIKNPPPANSGNTPNTL------LDKNKKIEEHEK-----EIKEIAKTIKF
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The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (I) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).
(I) and (II) are useful for the development of vaccines against antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat for prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by It will help to expand
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   --EDYDDLGQV 1259
                                                                                                                               -DILNSRFNKRENFKNVLESDLIPYKDLTSSNYV----VKDPYKFLNKEKRDKFLSSYNY 1367
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                                                                                                                                                   1260 VIGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLEN----NVMTFNVNVK--
                                                                                              -----DKINDISSRATNEEKQIFVSKLKALINRTHKQIDEAETFVSVETIVRNFKVE
                                                                                                                                                                                             IKDSIDTDINFANDVLGYYKILSEKYKSDLDSIKKYINDKOGENEKYLPFLNNIETLYKT
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and in the
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vaccines
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Plasmodium falciparum, useful as antimalarial
diagnosis of P.falciparum infection -
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our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70078 and AAB1814 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification.
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                                                                                                                                                                                                         ESEEDYDDL---GQVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNV 1304
GEFFFDEVEEKFDEKMGEFFFDEVEEKFDEKMGENIFEEIPK----KDDVEIBETYSEK 723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome 2; human malaria parasite; vaccine; protozoacide; infection; insecticide.
                                                                                    PEGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNV--DDEVDDVIIVPIFG
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                           LERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAET
                                                                      ENTLENTKILLKHYKGLVKYYNGES----SPLKTLSEESIQTEDNYASLENFKVLSKLEG
                                                                                                                 KLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYK-KFL
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                                                MWEIHDEK ----
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The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (I) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

C (I) and (II) are useful for the development of vaccines against P. falciparum infection or a monochonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in confection, or they can be used to identify drug resistance in subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasite biology, a process hampered by the vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. Ama70078 to ham70287 and Ama181852 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification.
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18.7%; Pred. No. 2.1e-08;
iive 288; Mismatches 625; Indels 643;
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                                                                                                                                                                                                  Proteins encoded by chromosome 2 of the human malarial Plasmodium falciparum, useful as antimalarial vaccines diagnosis of P.falciparum infection -
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Matches 359; Conservative 288; Mismatches
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               HOFFMAN S.
CARUCCI D.
GARDNER M.
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500 FUNNIDLINFEK----MMGKRYSYKVEKLTH------HNTFASYENSKH-----NLEKLTK 545

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Db 1497 SNYNEGNDPFIFQQLNEGIYINDIFINLNNKKRLESLEWSNEDIENLKFYFKQFKHMHNF 1556	RESULT 48 AMB18254 standard; Protein; 2206 AA. ABB18254 ABB18254 ABB18254 ABB18254; A O'NOV-2000 (first entry) E Plasmodium falciparum chromosome 2 related protein SEQ ID No:111. XX Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; XX AD ALIMALARIA: AND ALIMALARIA: B DISCOORS728-A2. XX AD ALIMALARIA: B DISCOORS738-A2. XX AD ALIMALARIA: B DISCOORS738-A2. XX AD ALIMALARIA: B DISCOORS738-A3. XX AD ALIMALARIA: B DISCOORS738-A3. XX AD ALIMALARIA: B DISCOORS ABBRER M. B CARWIY) CARWICT D. CARWIY CARWIT CARWICT D. CARWIY CARWICT D. CARWIY CARWIT CARWICT D. CARWIY CARWIT CAR
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Db 546 HNSN-DHTHFSNDHTHFSNDHTHFSNDHTHNSNDHTHNSKNHAHFSNEVDKTN Qy 546 ALKYMEDYSLRNIVVEKELKYYKNLISKIENEIETLVENIKKDEEQLFE Db 605 DYKYHSEKKKKNNVIRSKMYNIKKRISKINDELHELSNFFLIDKTKR-EKLMFEYNENVF Qy 595KKITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKT-QLILKNVE	831 NNIPVMYSMEDSLANSLSQLEMEIYEKE

(I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasite lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification. 72; TFYNESFTNFVKSKADDINSL---NDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLER 1017 471 : | | | | | : : | | : | : | | 328
IINKKKDRSRDTYEDEESREGAYGENTTEDLNEDTQEGHKNKKKEILMNILYNDINIKKN 328 296 HNLISVLEKRIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIK 355 356 EIAKTIKFNIDSLFTDPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYND 415 268 723 427 781 900 240 DYIKKNKKTIENINEL----IEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEA 295 ----INYNKKYFN 124 472 KSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFE-----KMMGKRY---SYKV 521 EKLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEIETL 581 619 VQKVLLMN------KIDELKKTQLILKN-VELKHNIHV-----PNSYKQENKQEPYYL 664 :|:: |::: |: : |: : | : : |
EYLESEKSSSDDRREVNNFENDYSKDSSHSNINSDLDVDRKKHSDNVYEESEQDGKQTEG 61 RKKI----KGFFKLKKGDS-----------EDENKEKETKDHRLK 91 : : : | : | : | : | | | DSPQYMS-----RNQSTWILINNIKNFCNTY 116 IN----NALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKEKIKIEKKKIESDK VENIKKD------EEQLFEKKITKD------ENKPDEKILEV--SDI-VKVQ 724 ALEGDSVQAQAQEQKQAQPPVPVPEAKAQVPTPPAPVNNKT--ENVSKLDYLEKLYEF 665 IVLKKEIDKLKVFMPKVESLINEEKKNI-KTEGQSDNSEPSTEGEITGQATTKPGQQAGS ----- KDKIKEY----DYLDNEKQKNVNKMIHPKDGNNNNNNILLSQ----------NSSTILSHVVQEDYADGIKKF 782 LNTSYICHKYILVSHSTMN-EKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMF NKNSFYNN---LENRKLININNIYDKYKI------ILSEIKSG-----DSLNNSLSQLFMEIYEKEMVCNLYKLKDNDKIKNLLEEAKKVSTSVKTLSSSSMQPLSLT PQDKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQELIGQKSSENFYEKILKDSD Length 2206; 515; 4.5%; Score 379.5; DB 21; Length ilarity 19.9%; Pred. No. 2.6e-08; Conservative 214; Mismatches 451; Indels h Similarity 19.9%; 2206 AA; Matches 294; Seguence Query Match Local 269 ~ 62 92 168 522 217 582 329 841 483 901 961 428 Best 8×866666666668×8 ŏ а ò g ò g δý g οy QQ οŽ q οy QQ δ Ор δ g δý qq ò g ò qq ò ò

1344 1195 SEEDYD-----DLGQVVTGEAVTPSVIDNILSKIENEYEVLYLK---PLAGVYRSLKKQ- 1299 LENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLN 1137 -------VVKD--PYKFLNKEKR--DKFLSSYNYIKDSIDTDINFA 1379 -----1457 -----KELNYLK--TIQDKLADFKKNNNFVGIADL----STDYNHNNLLTKFLSTGMV 1504 nootropic; immunosuppressant; cytostatic; gene therapy; cancer; KKNEVHYLHLYNLNI--NSKMLSIIDGYLECI----DVVYLNNFFLESFYNSVKNYY 820 707 peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's, Parkinson's disease; heamostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation; DNIXYINKLRNINNVNDMND-MYHHNDENDVINQKLYYDEIDYTKKGILDKIHVLMFYE 994 YCDDLHDYPIKFYLKKIISTYFIKYFAFFKNKVKKIIIDNERSILYVLYENSDLYVKLLS LFDKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENT -----NKK-----NKK-----NMK LEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSEN--NTDVNNALESYKKFLPEGTDV 1196 ATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVD------DVIIVPIFGE NDVLGYYK ---ILSEKYKSDLDSIKKYINDKQGEN----EKYLPFLNN---IETLYKTV 934 NEKIFHHSRNYMIEHTANDDNSSFNYYDNGKSSINSYNISNTYPEYMDNKSFIDEYNKNI LYYNNIYKINY---IKSNNKNKDILYNIHCRNIHL------YLILSSHEG-------LENNVMTFNVNVKDILNSRFNKRENFKNVLESDLIPYKDLTSSNY--FENLAKTVLSNLLDGNLQGMLN----ISQHQCV 1533 Š AAM38681 standard; Protein; 1780 Human polypeptide SEQ ID NO 1826. 26-DEC-2000; 2000WO-US34263 WO200153312-A1. Homo sapiens 22-OCT-2001 26-JUL-2001 Leukaemia. 1018 1078 1249 1300 1505 RESULT 49 AAM38681 614 655 167 1345 1380 1458 1108 592 1138 708 οý ΩD ò δλ g ò Dp g q g qq Dp ò g ò ö 셤 ò a ŏ οχ à

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Zhang J;
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18.9%; Pred. No. 3.1e-08;
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Xu C, Xue AJ,
R, Drmanac RT;
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Wehrman T, Xu
Goodrich R,
2000US-0488725.
2000US-0552317.
2000US-0598042.
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Wang 2, F
Zhou P,
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---EQLSDATLNRYFLECSQRNTESLCNESLSDPYMNNDNSHSQYSNS 1182

1183 YETENDNLSSENPNVDDLSGHIONNDNSFNSSSSNVPLNVNPTNIENSNILPLSIEGTNS

SGGSGGSVASGG---SVASGGSVASGGSVASGGSGNSRRTNPSD

1128 QCLIDKNVRN-

75

qq δ

117

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Infection, or they can be used to identify drug resistance in the control of the plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many drugs. AAA70078 to AAA7028 and AAB1814 to AAB18352 represent nucleotide specifically mentioned within the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (I) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

(I) and (II) are useful for the development of vaccines against antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) and and the identification of drugs to treat or prevent P. falciparum furthermore.
                                                                                                                                                                                                                                                             chromosome 2; human malaria parasite; vaccine; protozoacide; infection; insecticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     parasite,
and in the
                                                                                                                                                                                                                             Plasmodium falciparum chromosome 2 related protein SEQ ID NO:129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proteins encoded by chromosome 2 of the human malarial Plasmodium falciparum, useful as antimalarial vaccines
QY * 1391 EKYKSD---LDSIKKYINDKQGENEKYLPFLNNIETLYKTVND 1430
                     | | : : | | : : | : | : | : | ETSKIETQIMDIKPKRISSADPDKLQTEPLSTSFEISRNKIED 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter JC;
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                                                                                                                         AAB18272 standard; Protein; 2500 AA
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                                                                                                                                                                                                                                                             Plasmodium falciparum;
antimalarial; malaria;
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CARUCCI D.
GARDNER M.
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1821
                                  1243 AHLNFGRSYSD-------PPPFHSPNTSILEFCCSRYFSSNFPFEKTMIQ 1285
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   SDSD-AKSYADLKHRVRNYLLTIKELKYPQLFDLTN-HMLTLC-----DNIHGFKYLID 169
                                                                                                                                                                                                                                                                             334 GNT----PNTLLDKNKKIEEHEKEIKEIAKTIKFNI-----DSLFTDPLELEYYLR--- 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            590 EQLF----EKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELKH 645
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                                                                                                   1286 N-EQVQESLYISNNFI-----KANHV------ERIKITHIDTFTS------N
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*Match 4.4%; Score 372; DB 21; Length 2500; Local Similarity 20.5%; Pred. No. 6.3e-08; les 328; Conservative 231; Mismatches 574; Indels 466;

Query Match

Matches

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73;

Gaps

Tue Apr

CC specific auto-antibo CC in the removal of au CC coupled to a cytotoxa CC producing lymphocyte		걸	Matches 266; Conserva Qy 232 KDNVGKMEDYIKKNK	Db 82 RDDVTLLRQEVQDLQ	QY 290 KQLEEAHNLISVLEK	Db 142 QQLEEAQT		Qy 410 PLSYNDINNALNELN	Db 219GIEDVAVLKKELV		QY 519 Y-KVEKLTHHNTFAS	Db 318 YTKLEE	QY 560 VEKELKYYKNLISKI	Ov 610 EVSDIVKVOV	425 ETEROLGEA			Qy 688 EKKNIKTEGOSDNSE	Db 545 EREDLYAKIQAGEGE	QY 742 PPVPVPVBEAKAQVF	Db 596 ENLHDQVQEQKAHLR	QY 802 KILKQYKITKEEESK	Db 645 KAKTELLESAEAAKT	Qy 862 NLYKLKD-NDKIK	705	LNTDL LNTDL	Qy 961TEYNESE'	-
DINKLKKTLQLSFDLYNK-YK 1012 ::	PKHVLQNFSVFFNKKK		SSPLKTLSEESIQTEDNYASL 1119 : ::: PSNIKVKLEEEEKSDD 2251	EVIKNKNYTGNSPSENNTDVN 1179	EEEKSDDKRDDKKNDNTREKN 2303	HVGAESNTITTSQNVDDEVDD 1239	TPSVIDNILSKIENEYEVL	:	KRENFKNVLESDLIPYKDLTS 1341	1380	1 2496						gen; diagnosis;						ARGEN.			on - useful for exact apy and for removal of		the antigen p162, for use ic disease, i.e. they
960 - DTFYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNK-YK 	LKLERLFDKKKTVGKYKMQIKKLTLLKEQLE	: : EKYSRKFNYNHSSGSYH	1068 EAEIAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASL. : : : : : : :	1120 ENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVN	2252KRDDKKNDNTR-EKNNLDNKKSFPSNIKVKLEEEEKSDDKRDDKKNDNTREKN	1180 NALESYKKELPEGTDVATVVSESGSDTLEGSQPKKPASTHVGAESNIITTSONVDDEVDD	VIIVPIFGESEEDYDDL	: :	1285 YLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFKNVLESDLIPYKDLTS 1341 ::	SNYVVKDP	2461 KNEIKNDKKNNKKNNKKVAKKNEIKNEIKDEIKDEN 2496	E E	AAW02258 ID AAW02258 standard; Protein; 1411 AA. XX	AAW02258;	09-MAR-1997 (first entry)	Nucleolar/endosomal auto-antigen p162.	Auto-antibody; p162; rheumatic disease; antigen; diagnosis; gene therapy.	Homo sapiens.	DE19515514-C1.	12-SEP-1996.	27-APR-1995; 95DE-1015514.	27-APR-1995; 95DE-1015514.	(PRIV-) PRIVATES INST IMMUNOLOGIE & MOLEKULARGEN	Renz M, Seelig HP;	WPI; 1996-403153/41. N-PSDB; AAT58751.	DNA encoding nucleolar-endosomal auto-antigen diagnosis of rheumatic disease, in gene therapy specific auto-antibodies	Claim 1; Fig 2; 15pp; German.	Transformed cells can be cultured to produce the antigen p162, for in exact (differential) diagnosis of rheumatic disease, i.e. they can about in immunoseme

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNE 801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVC 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEE
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SELAKGPQEVAVYVQELQKLKSSVNELTQKNQ---TLTENLLKKEQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 382;
                                                                                                                                                                                                                                                                                                                                                       4.4%; Score 370; DB 17; Length 1411;
17.8%; Pred. No. 3.9e-08;
ative 270; Mismatches 574; Indels 382.
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1434
                                                                                                                                                                    1249 NLGTVKKEWQSSQRRVSELEKQTDDLRGE------IAVLEATVQNNQDERRALLER 1298
                                                                                                                                                                                                                                                                                              1149 SH-------KLESIKEITNIKDAKQLLIQQKLELQGKA------DSLKAAVEQ 1188
                                                                                                                                                                                                                                                                                                                                                         1189 EKRNQQILKDQVKKEEEELKKEFIEKEAKLHSEIKEKEVGMKKHEENEAKLTMQITALNE 1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                ----FVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIAD---L 1485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1299 CLKGEGEIEKLOTKVLELORKLDNTTAAVOELG------RENQSLQIKHTQAL 1345
                                 1064 NKKKEAEIAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFK 1123
                                                                                                          ::||::|
LENKLQQQLTQAAQELAAEKEKISVLQNNYEKSQETFKQLQSDFYGRESELLATRQDLKS 1051
                                                                                                                                                                                                           1209 QSQPKKPASTHVGAES-----NTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVT 1261
                                                                                                                                                                                                                                                                    1262 GEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNK 1321
                                                                                                                                                                                                                                                                                                                              RENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFAND 1381
875 FFEKENQKGKAAILDLEKTCKELKHQLQVQMENTLKEQKELK-KSLEKEKEASHQLKLEL 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant multivalent protein comprising antigenic determinants derived from more than one stage in a life cycle of Plasmodium vivax, useful as a vaccine for treating, preventing and reducing malarial
                                                  1160 V------IKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSESGSDTLE
                                                                                                                                                                                                                                                                                                                                                                                       VLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Multivalent protein; immune response; Plasmodium vivax; parasite; protozoacide; vaccine; malaria; recombinant; ViVacl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STDYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQC 1537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----VTVRRHHC--RQC 1377
                                                                                         1124 VLSKLEGKL---KDNLNLEKKKLSYLSSGLH-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB85697 standard; Protein; 1807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RKWAEDNEVQNCMACGKGFS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant protein ViVaclp.
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N-PSDB; AAH47058.
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The invention relates to recombinant multivalent proteins (I) that
stimulate an immune response to Plasmodium vivax. (I) comprises antigenic
determinants, fragments or conservative substitutions, derived from more
than one stage in a life cycle of a Plasmodium vivax parasite. (I) is
useful as a vaccine for stimulating an immune response, specifically a
protective immune response that confers increased resistance to infection
by Plasmodium parasites, such as p. vivax. (I) is especially useful in
the treatment, prevention and reduction of malarial infection, as
the treatment, prevention and reduction of malarial infection, as
the treatment, prevention and reduction of malarial infection, as
the treatment, prevention and reduction of malarial parasite. The antibodies produced are useful for
stages of the malarial parasite. The antibodies produced are useful for
the detection or measurement of antigenic epitopes derived from one or
more stages in a life cycle of a parasite, particularly P. vivax. The
vaccine comprising the recombinant proteins, is cost-effective, health-
promoting intervention for controlling, preventing or treating the
incidence of malaria. The present sequence represents the amino acid
sequence of the recombinant protein Vivaclp, a multivalent and
multistage vaccine against P. vivax.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    501. HAASFVMAGDQNSSYRHPAVYDEKEKTCHMLYLSAQENMGPRYCSPDAQNRDAVFCFKPD 560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 GSVASGGSGGSVASG---GSVASGGSVA--SGGSVASGGSGNSRRTNPSDNS-SDSDAKS 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIMANFDSVKKKCYIFNTKPTCLINDKNFIA-----TTALSHPQEVDL----E 721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           341 YYIIFLSAQCLVHIGKCGRNQKPSRLT-RSANNVLLEKGPTVER---STRMSNPWKAFME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245 YLD---KVRATVGT----EWTPCSVTCGVGVRVRRRVNAAYKKPEDL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----VGKMEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         372 PLELEYYLREKNKNIDISAKVETKEST-----EPNEYPNGVTYPLSYND----INNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                561 KNE--SFENLVYLSKNVRNDWD-KKCPRKNLGNAKFGLWVDGNCEEIPYVKEVEAEDLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 FDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYR-----KPLDNIKDN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282 QYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIK-----ELLDKINEIKNP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ^ Match 4.4%; Score 369.5; DB 22; Length 1807; Local Similarity 19.2%; Pred. No. 5.5e-08; les 357; Conservative 272; Mismatches 684; Indels 545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKKI-----ESDKKS-YEDRSKSLNDITKEYEKLLNEIYDSKF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 LNELNSFGDLI -----NPFDYTKEPSKN-
                                            Claim 5; Page 39-45; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1807 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Sim:
Matches 357;
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: : : Db 1709 VDNAAKSPV Qy 1561 QEGDKCVENPN : Db 1754 EEGGKCVPASN	RESULT 53 AAY19935 ID AAY19935 standax XX AC AAY19935; XX DT 19-JUL-1999 (£)	XX DE B. burgdorferi & XX KW Antigenic protes XX OS Borrelia burgdox XX PN W09859071-A1.	XX 30-DEC-1998, XX PF 18-JUN-1998; SX XX 03-SEP-1997; PR 20-JUN-1997; PR 22-JUL-1997; SPR 2			CC invention, which cc an be used in vertice record to the Borrelia get cc the Borrelia get cC infection caused CC be used for detax XX Sequence 1087	Query Ma Sest Loc Matches	Db 1 KLNDKNREIM Qy 321 KINEIKNPPP- ; bb 49 TLAEIANSSP Qy 374 ELEYYLREKN bb 107NYSDRNDD
OY 619 VOKULLMNKIDELKKTQLILKNVELKHNIHV	QY 713 ATTRPGQQAGSALEGDSV	814 993 872 1042	Qy 894	QY 984 ESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLER-LFKKKTVCKYKMQIKKLTLLK 1039 Db 1214 EQEVPQ-DNNVNEPERSDSNGYGVEKVIPNPLDNERDMANKNKTVHPGRK 1263 QY 1040 EQLESKLNSLNNPKHVLQNFSVFFNKKEAEIAETENTKILLKHYK 1089 Db 1264 DSANDKYARPHGSTHVNNRANENSDIPNPVPSOYEOPENKK- KSSNNGYKIAGGVI 1321	1090GLVKY-YN	Qy 1186 KKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDDV 1240 b : : :	OY 1281 YEVLYLRPLAGUYRSLKKOLENNVMTENVVKDILNSŘPNKRENFKNVLESDLIPYK 1337 1	OY 1384 GYYKILSEKYKSDLDSI-KKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLFVIHLEAK 1442 : :: : : : Db 1624 SYDQWITRK-KNQMDVLSNKFISVKNAEKVQTAGIVTPYDILKQELDEF 1671 Qy, 1443 VLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGLADLSTDYNHNNLLTKFLSTG 1502 L672 - NEVAFENEINKRDGAYIELCVCSVEGAKKNTQEVVTN 1708 Qy 1503 MVFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQN\$GCFRHLDEREECKCLLNYK 1560
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represents a Borrelia burgdorferi (Bb) protein of the ch is suitable for use in a vaccine. The Bb polypeptides of vaccines for eliciting protective antibodies to members of fenus, particularly for the use against Lyme disease in manls. They can be used for preventing or attenuating an sed by a member of the Borrelia genus. The products can also stection of members of the Borrelia genus.
TKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLD 320
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                                                                                            orrelia burgdorferi nucleic acids - used to develop
he diagnosis, prevention and treatment of diseases
elia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                  ein; vaccine; Lyme disease; infection; detection.
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rity 21.3%; Pred. No. 3.2e-08;
inservative 208; Mismatches 472; Indels 378.
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|::| | | ::| | | ::| | | | |::| | | |::| | | |::| | | |::| | |::| | |::| |::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| 
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21.3%; Pred. No. 3.3e-08;
tive 208; Mismatches 472;
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                                                                               IADLSTDYNHNN-----1LLTKF 1498
                                                                                                                                    I --- IEYNENNNDQTLRELIKKF 1072
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MEDIMMUNE INC
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the encoded polypeptides (AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM38642-AAM3864AAM3864AAM3864AAM3864AAM3864AAM3864AAM3864AAM3864AAM3864AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM386AAM3
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1029 KAIEIF----EKAIINSDIEAKYNLATTLIEINDNTRAKDLLREYTKLKPNNPEALHALG 1084
                                                                                                                                                                                                                                                                                                                                                                                                                Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance; peripheral nervous system; neuropathy; central nervous system; CNS; Alzhehmer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human nucleic acids (AAI57798-AAI61369) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries
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Yang Y,
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Wehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
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                                                                                                                                                                                                                                      A.
                                                                       1498
                                                                                                                   I----IEYNENNNDQTLRELIKKF 1104
                                                                                                                                                                                                                                   AAM40467 standard; Protein; 1788
                                                                                                                                                                                                                                                                                                                                                                       Human polypeptide SEQ ID NO 5398.
                                                                       IADLSTDYNHNN-----LLTKF
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2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-065345.
2000US-0652191.
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Wang Z, V
Zhou P,
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19-JUL-2000;
03-AUG-2000;
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19-OCT-2000;
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25-APR-2000;
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Wang
Zhao
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TL--QLSFDLYNK---YKLKLERLFDKKKTVGK-
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CARUCCI D.
GARDNER M.
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AAB18315
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                                                                                                                                                                             | | | : : | | | : : | SFIKDLQWIQVSDSK-EAYRLKLGIKHQSVAFTKLNNASSRSHSIFTVKILQIEDSEMS 375
                                                                                                                                                                                                                                                                                                                                                                                                                566 YYKNLISKIENEIETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLM 625
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                                                                                          203 HRSREYLRLSSEQEKEEIASKSALLRQIKEVTVHNDSDDTLYGSLTNSLNISEFEESIKD 262
                                                                                                                171 YEEIN-ELLYKLNF----YFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGY 224
                                                                                                                                                                                                                         ----NIKELL----DKINEIKNPPPANSGNTPNTLLD 342
                                                                                                                                                                                                                                                                       435 HVPFRESKLTHYFQSFFNGKGKICMIVNISQCYLAYDETLNVLKFSAIAQKVCVPDTLNS 494
                                                                                                                                                                                                                                                                                                       343 KNKKIEEHEKEIKEIAKTIKFN--IDSLFTDPLELEYYLREKNKNIDISAKVETKESTEP 400
                                                                                                                                                                                                                                                                                                                              SQEKLFGPVKSSQDVSLDSNSNSKILNVKRATISWENSLEDLMEDEDLVEELENAETE- 553
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                                                                                                                                                                                                                                                                                                                                                                  ---DVGETKLLD-EDLDKTLEENKAF------ISHEEKRKLLDLIEDLKKKLINEKKE 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     648 AIFKDLVGKCD-----TREEAAKDICATKVETEEATACLELKFNQIKAELAKTKGELI 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KTKEELKKRENESDSLIQELETSNKKI----ITQNQ------RIKELINIIDQKEDTI 748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       837 P-----NIAELEDIRVLOE-----NNEGL 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              805 KQYKITKEEESKLSSCDPLDL---LFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVC 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----NLYKLKDNDKIKNLLEEAKKVSTSVKTLSSSSMQPLSLFPQDKPEVSANDDTSHST 917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKBIDKLKVFMPK-VESL 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKIL 804
                                                                                                                                                                                                            KLYQAQYDLSIYN------KQLEEAHNL---ISVLEKRIDTLKKNE----
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                        Length 1788;
                                                441;
                      4.4%; Score 368.5; DB 22; Length ilarity 19.0%; Pred. No. 6e-08; Conservative 266; Mismatches 551; Indels
                                                                   130 HRVRNYL-----LTIKELKYPQLFDLTNH-
1788 AA;
                                   Best Local Similarity
Matches 295; Conserv
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SQ • Sequence
                         Query Match
Best Local 9
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HILLI III HEAKLEQDILEKESIILKLERNLKEFQEHLQDSVKNTKDLNVKELKLKE-EITQLTNNLQ 1205 : | ||: : : |: || || || || : DMKHLLQLKEEEEETNRQETEKLKEELSASSARTQNLNADLQRKEEDYADLKEKLTDAKK 1265 NFKVLSKLEGKLKD-------NLNLEKKKLSYLSSGL---HHLIAELKEVIKNKNYTGNS 1170 LOESEQKYNA------DRKKWLEEKMMLITQAKEAENIRNKEMKKYAEDRERFFK 1464 RENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYN-YIKDSIDTDINFAN 1380 -YKMQIKKL-TLLKEQLESKL 1046 -----VEEAIQQYERACKDLNVKEKIIEDMRMTLEEQEQTQVEQDQVLEAKLEEVERL 1373 -----GAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDNI 1273 LSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTF-----NVNVKDIL-----NSRFNK 1321 human malaria parasite; vaccine; infection; insecticide. NTKILLKHYKGLVKYYNGESSPLK-TLSEESIQT-----EDNYASL----E 1171 PSENNTDVNNALESYKKFLPEGT-----DVATVVSESGSDTLEQSQPKKPASTHV---1374 ATELDRWRVKCNDLETKNNQRSN-----KEHENNTDVLGKLTN-----LQDE NSLNNPKHVLQNFSVFFN--------KKKEAEIAETENTLE Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection Plasmodium falciparum chromosome 2 related protein SEQ ID NO:173 :: : | : | : | : | : | 1514 EIEQLKRIISETSKIETQIMDIKPKRISSADPDKLQTEPLSTSFEISRNKIED 1566 1381 DVLGYYKILSEKYKSD---LDSIKKYINDKQGENEKYLPFLNNIETLYKTVND 1430 Venter Plasmodium falciparum; chromosome 2; antimalarial; malaria; protozoacide; Ā

- - VNNSNMF -

1260 ITKVIFFPVHMKEHDHVMNKNYYNNQY----

Also described are: (1) nucletide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

Vaccines against P. falciparum infection comprising (I) or (II).

CC (I) and (II) are useful for the development of vaccines against

D. falciparum infection. (I) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum (C) (aspecially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum (C) (I) (especially when they can be used to identify drug resistance in flection, or they can be used to identify drug resistance in complexity of the parasite biology, a process hampered by the subsequent identification of proteins encoded by it will help to expand cour understanding of parasite biology, a process hampered by the complexity of the parasite lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB18135 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification. present invention describes proteins and their fragments (I) encoc chromosome 2 of the human malarial parasite, Plasmodium falciparum Disclosure; Page 395-401; 577pp; English.

2380 AA; Sequence

83; EKIVY-----KFLLNNKNFEYIEKQYSSKEDMNELDILVNYYDMKYDKIIEFLKNNGYLK 1199 ----NNNNNIFNN-NIF-----NNNIFNNNMNSCVGVSEKDFISTVASF 1024 876 408 928 YEEEEYEDEGEEYEEEDDDEEED--EEEYGHNNDNQDDEGDKNKTTNEKNKKKKNKNN-- 983 ---EINELLYKLNFYFDLLRAKLNDVCANDYCQI 203 KTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNI 692 711 NKCYFLIENIISNVYKHGCYQKLENILNIELNKYLYEDSYİY--LNNRIGNVFVGITQIL 204 PFNLKIRANEL - - - - DVLKKLVFGYRKPL - - - DNIKDNVGKMEDYIKKNKKTIENINELI -HEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVT EKLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIEN----E -----RNKKCIDG---FF --LEEAHNLI----SVL EKRIDTL--KKN-----ENIKELL-----DKINEIKNPPPANSGNTPNTLLDKNKKIEE------ERKKFIN-----IETLV - - - ENIKKDEEQLFEKKITKDEN - - - KPDEKILEVSDIVKVQVQKVLLMNKIDELK Length 2380; Indels DB 21; Query Match 4.3%; Score 365.5; DB|21; Best Local Similarity 18.7%; Pred. No. 1.2e-07; Matches 344; Conservative 264; Mismatches 600; 877 HKYINNLWIEKDYLFLIENLKDILERKIFDYYTFVKR----YPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDN-EESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQ-----EIKEKI --KIEKKKIESDKKSYEDRSKSLNDITKE-----YEKLLNEIYDSKFNNNIDLTNFE--152 NHMLTLCDNIHGFKYLIDGYE----_ = :: -: 1085 578 633 257 1145 694 818 303 409 984 455 522 488 ò g ô qq ò g ò qq ð QQ ò qq ò g ö g ò 셤 ŏ ò

1: | 1: | : 1603 CLQNDNDKNVNNNFKFIENNGTNEIKKELYRNDMYNDGIINFDINNEYFFRNLNNMNECQ 1662 FFKYTLFDKNDNVFDHINNKDNTDYNKYFYKFENLIIFNYDFTLISKIEDF----YQSNR 1718 ESSPLKTL-----SEESIQTEDNYASLENFK-----VLSKLEGKLKDNLNLEKKKL 1143 SYLSSGLHHLIAELKEVIKN-----A 1181 1543 DKKKKKNDKTIERNESAENKIEKNIIENNYTIDNDKREFNMDNTIKNEKRESENNNKHME KTEGQSDNSEPSTEGEITG--QATTKPGQQAGSALEGDSVQAQAQEQKQAQPPVPVPVF ---KPEVSANDDTSHSTNLNN --LERLFDKKKTV------GKYKMQIKKLTLLKEQ--LESKLNSLNNPKHVLQN ----AETENTLENTKILLKHYKGLVKYYNG | : |: :: | | : :::| | XKKKYKDMRVPYINLHMEQGGDKKGNHENIQHRKNNEVDIVYNNRVEDIRENMN-----LESYKK--FLPEGT-----KKPASTHV ----NNIYSNNN------LYGDDNMNYPTSS---TGKGTPRRLFEGSNNDGNNS 1972 VILSK--SEY-----VRKKRLRYLEGNDSDFVEDLKTNIEDELYDKYKTYFVKNV 2020 YSMRKLFKIALEGSEEKVIKKIYDLGRSDAHLWLFVEYLNVGIYLYKRIYTIYIKLLTVF ESLIYLTNINKKKKKVDISTFLASIEYAVIYVNGNPFDLFKFCNLLVLCYTYYSMPYVKA QTSVLNNNDDHKLGTVYDKNIMNKESVHANGISKELIKNDKTSEKLRKKDEKKKMKKIKK 1427 TVNDKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLAD---FKKNNNFVGIA 2200 NSTSSIDMDI------NNYEKGKIDVR-QNIDYNNKKEDNVNSDHIKRKNR---IK 751 AKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKIT KEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKDND TLQ------LSFDLYNKYKLK-----YKIFDINKKKKKEIFYHLYYIYIYRDILFLLKFVFTLNFCENTK----YKFLKRRENT SIDTDINFANDVLG--YYKILSEKYKSDLDSIKKYI--NDKQGENEKYLPFLNNIETLYK SLK------LFENILSLGKNKNIYQELIGQ--KSSENFYEKILKDSDTF----1294 NTRGDHNNNOTNDNHYNHHYDDTHNNNNNNSKYYKNKNKNKINTENERERK-----ILSKIENEYEVLYLKPLAGVYRSLKKQLENN----VMTFNVNVKDILNSR-------YVVKDPYKF--GAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDN---YNESFINFVKSKADDINSLNDESKR----871 KIKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQD---------LNKEKR----DKFLSSYN----FNKRENFKNVLESD ----LIPYKDLTSSN ----FSVF-FNKKKEAEI-------693 1345 1390 1433 922 1719 1098 1144 1273 1319 2080 1483 1663 1182 2140 1871 1931 963 g g g g ò q δ a g ŏ q Q ŏ δλ Dp ò ŏ ò a ò ò ŏ a q ŏ g ò g δλ a δ δ ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
               2247 KTNKQRNNKEKLKRSISLPL---NLKRTVVKII----NLKNKINLNKNIIDAINNDILKGT 2300
  ---HQCVKKQC 1537
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                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
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1484 DLSTDYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQ--
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-- NKQLEEAHNLISVLEKRIDTLKKNENIKELLDKINEIKNP 328
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                                                                                                                                         PPANSGNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKN-----
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Also described are: (I) nucleotide sequences (II) encoding (I): and (2) vaccines against P. falciparum infection comprising (I) or (II).

C (I) and (II) are useful for the development of vaccines against CC (I) and infection. (I) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, CC useful in the detection of infection with P. falciparum. Furthermore, CC (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in curedation of proteins encoded by it will help to expand or subsequent identification of proteins encoded by it will help to expand or understanding of parasitic biology, a process hampered by the CC complexity of the parasitic lifecycle, and provide new targets for complexity of the parasitic lifecycle, and provide new targets for complexity of the parasitic lifecycle, and provide new targets for complexity of the world, and there is a pressing need for vaccines and mean coresistance to insecticides have led to a resurgence of malaria in many creatings. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide
                                                                                                          1280 EYEVLYLKPLAGUYRSLKKOL.--ENNVMTFNVN-VKDILNSRFNKRENFKNVLESDLIPY 1336
                                                                                                                                           1644
1479 RYKDFYIGLQSQGGGTESAAELEKVRSELEEVNNQLRALKDEHEKITKECDEVKK----R 1534
                                            1220 VGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVV TGEAVTPSVIDNILSKIEN 1279
                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
                                                                   TEPETDTSAIRQEYKAKLDKLVVDLTVART-----DLVNQETTFAGTKSSYDETIARLEK
                                                                                                                              malarial parasite,
vaccines and in the
                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum chromosome 2 related protein SEQ ID NO:62.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteins encoded by chromosome 2 of the human Plasmodium falciparum, useful as antimalarial
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CARUCCI D.
GARDNER M.
VENTER J C.
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and protein sequences given in the present invention, but which are not specifically mentioned within the specification.
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4.3%; Score 302.3; De 21.
Best Local Similarity 20.0%; Pred. No. 1.1e-07;
Matches 317; Conservative 262; Mismatches 574;
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963 NL------IKKENSYAAEMNVGLVFRKYIPILINLSCNYLLIKKNEKNVITCISYTNII 1015
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                                                     ---LONFSVF----FNKKKEAEIAETE-----NTLENTKILLKHYKGLVKYYNGESS 1100
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                  845 QDEELCSNNILVKDIEEKKMCGKLFFEEICVFRINEKNEHGHENLRKNNHNDDTHKMYSS 904
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CARUCCI D.
GARDNER M.
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The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, Also described are: (I) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

Cand (II) are useful for the development of vaccines against P. falciparum infection or a monochonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) despecially when they are rifins or secreted or membrane proteins) can aid the identification of infection with P. falciparum. Furthermore, infection, or they can be used to identify drug resistance in infection, or they can be used to identify drug resistance in confiction of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasite infection, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70287 en AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification.
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                                                                                       Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 KKRFDKFNDIYEIITNHKNKQPHIKENNIK---YITRN----VWYDRLSVDEKKKKNDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 KGNDNRLGVSSTSNDKKKNNKKRYNNNNNNDNNNDINNDCNNNKYNPCCSSCNGNVLSSS
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  Venter JC;
                                                                                                                                                                                      Disclosure; Page 312-316; 577pp; English.
  Gardner M,
Carucci D,
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ογ	632	KKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKN 691
QQ	544	RGQKIGQEKKHKKKDENKKKOPKN 568
Οy	692	IKTEGOSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQAQPPVPVPEA 751
qq	569	KNKNNNNSNNINNKHGRVIQYTDEKIQNDYCKNKESSKRGNHKMMRK 615
οy	752	KAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYI-CHKYILVS 795
ор	616	GRKGEKYIY
δy	196	HSTMNEKILKQYKITKEEESKLSSCDPLDLLFNIONNIP 834
g	675	HKRNNILNEENFIKEHQINGRNKEHVNEKNKEEDTFNISKENTKEGSYIITHKNKRNMDN 734
δy	835	VMYSMPDSLNNSLSQLFMEIYEKEMVCN-LYK-LKDNDKIKNLLEE 878
QΩ	735	IKIGRYDNINDKKEFSSNILYKCVKKNDKINKSQTSLFFEFMKGKGDQKH 784
λo	879	KPEVSANDDTSHSTNLNNS
qq	785	NVIKKEDVEIKTFRTNK-SPTELTKKISDYKCNLLYTSLDRIHKNV 829
ογ	937	NIYQELIGQKSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDESK 986
g	830	SIXNERIERTKHVPQKKNDNIDIRGIYKSYNFFKSMNMMNSLSKCYHT 877
ΟŊ	486	RKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKLTLLKE 1040
DP,	878	KTCDYSNYDFMKNKMSKKAQNKLVSKCISKYKKKAIKKKERERETTTTKKKYIYRKNEISI 937
ογ	1041	QLESKLINSLANPKHVLQNFSVFFNKKKBABIAETENTKILLKHYKGLVKYYNGESS 1100
qq	938	SFDGNVFGHENRKRTKENNKSKESAYTSKSRKNNKIKGEEKKTKRSLCSYKLR 990
οy	1101	PLKTLSEESIQTEDNYASU-ENFWLSKLEGKLKDNLN 1137
qq	991	KWKHLCVENKMHIKKNVRQIIKKKKKNIYKTIKCLNSYKTLIDOVNVKGDEBHKLSNHVN 1050
ογ	1138	LEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVN-NALESYKKFLPEGTDVA 1196
QQ	1051	NKKKKKKNCINENNDDNNNDNYNDNNNDNYNDNNNDNY 1092
οy	1197	EQSOPKKPASTHVGAESNTITTSONVDDEVDDVIIVPI
qq	1093	NDNNNDHNDHNNNDNNNDLNNDHRNDNNQREHSCEEI 1129
οy	1257	GQVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVK 1312
Op	1130	NIQNVEQKCEGEKYEGKRKNKYTYYNNYKINGKNEIHDDYNIKSHGS 1177
Οÿ	1313	DILMSRENFRNENFKNVLESDLIPYKDLTSSNYVVKDPY 1350
qq	1178	RINYNIFNIKDNKHNNNDKGEKSCELKKCSIPYVEKYNLENNTYEIIGLIYYGDKSQVY 1237
Οy	1351	KFLNKEKRGYYKILS 1390
QQ	1238	KCINMNNKRVYAMKVVLKECNEIFVDNFIKKYLFLKNNPHKNIISIYDIFCNNNYICIIM 1297
οy	1391	۵
Op	1298	D-YCEGSTLLDYFMSLVPGSLDVYEIKKIMKNIFIALDFFHSNNIHRDIKLENI 1351
٥y	1447	TYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLSTDYNHNNLLTKFLS-TGMVF 1505
op D	1352	MFKNKKRKKKRRNYEKYGSFLFNNHEEISFSTSCSNLHKKDLQLRGM 1398
٠ مy		EINLAKTVLSNLLDGNLQGMLNISQHQCVKRQCPQNSGCFRHLDEREECKC 1555
Dp	1399	

Qy 1556 LLNYKQEGD 1564 : | | | Db 1456 YIKYNNNMD 1464 Search completed: March 31, 2003, 07:20:42 Job time : 161 secs

Q25645 plasmodium Q9u6d4 plasmodium Q25665 plasmodium Q25668 plasmodium Q25924 plasmodium Q03999 plasmodium Q9bmg8 plasmodium Q9bmg8 plasmodium Q9bmg75 plasmodium Q55975 plasmodium Q55975 plasmodium Q55975 plasmodium Q55975 plasmodium Q55975 plasmodium Q5000000000000000000000000000000000000		Q25665 plasmodium Q9tzu2 plasmodium Q9tzu7 plasmodium Q9tzu7 plasmodium Q9tzu9 plasmodium Q9tzu9 plasmodium Q9tzu1 plasmodium Q9tzu1 plasmodium Q9tzu1 plasmodium Q9tzu1 plasmodium Q9tzu1 plasmodium Q9tzu4 plasmodium Q9tzu6 plasmodium Q9tzu7 plasmodium Q9tzu7 plasmodium Q9tzu9 plasmodium	09tzu0 plasmodium 09tzu4 plasmodium 09tzw4 plasmodium 09tzw4 plasmodium 09tzw4 plasmodium 09tzw6 plasmodium 09tzw9 plasmodium 09tzv9 plasmodium 09tzv9 plasmodium 025724 plasmodium 025725 plasmodium 025722 plasmodium 025722 plasmodium 025722 plasmodium 09ncm4 plasmodium 09ncm2 plasmodium 09ncm2 plasmodium 09ncm2 plasmodium 09ncm2 plasmodium 025719 plasmodium 025719 plasmodium 025719 plasmodium 025719 plasmodium 025771 plasmodium 025777 plasmodium 025777 plasmodium 025777 plasmodium
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                                                                                                                                                                                                                                                                                     TEEDSGSNGKKITCECTKPDSYPLFDGIFCSSSNFLGISFLLILMLILYSFI 1639
                                                                                                                                                                                                                                                                                                      1653 TEEDSGSNGKKITCECTKPDSYPLFDGIFCSSSNFLGISFLLILMLILYSFI 1704
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Shan Z.X., Yu X.B., Li X.R., Ma C.L., Fang J.M.;
"Molecular cloning and sequence analysis of major merozoite
antigen(gpl95)gene of Plasmodium falciparum isolate FCC1/HN.
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF218248; AAF27526.1;
InterPro; IPR00063; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium
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                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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   YIKDSIDTDINFANDVLGYYKILSEKYKSDLDSIKKYI
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01-OCT-2000 (
01-JUN-2002 (
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SEQUENCE
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Q9NHX1
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NDKQGENEKY 1414
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SERVAIN-HNI;
Jiang G., Liu R., Daubenberger C.A., Pluschke G.;
Sequence analysis of the MSP 1 gene of Plasmodium falciparum from "Sequence analysis of the MSP 1 gene of Plasmodium falciparum from Hainan, China.";
Chung Kuo Chi Sheng Chung Hsueh Yu Chi Sheng Chung 17:294-297(1999).
EMBL; APO62448; AAC72884.1;
TinterPro; IPR000561; EGF-11ke.
Pfan; PP00008; EGF: 1.
SEQUENCE 1694 AA: 192795 MW; 84CFCOE709F5673B CRC64;
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                                                                   KNNNFVGIADLSTDYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVK
                                                                                                                       KOCPONSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGS
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                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Merozoite surface protein 1.
MSP1.
Plasmodium falciparum.
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCB1_TAXID=5833;
                                                                                                                                                                                                                 NGKKITCECTKPDSYPLFDGIFCSSSNFLGISFLLILMLILYSFI 1639
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 TDINFANDVLGYYKILSEKYKSDLDSIKKYI
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Q9TZT5;
01-MAY-2000 (
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KTIKENIDSLFTDPLELEYYLREKNKNIDISAKVETKESTEPN-EYPNGVTYPLSYND 	INNALNELNSFGDLINPFDYTKEPSKNIYTDN-ERKKFINEJKEKIKIEKKKI	ESDKKSYEDRSKSLNDITKEYEKLLNEIVDSKFNNNIDLTNFEKMAGKRYSYKVEKLTHH :	NTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYRNLISKIENEIETLVENIKK	DEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELK :	HNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEPS :	TEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQAQPPVPVPVPEAKAQVPTPPAPV	NNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEE	ESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFWEIYEKEWVCNLYKLKDNDKIK :::	NLLEEAKKYSTSVKTLSSSSMQPLSLTPQDKPEVSANDD ::	TSHSTULNNSLKLFENILSLGKNKNIYQEL-IGQKSSENFYEKILKDSDTFYNESF 	TNFVKSKADDINSLNDESKRKLEEDINKLKKTLQLSFDLYNKYKLKLEELFDKKKTVGK : ::: ::	YKMQIKKLTLLKEQLESKLNSLNNPKHVLONFSVFFNKKKEAETAETENTLENTKILLKH 	YKGLVKYYNGESSPLKTLSEESIOTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLS 	SCLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKELPEGTDVATVVSE	SGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDDIVJFFGESEEDY	DDLGQVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKD :	ILNSREKKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSID : : : : :: : :
359 355	416	468	528	588 590	645	705	763	814	874	913	968	1028	1088	1148	1202	1254 1292	1314
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-----NDKQGENEKY 1414
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STRAIN=NF54;
MEDLINE-96123395; PubMed=8577332;
Pan W., Tolle R., Bujard H.;
"A direct and rapid sequencing strategy for the Plasmodium falciparum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Precursor of the major merozoite surface antigens.
Plasmodium falciparum (isolate NF54).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TAXID=5843;
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SEQUENCE 1720 AA; 195725 MW; 717B2FD1E637A8A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases
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Mol. Biochem. Parasitol. 73:241-244(1995).
EMBL, 235327; CAA84556.1;
Pfterpro; IPR000561; EGF-like.
Pfam; PF00008; EGF; 1.
Merozoite; Signal.
1374 TDINFANDVLGYYKILSEKYKSDLDSIKKYI---
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Tolle R., Bujard H., Cooper J.A.;
Exp. Parasitol. 0:0-0(1995).
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Tolle R.;
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Tue Apr 1 10:57:16 2003

QY 61 AVTTSTPGSKGSVASGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDS 120 Db 51	Db 127 INFHYDLIRAKLHDMCAHDYCKIPEHLKISDKELDMLKKVVLGYRKPLDNIKDDIGKLET 186 Qy 241 YIKKNKKTIENINEL-IEESKK	Db 307 LORAQKLIAVUEKRYVUKEHKDIKVULEQVAKEKEKLPSDYPNTTULTNVHKEAESKIA 366 Qy 349 EHEKEIKETAKTIKFNIDSLFTDPLELEYYLREKNKNI-DISAKVETKESTEPNE 402	Db 486 IMNKIKIEEDKIPDLKKEYEEKYKVYEAKVDEYRPAHFYEARLDNTLVENKFDDFKKK 545 Qy 516 RYSYKVEKLTHHNTFASYENSKHULEKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIE 575	691NIKTEGOSDNSEPSTEG	QY 830 QNNIPVMYSMPDSLANSLSQLFMEIYEKEMYCNLYKLKDND-KIKNLLEBAKKVS 883
	320 DKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLETDPLELEYYL 1111111111111111111111111111111	500 FUNNIDLTNPEKMAGKRYSYKVEKLTHHNTFASYENSKALDUINGIERLEN 500 FUNNIDLTNPEKMAGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYMEDYK 111111111111111111111111111111111111	SULT 6 1194 Q26194 PRELIMINARY; PRT; 1751 AA. Q26194: 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) PV200 protein precursor. Plasmodium vivax. Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.	1 8 1 1 · · D 1 0	Oue Mat Mat

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Olafsson P., Matile H., Certa U.;
Plasamodium falciparum: the repetitive MSA-1 surface protein R0-71 isolate is recognized by mouse antibody against the nonrepetitive repeat block of R0-33.";
Exp. Parasitol. 74:381-389(1992).
Exp. Parasitol. 74:381-389(1992).
InterPro: IPR000087; Collagen.
NON_TER 1087
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Major surface antigen (Fragment).
Plasmodium falciparum.
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
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SEQUENCE FROM N.A.
STRAIN-RO-71;
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                                                                                              VAVSSGPAVVEESHDPLTVLSISNDLKGIVSLLNLGNKTKVPNPLTISTTEMEKFYENIL
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                                                                                   ----GTSGTAVTTSTPGSKGSVASGGSGSVASGGSVASGGSVASGGSVASGGSGNS
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 Length 1087
                                          1 MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNE--
                     Indels
 DB 5;
35.7%; Score 3003.5; DB llarity 57.4%; Pred. No. 1.8e-86; Conservative 147; Mismatches 238
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                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BELEM;
MEDLINE-91219506; PubMed-2023952;
Mel Portillo H.A., Longacre S., Khouri E., David P.H.;
Primary structure of the merozoite surface antigen 1 of Plasmo vivax reveals sequences conserved between different Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 36.9%; Pred. No. 1.2e-84;
Matches 678; Conservative 324; Mismatches 518; Indels 316;
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                                                                                                                                                                                                                                                                                                                                        Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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18 1726 MEROZOITE SURFACE ANTIGEN 1.
1726 AA; 194434 MW; BAODCD8333C6C727 CRC64;
                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Merozoite surface antigen 1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 88:4030-4034(1991)
EMBL; M60807; AA563427.1; -.
Interpro; IPR000561; EGF-like.
Pfam: PF00008; EGF; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.0%; Score 2951; DB 5; 36.9%; Pred. No. 1.2e-84;
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Best Local 9
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Jongwutiwes S., Tanabe K., Kanbara H.;
"Sequence conservation in the C-terminal part of the major merozoite surface proteins (MSP1) of Plasmodiu; field isolates.";
Mol. Blochem. Parasitol. 59:95-100(1993).
EMBL, D13360; BAA02621.1;
InterPro: IPR000561; EGF-like.
InterPro: IPR001245; Tyr_pkinase.
Pfan, PP00008; EGF:
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
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Matches 538; Conservative
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NCBI_TaxID=5833;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
101-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Major merozoite surface protein (Fragment).
MSP1.
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llarity 100.0%; Pred. No. 1.8e-80;
Conservative 0; Mismatches 0;
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EMBL, D13158; BAA02619.1; -.
InterPro: IPR001545; EGF-like.
Pfam; PF00008; EGF: 1.
PROSITE; PS00109; PROTEIN_KINASE_IYR; 1.
EGF-like domain; Merozoite.
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MEDLINE-913295445; Pubwed-8515786;
MODULIWES S., Tanabe K., Kanbara H.;
"Sequence conservation in the C-termina
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99.8%;
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Matches 538; Conservative
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"Sequence conservation in the C-terminal part of the precursor to major merozoite surface proteins (MSP1) of Plasmodium falciparum field isolates.";
Mol. Biochem. Parasitol. 59:95-100(1993).
BMBL; D1337; BAA0261B.1; -.
Interpro; IPR001045; Tyr_pkinase.
Pfam; PF00008; EGF: 1.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Major merozoite surface protein (Fragment).
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Pred. No. 2.6e-80;
0; Mismatches 1;
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les 538; Conservative
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Jongwuliwes S., Tanabe K., Kanbara H.;
Sequence conservation in the C-terminal part of the precursor to the major merozoite surface proteins (MSP1) of Plasmodium falciparum from field isolates.";
Mol. Biochem. Parasitol. 59:95-100(1993).
EMBL; D13361; BAA02622.1;
EMBL; D13361; BAA02622.1;
InterPro; IPR001245; Tyr.pkinase.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
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NCBI_TaxID=5833;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Major merozoite surface protein (Fragment).
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Jongwutiwes S., Tanabe K., Kanbara H.;
Sequence conservation in the C-terminal part of the precursor to the major merozoite surface proteins (MSP1) of Plasmodium falciparum from field isolates.";
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20, Last annotation update)
protein (Fragment).
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EMBL; D13362; BAA02623.1; -.
InterPro; IPR001561; EGF-11ke.
PrinterPro; IPR001245; Tyr_pkinase.
Pfam; PF00008; EGF:
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
EGF-11ke domain; Merozoite.
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01 MAR-2002 (TrEMBLrel.
Major merozoite surface i
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538; Conserv
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01-NOV-1996
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Jongwutiwes S., Tanabe K. Kanbara H.;
Jongwutiwes S., Tanabe K. Kanbara H.;
Sequence conservation in the C-terminal part of the precursor to the major merozoite surface proteins (MSP1) of Plasmodium falciparum from filed isolates.";
Mol. Blochem. Parasitol. 59:95-100(1993).
EMBL; D13363: BAA02624.1;
EMBL; D13363: BAA02624.1;
InterPro: IPR001545; Tyr_pkinase.
Pfam: PF00008; EGF:1ike.
InterPro: IPR001155; Tyr_pkinase.
FGF-like domain; Merozoite.
NOM_TER 1 1
SEQUENCE 539 AA; 61046 MW; 3EED87473EE87B65 CRC64;
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CDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSSNFLGISFLLILMLILYSFI 1639
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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Last annotation update)
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01, Last sequence upo
20, Last annotation of protein (Fragment).
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Matches 537; Conservative
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PRELIMINARY;
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                                                                                Eukaryota; Alveo.
NCBI_TaxID=5833;
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"Sequence conservation in the C-terminal part of the precursor to amajor merozoite surface proteins (MSP1) of Plasmodium falciparum field isolates.";
Mol. Biochem. Parasitol. 59:95-100(1993).
BMBL; D1336; BAA02617.1;
InterPro; IPR000561; EGF-like.
InterPro; IPR000261; EGF-like.
Pfam; PF00008; EGF; 1.
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                                                                                                     Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                               539 AA; 61115 MW; 3788015F3127CB9E CRC64;
                                                01, Created)
01, Last sequence update)
20, Last annotation update)
protein (Fragment).
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Pred. No. 4.2e-80;
0; Mismatches 2;
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                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=93295445; Pubmed=8515786;
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99.6%;
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01-NOV-1996 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
Major merozoite surface
                            PRELIMINARY;
                                                                                                    Plasmodium falciparum.
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RESULT 16

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                                                                                                                                                                    Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                           Last sequence update)
Last annotation update)
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99.6%; Pred. No. 4.6e-80;
live 0; Mismatches 2;
                                            01-NoV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence v
01-NAR-2002 (TrEMBLrel. 20, Last annotation
Major merozoite surface protein (Fragment).
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-92295445; PubMed-8515786;
Jongwutiwes S., Tanabe K., Kanbara H.;
"Sequence conservation in the C-terminal
539
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EMBL; D13359; BAA02620.1; -.
InterPro; PR0000561; EGF-like.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF000008; EGF; I.
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                                                                                                       Toebe C.S., Clements J.D., Cardenas L., Jennings G.J., Wiser M.F., "Evaluation of Immunogenicity of an oral Salmonella vaccine expressing recombinant Plasmodium berghei merozoite surface protein-1."; Am. J. Trop. Med. Hyg. 56:192-199(1997).
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                                                                                                                                                                                Jennings G.J., Toebe C.S., van Belkum A., Wiser M.F., The complete sequence of Plasmodium berghei merozoite surface protein-1 and its inter- and intra-species variability."; Mol. Biochem. Parasitol. 93:43-55(1998).
                                                                                                                                                                                                                                                                                                                    364;
                                                                                                                                                                                                                                                                                                   Length 1787;
                                               Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                               Wiser M.F., Jennings G.J.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
EMBL: U43521; AAC28871.1; -
SEQUENCE 1787 AA; 198156 MW; AS85D64F5148B4EA CRC64;
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Pred. No. 1.4e-71;
  01, Created)
05, Last sequence up
19, Last annotation
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                                                                                                                                                             STRAIN=K173;
MEDLINE=98324404; PubMed=9662027;
                                                                                              MEDLINE=97235961; PubMed=9080880;
                                                                          SEQUENCE OF 219-373 FROM N.A.
01-NOV-1996 (TrEMBLrel. 01, 01, 01-JAN-1998 (TrEMBLrel. 05, 101-DEC-2001 (TrEMBLrel. 19, Merozoite surface protein-1.
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32.0%;
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SEQUENCE FROM N.A.
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                                                        NCBI_TaxID=5821;
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1061 TLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENTLENTKILLKHYKGLVKYY 1095 SILKARLLKRKQNINGIFYILSGYVNFFNKRREADKQYVDNALKNNDMLLKYYKARIKYF 1239 NGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIA 1155 595 611 671 DKLKVFMPKVESLINEEKKNIKTE-----GQSDNSEPSTEGEITGQATTKPGQQAGSAL 725 942 KSILVKAGVIDPEPVASPPTPPTPPTPPTLPTTPTPTPTPAAPSEQTTTPEAATAASN 1001 ELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEG-------TDVAT--- 1197 | ||::||||||| : : :| || || ||: ||:|| EFKELLKNKNYTGKTNPDTVPEVTNAFEQYKELLPKGVTASASPAAATTPTSADAATQRA 1359 ---VVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYD 1254 537 761 758 821 DLGQVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDI 1314 LNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYME DYSLRNIVVEKELKYYKNLISKIENEIETLVENIKKDEEQLFEKKITKDENKPDEKILEV SDIVKVQVQKVLLMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEI DRLAQFIPKIENMIAKEKE--KTEQVPVVTGESEETS-SVSTEVSVQASSQSGTSSTVPA 762 AGAISPIVIPVIEEAQSSQNAPPITAATPATTPEAATTAATPATPEAATTSITISI TISTITETITEVMTKLYLEKLÖKFLVFSYSCHKYLLLQNSTINKDALSKYALITEEDK --KLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKD-NDKI -----LGKNKNIYQELIGQK-----SSENFYEKILKDSDTFYNESFTNFVKSKA ------KKVSTSVKTLSSS DDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKL ---PAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEES TPESGSGSGSGSVVSSTPEEVARS--GSGENAVVSGSSVDD-----NDDD 1375 D-----INFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKT LNSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDT EGDS-----VQAQAQEQKQAQP---PVPVPVPEAKAQVPTP-----VQAQAEQKQAQP SMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFENILS-

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                                             RHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECT 1604
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Merozoite surface antigen 1.
Plasmodium berghei (strain Anka).
Bukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TAXID-5823;
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--TLLDKNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKN
                   361 NTNTEVTQVQTVPTLTPEEKKKKKMDGLYAQIKEIAKTIKFNLDGIFVNPIELEYFKKEKK
                                                                    K---NIDISA--KVETKESTEP--NEYPNGVTYPLSYNDI-----NNALNELNSFGDLIN
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Merozoite surface protein-1 precursor.
Plasmodium chabaudi.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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"Nucleotide sequence analysis and epitope mapping of the new protein 1 from plasmodium chabaudi chabaudi AS.";
Mol. Biochem. Parasitol. 62:199-210(1993).
EMBL; L22982; AAA29499.1;
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"Plasmodium falciparum: the repetitive MSA-1 surface protein
RO-71 isolate is recognized by mouse antibody against the
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Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Tolle R., Bujard H., Cooper J.A.;

"Plasmodium falciparum: variations within the C-terminal region of merozoite surface antigen-1.";

Exp. Parasitol. 18.147-54(1995).

EMBL; 235329; CAA84558.1; -.

InterPro; IPR000561; EGF-1ike.

Pfam: PF00008; EGF-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      651 AA; 74134 MW; AA2137E699255150 CRC64;
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    RO-33.";
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repeat block of RO
1. 74:381-389(1992)
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01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 101, 101-NOV-1996 (TrEMBLrel. 19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11-19, 11
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                                    Exp. Parasitol.
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538 LNISQHQCVKKQCPENSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDAD 597
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                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                              Peterson M.G., Coppel R.L., McIntyre P., Langford C.J., Woodrow G., Brown G.V., Anders R.F., Kemp D.J.; "Variation in the precursor to the major merozoite surface antigens Plasmodium falciparum."
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                                                                                                                                                                                                                                region
                                                                                                                                                                                                                                                                                                                         25.2%; Score 2119.5; DB 5; Length 652; 63.8%; Pred. No. 3.8e-59;
          Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                    Tolle R., Bujard H., Cooper J.A.; "Plasmodium falciparum: variations within the C-terminal
                                                                                                                                                                                                                                                                                                                                              84; Mismatches 116; Indels
                                                                                                                                                                 Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                    652 AA; 74292 MW; 2B6A87737B490A62 CRC64;
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                                                                                                             Biochem. Parasitol. 27:291-302(1988).
                                                           MEDLINE-88142999; PubMed-2449612;
                                                                                                                                                                                                         MEDLINE=95354793; PubMed=7628566;
                                                                                                                                                                                                                                       merozoite surface antigen-1.";
Exp. Parasitol. 81:47-54(1995).
EMBL: 253228; CAA84557.1; -.
InterPro: IPR000561; EGF-11ke.
Pfam; PF00008; EGF: 1.
                                         SEQUENCE OF 1-298 FROM N.A.
                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 63.8%
Matches 418; Conservative
Plasmodium falciparum
Eukaryota; Alveolata;
                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                 SEQUENCE FROM N.A.
                    NCBI_TaxID=5833;
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1360 KFLSSYNYIKDSIDTDINFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLN 1419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein-1 produces a membrane-bound fragment containing two epidermal
growth1 factor-like domains.";
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400;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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MEROZOITE SURFACE PROTEIN 1.
MEROZOITE SURFACE PROTEIN 1.
377F075058626AC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-1991) to the EMBL/GenBank/DDBJ databases EMBL, M4681, AAA29709.1. .
InterPro: IPR00561; EGF-11ke.
InterPro: IPR001245; Tyr_Pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blackman M.J., Ling I.T., Nicholls S.C., Holder A.A.; "Proteolytic processing of the Plasmodium falciparum 1
                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Merozoite surface protein 1 precursor (Fragment).
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Pred. No. 8.8e-59;
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100.0%; Pred. No. c...
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PROSITE, PS00109; PROTEIN_KINASE_TYR;
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KILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKK 1141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-93295445; PubMed-8515786;
MEDLINE-93295445; PubMed-8515786;
MEDLINE-93295445; PubMed-87186;
Mandouvitiwes S., Tanabe K., Kanbara H.;
Sequence conservation in the C-terminal part of the precursor to the major merozoite surface proteins (MSP1) of Plasmodium falciparum from field isolates.";
MOL. Biochem. Parasitol. 59:95-100(1993).
EMBL; D1349; BAA02510.1;
EMBL; D1349; BAA02510.1;
PinterPro; IPRO00561; EGF-like.
Pfam: PF00008; EGF.
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                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   902 QDKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQELIGQKSSENFYEKILKDSDT
                                                                                                                                                                                                                                                                                                                                  1022 KKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENTLENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "38 kDa subfragment of MSP-1 gene of FCB-1 strain of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36;
                                                                                                                                                                    ;
0
                                                                                                                                     Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum.
Eukaryota; Alveelata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                    Indels
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                  falciparum.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF286876; AAF87595.1;
                                                                                                     9A5E9DE65E5A680B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1161 IKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               569 AA; 64459 MW; ED4284B2867C9703 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAX-2002 (TrEMBLrel. 20, Last annotation update)
Major merozoite surface protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.1%; Score 1778; DB 5; 60.8%; Pred. No. 1.5e-48; iive 79; Mismatches 109;
                                                                                                                                  Score 1818; DB 5;
Pred. No. 5.2e-50;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                     360 AA; 40993 MW;
                                                                                                                                  21.6%;
illarity 99.7%;
Conservative
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                                                                                                                                                   Best Local Similarity
Matches 359; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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SEQUENCE
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Q25975;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1264 AVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRE 1323
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                                                                                                                                  Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                          Li X.R., Goel V.K., Liu S.C., Chishti A.H., Oh S.S.;
"42 kDa subfragment of MSP-1 gene of Plasmodium falciparum
isolate.";
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NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                            Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF325919; AAK07641.1; -. InterPro; IPR001245; Tyr_pkinase. InterPro; IRR011245; Tyr_pkinase. Pfam; PF00008; EGF; I. PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 376 AA; 43218 MW; EB2A72EDF231A5AF CRC64;
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Last sequence update)
Last annotation update)
                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Merozoite surface protein 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                            23.5%; Score 1979; DB 5;
100.0%; Pred. No. 5.2e-55;
tive 0; Mismatches | 0;
376 AA
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Goel V.K., Liu S., Chisthi A.H., Oh S.S.
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 PRT;
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01-0CT-2000 (TrEMBLrel. 15, Ls
01-0CT-2000 (TrEMBLrel. 15, Ls
Merozoite surface protein 1 (1
MSP-1.
Flasmodium falciparum.
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Matches 376; Conservative
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 PRELIMINARY;
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                                                                                                               Plasmodium falciparum.
                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-FCB-1;
                                                                                                                                Eukaryota, Alveo.
NCBI_TaxID=5833;
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RESULT 25 Q9NAT3

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PLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEV 1160
                                                                                          PSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFK 1326
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                             180 VT-MDNILSGFENEYDVIYLKPLAGVYRSLKKQIEKNIITFNLNLNDILNSRLKKRKYFL 238
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MEDLINE=93295445; PubMed=8515786;
Jongwutiwes S., Tanabe K., Kanbara H.;
Sequence conservation in the C-terminal part of the precursor to major merozoite surface proteins (MSPI) of Plasmodium falciparum field isolates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36;
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Pukarvota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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20, Last annotation update)
protein (Fragment).
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EMBL; D13350; BAA02611.1; -.
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Pfam; PF00008; EGF; 1.
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Best Local Similarity 60.79
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01-NOV-1996 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
Major merozoite surface
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SEQUENCE
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                                              1207 LEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVT 1266
                                                                                                          PSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFK 1326
                                                                                                                                                                                                                                    -----NDKQGENEKYLPFLNNIETLYKT 1427
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STREETQIPTSGSLLTELQQVVQSQNYDEEDDSLVVLPIFGESEDNDEYLDQVVTGEAIS 179
                                                                                                                          180 VT-MDNILSGFENEYDVIYLKPLAGVYRSLKKQIEKNIITFNLNLNDILNSRLKKRKYFL 238
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of Plasmodium falciparum
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Major merozoite surface protein (Fragment).
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Jongwutiwes S., Tanabe K., Kanbara H.;
Sequence conservation in the C-terminal panador merozoite surface proteins (MSP1) of I field isolates.";
Mol. Biochem. Parasitol. 59:95-100(1993).
EMBL. D13466; BAAQ2607.1;
InterPro; IPR000561; EGF-like.
Pfam; PF00008; EGF; 1.
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Matches 347; Conservative
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Eukaryota; Alveolata;
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60.5%; Pred. No. 3e-48;
ive 79; Mismatches 111;
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MEDLINE=93295445; PubMed=8515786;
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Eukaryota; Alveolata;
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MEDLINE-93205445; PubMed=8515786;
Jongwutiwes S., Tanabara H.;
Sequence conservation in the C-terminal part of the precursor to the major merozoite surface proteins (MSPI) of Plasmodium falciparum from field isolates.";
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                 STREETQIPTSGSLLTELQQVVQLQNYDEEDDSLVVLPIFGESEDNDEYLDQVVTGEAIS
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                                                                                          NVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYY
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Major merozoite surface protein (Fragment).
MSP1.
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BMBL; D13348; BAA02609-1; -.
InterPro; IPR000561; EGF-like.
Pfam; PF000008; EGF:
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"Sequence conservation in the C-terminal part of the precursor to the major merozoite surface proteins (MSP1) of Plasmodium falciparum from field isolates.";
Mol. Biochem. Parasitol. 59:95-100(1993).
EMBL: D13352: BAA02613.1; -.
InterPro: IPR000561; EGF-11ke.
Pfam; PF000008; EGF; L DDTKKDMLGKLLSTGLV-QNFPNTIISKLIEGKFQDMLNISQHQCVKKQCPENSGCFRHL VNDKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLST DYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQNSGCFRHL 36; Length 569; Alveolata; Apicomplexa; Haemosporida; Plasmodium Indels A2691FE569E80396 CRC64; 01, Created) 01, Last sequence update) 20, Last annotation update) IKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSE---δ

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PSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFK 1326
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STREETQIPTSGSLLTELQQVVQLQNYDEEDDSLVVLPIFGESEDNDEYLDQVVTGEAIS 179
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NCBI_TaxID=5833;
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Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence u
01-NOV-1996 (TrEMBLrel. 01, Last sequence u
01-MAR-2002 (TrEMBLrel. 20, Last annotation
Major merozoite surface protein (Fragment).
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EMBL; D13344; BAA02605.L; -.
InterPro; IPR000561; EGF-like.
Pfam; PF00008; EGF; I.
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"Sequence conservation in the C-terminal part of the precursor to major merozoite surface proteins (MSP1) of Plasmodium falciparum field isolates.";
                                                         KILSEKYKSDLDSIKKYI--------NDKQGENEKYLPFLNNIETLYKT
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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EMBL; D13355; BAA02616.1; -.
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01-NOV-1996 (TrEMBLrel. 01, Last sequ
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Pfam; PF00008; EGF; 1.
EGF-like domain; Merozoite.
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SEQUENCE FROM N.A.
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MEDLINE-93295445; PubMed-8515786;
Jongwutiwes S., Tanabe K., Kanbara H.;
"Sequence conservation in the C-terminal part of the precursor to the major merozoite surface proteins (MSP1) of Plasmodium falciparum from field isolates.";
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                                                                                                             EKVLAKYKDDLESIKKVIKEEKEFPSSPPTTPPSPAKTDEQKKESKFLPFLTNIETLYNN 358
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          359 LVNKIGDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNTDDFEAIKKLIN
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                                                                                       1387 KILSEKYKSDLDSIKKYI--------NDKQGENEKYLPFLNNIETLYKT
                                                                                                                                    VNDKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQÖKLADFKKNNNFVGIADLST
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Last sequence update)
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Eukaryota; Alveolata; Apicomplexa; Haemosporida;
NCBL_TaxID-5833;
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. 20, Last annotation
. protein (Fragment).
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EMBL: D13345; BAA02606.1; -.
Interpro: IPR000561; BGF-like.
Pfam: PF00008; EGF: I.
EGF-like domain; Merozoite.
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01-NOV-1996 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
Major merozoite surface
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345; Conserv
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PSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFK 1326
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Plasmodium falciparum f
                       NVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYY
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Major merozoite surface protein (Fragment).
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Jongwutiwes S., Tanabe K., Kanbara H.;
"Sequence conservation in the C-terminal part of
major merozoite surface proteins (MSP1) of Plasmo
field isolates ";
Mol. Biochem. Parasitol. 59:95-100(1993).
EMBL; D13354; BAA02615.1;
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Pfam; PF00008; EGF; 1.
EGF-like domain; Merozoite.
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NCBI_TaxID=5833;
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Matches 344;
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NVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYY 1386
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EKVLAKYKDDLESIKKVIKEEKEFPSSPPTTPPSPAKTDEQKKESKFLPFLTNIETLYNN 358
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MEDLINE=91295445; PubMed=8515786;
JONGWULHWS S., Tanabe K., Kanbara H.;
Jongwulhws S., Tanabe K., Kanbara H.;
Sequence conservation in the C-terminal part of the precursor to major merozoite surface proteins (MSP1) of Plasmodium falciparum field isolates...
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NCBL_TaxID=5833;
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MEDLINE-88011243; PubMed-3079521;
Tanabbe K., Mackay M., Goman M., Scaife J.G.;
"Allelic Dimorphism in a Surface Antigen Gene of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13, Created)
13, Last sequence update)
20, Last annotation update)
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MSP1.
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ERBL; D13343; BAA02604.1; -.
InterPro; IPR000561; EGF-11ke.
Pfam; PF000008; EGF;
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J. Mol. Biol. 195:273-287(1987).
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                                                                                                                                                                                                                                                                                                                                          DYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQNSGCFRHL 1547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREETQIPTSGSLLTELQQVVQLQNYDEEDDSLVVLPIFGESEDNDEYLDQVVTGEAIS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jongwutiwes S., Tanabe K., Kanbara H.;
"Sequence conservation in the C-terminal part of the precursor to major merozoite surface proteins (MSP1) of Plasmodium falciparum failed isolates.";
Mol. Biochem. Parasitol. 59:95-100(1993).

EMBL; D13347; BAA0260B.1; -.
Interpro; IPR000561; EGF-like.
Pfam; PF0000B; EGF.
                                                                      NVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYY
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Last annotation update)
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60.0%; Pred. No. 1.2e-47;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence
01-NR-2002 (TrEMBLrel. 20, Last annotatio
Major merozoite surface protein (Fragment)
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Matches 343; Conservative
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01-NOV-1996 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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Eukaryota; Alveolata;
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                                                                           STREETQIPTSGSLLTELQQVVQLQNYDEEDDSLVVLPIFGESEDNDEYLDQVVTGEAIS 179
                                                                                                                                                                                                                                     PSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFK
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1.6e-47;
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EMBL; D13353; BAA02614.1; -
InterPro; IPR000561; EGF-like.
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EGF-like domain; Merozoite.
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Matches 342; Conserv
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1207 LEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVT 1266
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Jongwutiwes S., Tanabe K., Kanbara H.;
"Sequence conservation in the C-terminal part of the precursor to the major merczotte surface proteins (MSP1) of Plasmodium falciparum from field isolates.";
                      STREETQIPTSGSLLTELQQVVQLQNYDEEDDSLVVLPIFGESEDNDEYLDQVVTGEAIS 179
                                                                                               Gaps
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                                                                                                                                                        NVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYY
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Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence u
01-MAR-2002 (TrEMBLrel. 20, Last annotation
Major merozoite surface protein (Fragment).
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EMBL; D13351; BAA02612.1; -.
Interpro; IPR000561; EGF-like.
Pfam; PF00008; EGF; I.
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NCBI_TaxID=5833;
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SEQUENCE
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5 1101 PLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEV 1160 1207 LEGSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVT 1266 VNDKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLST 1487 DYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQNSGCFRHL 1547 DEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPD 1607 1161 IKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSE------SGSDT 1206 Jongwutiwes S., Tanabe K., Kanbara H.; "Sequence conservation in the C-terminal part of the precursor to the major merozoite surface proteins (MSP1) of Plasmodium falciparum from field isolates."; DDTKKDMLGKLLSTGLV-QNFPNTIISKLIEGKFQDMLNISQHQCVKKQCPENSGCFRHL 477 Gaps 36; Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. NCBI_TaxID=5833; Length 569; Indels 569 AA; 64536 MW; 8008861DECECD8DC CRC64; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NAR-2002 (TrEMBLrel. 20, Last annotation update) Major merozoite surface protein (Fragment).

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KTIDKNKNATKEEEKKKLYQAQYDLSIYNKOLEEAHNLISVLEKRIDTLKKNENIKELLD 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AVTTSTPGSK---GSVASGGSGGSVASGGSVASGGSVASGGSVASGGSGNSRRTNPSDNS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 356;
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falciparum in clinical isolates from the Kilombero District.
Tanzania.";
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                               Jiang G., Daubenberger C., Huber W., Matile H., Tanner M.,
                                                                                                                                                        KINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNIDSL 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Indels
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                (Fragment).
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MEDLINE=20106724; Pubmed=10643908;
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EMBL, AF061143; AAC69742.1;
NON_TER 356 356
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Q9TZU5;
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                     NVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYY 1386
                                                                                                                                                                             VNDKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLST 1487
                                                                                                                                                                                                                             DYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQNSGCFRHL 1547
                                                                                                                                                                                                                                                                                  DEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPD 1607
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EKVLAKYKDDLESIKKVIKEEKEFPSSPPTTPPSPAKTDEQKKESKFLPFLTNIETLYNN 358
STKEETQIPTSGSLLTELQQVVQLQNYDEEDDSLVVLPIFGESEDNDEYLDQVVTGEAIS 179
                                                                                                                                                                                                                                            81 SVASGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDSDAKSYADLKHRVRNYLLTIK 140
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                                                                                         1 THESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGTAVTTSTPGSKGSVASGG---
                                                                                                                            KILSEKYKSDLDSIKKYI--------NDKQGENEKYLPFLNNIETLYKT
                                                                                                                                                                                                                                                                                              21 THESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGTAVTTSTPGSKGSVASGGSGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
(Fragment).
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Kerr P.J., Ranford-Cartwright L.C., Walliker D.;
"Proof of intrapenic recombination in Plasmodium Mol. Blochem. Parasitol. 66:241-248(1994).
EMBL; X52962; CAA37135.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida;
NCBL_TaxID=5833;
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Kerr P.J., Ranford-Cartwright L.C., Walliker D.;
"Proof of intragenic recombination in Plasmodium
Mol. Biochem. Parasitol. 46:185-187(1991).
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NCBL_TaxID=5833;
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falciparum in clinical isolates from the Kilombero District,
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01-DEC-2011 (TrEMBLrel.), Last annota-
Merozoite surface protein 1 (Fragment).
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MEDLINE=20106724; PubMed=10643908;
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Acta Trop. 74:51-61(2000).
BMEI, AF061146; AAC6945.1; -...
AG943.1; -...
AG943.1; -...
                                          (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 19,
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Matches 324; Conservative
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PRELIMINARY;
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61 AVTTSTPG---SKGSVASGGSVASGGSVASGGSVASGGSVASGGSGNSRRTNPSDNS 117
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Acta Trop. 74:51-61(2000).
EMBL; AF061140; AAC69739.1; -.
NON_TER 357 As; 39850 MW; 498FCDF8E2DF1AID CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequen
01-DEC-2001 (TrEMBLrel. 19, Last annota
Merozoite surface protein 1 (Fragment)
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Acta Trop. 74:51-61(2000).
EMBL; AF061141; AAC69740.1; -.
NON_TER 357 357
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360 AA; 40170 MW; 224E3CD345BD2F7A CRC64;
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EMBL, AF061136; AAC69735.1; -..
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Matches 325; Conservative
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NCBI_TaxID=5833;
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                                                                                                                  plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                            MEDLINE-20106724; PubMed-10643908;
Jiang G., Daubenberger C., Huber W., Matile H., Tanner M.,
Pluschke G.;
                                                                                                                                                                                                                                                                                                                                                   19.3%; Score 1625.5; DB 5; Length
89.0%; Pred. No. 5.3e-44;
.ive 15; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                          363 AA; 40398 MW; C25F38CB636941B7 CRC64;
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                                                                                         Merozoite surface protein 1 (Fragment).
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01-DEC-2011 (TrEMBLrel. 19, Last annota
Merozoite surface protein 1 (Fragment).
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Tanzania.";
Acta Trop. 74:51-61(2000).
EMBL; AF061139; AAC69738.1; -. 363 363
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Matches 323; Conservative
                          PRELIMINARY;
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Plasmodium falciparum.
                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=IFA11;
                                                                                                                                   Eukaryota; Alvec
NCBI_TaxID=5833;
                                                  01-MAY-2000
01-MAY-2000
01-DEC-2001
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01-MAY-2000 (
01-MAY-2000 (
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Q9TZU1
45
RESULT
09TZU9
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

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301 VLEKRIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKT 360
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Acta Trop. 74:51-61(2000).
BEMBL: AF061137; AAC69736.1; -.
NON_TER 365 365
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                              1 MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFHKEKMILNEEEITT
                                                                          AVTTSTPGSKGSVASGGSVASGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDS
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NCBL_TaxID=5833;
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Last annotation update)
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MEDLINE=20106724; Pubmed=10643908;
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01-MAY 2000 (TrEMBLrel. 13, 0
01-MAY -2000 (TrEMBLrel. 13, 1
01-DEC 2001 (TrEMBLrel. 19, 1
Merozoite surface protein 1
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Matches 317; Conserv
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Tanzania.";
Acta Trop. 74:51-61(2000).

EMBL: AF061135; AAC69734.1; -.
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                                                                                                                                                                                                                                  Length 344;
                                                                                                     Sequence diversity of the merozoite surface protein 1 of Pl falciparum in clinical isolates from the Kilombero District, Tanzania.";
Acta Trop. 74:51-61(2000).
EMBL. AF061147; AAC69746.1; -.
NON_TER SEQUENCE 344 AA, 38767 MW; 1225C0E1683007DF CRC64;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Last annotation update)
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                                                                          Jiang G., Daubenberger C., Huber W., Matile H
Pluschke G.;
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86.8%; Pred. No. 1e-43;
tive 11; Mismatches ;
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                                           STRAIN-HN6.27;
MEDLINE-20106724; PubMed-10643908;
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STRAIN-IFA9.16;
MEDLINE-20106724; PubMed-10643908;
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Les 322; Conserv
NCBI_TaxID=5833;
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Pluschke G.
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Best Local S:
Matches 322,
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241 VGKMEDYIKKNKTTIANINELIEGSKKTIDQNKNADNEEGKKKLYQAQYDLSIYNKQLEE 300
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID-5833;
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Acta Trop. 74:51-61(2000).
EMBL; AF061144; AAAC69743.1; ...
NON_TER 351 351
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Last annotation update)
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361 KIKEI 365
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RESULT 50 Q9TZU3

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DAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence diversity of the merozoite surface protein 1 of Plasmodium falciparum in clinical isolates from the Kilombero District, Tanzania.";
Acta Trop. 74:51-61(2000).
BEMBL: AF061145; AAC69744.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AVTTSTPGSKGSVASGGSGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295 VLEKRIDTLKKNENIKKLLEDIDKIKTDAEKPTTGSKPNTLLDKNKIEEHEEKIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                               Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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BEDLINE-20106724; PubMed=10643908;
Jiang G., Daubenberger C., Huber W., Matile H., Tanner M.,
Pluschke G.;
                                                                                                                                                                                                                                                 Jiang G., Daubenberger C., Huber W., Matile H., Tanner
Pluschke G.;
                                                                                                                                                                                                                                                                                                                                                                                                  351 AA; 39465 MW; 06481719E004278D CRC64;
                                       Last sequence update)
Last annotation update)
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Last annotation update)
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Pred. No. 9e-43;
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                                                                           Merozoite surface protein 1 (Fragment).
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MEDLINE=20106724; Pubmed=10643908;
                                                                                                                                                                                                                                                                                                                                                                                                                                          18.8%;
88.2%;
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Q9TZU3;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
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121 DAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence diversity of the merozoite surface protein 1 of Plasmodium falciparum in clinical isolates from the Kilombero District, Tanzania."; Acta Trop. 74:51-61(2000).

EMBL. AFVG1131; AAC69730.1; -.

NON_TER 347 AA; 39603 MW; 5E155E74DB6CDOCB CRC64;
             61 AVTTSTPGSKGSVASGGSGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 KGASAQSGTSGT---SGPSGTSGPSGTSPSSRNTLPRSNTSSGAS-----PPADASDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 YIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLIS
                                                    LLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 347;
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NCBL_TaxID=5833;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Jiang G., Daubenberger C., Huber W., Matile Pluschke G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequen
01-DEC-2001 (TrEMBLrel. 19, Last annotai
Merozoite surface protein 1 (Fragment).
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MEDLINE=20106724; Pubmed=10643908;
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Best Local Similarity 86.25
Matches 307; Conservative
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                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum.
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SEQUENCE FROM N.A.
STRAIN=IFA9.26;
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                                                                                                                                                                                                                                          DNSSDSDAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEI 174
                                                                                                                                                                                                                                                                                              NELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDN 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 SGTAVTTSTPGSKG-SVASGGSGGSVASGGSVASGGSVASGGSVASGGSGNSRRTNPSDN 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence diversity of the merozoite surface protein 1 of Plasmodium falciparum in clinical isolates from the Kilombero District, Tanzania.";
Acta Trop. 74:51-61(2000).
EMBL. AF061133; Aac69732.1;
NON_TER 353
SEQUENCE 353 AA; 40089 MW; 93B3CF4E3AD5E757 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                          Gaps
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                                                                                                                                                1 MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGT
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                                                                             Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alveolata; Apicomplexa; Haemosporida; Plasmodium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tanner M.,
                                                                          18.7%; Score 1576; DB 5; Length 3 87.5%; Pred. No. 1.8e-42; rive 15; Mismatches 22; Indels
                                                   498DE127997E8B9B CRC64;
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Last annotation update)
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MEDLINE-20106724; PubMed-10643908;
Jiang G., Daubenberger C., Huber W., Matile H.,
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01-MAY-1999 (TrEMBLrel. 10, Last seque
01-DEC-2001 (TrEMBLrel. 19, Last annot
Merozoite surface protein 1 (Fragment)
                                     360
39814 MW;
        ACTA Trop. 74:51-01(201);
EMBL; AF061138; AAC69737.1;
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Matches 315; Conservative
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Plasmodium falciparum.
Eukaryota; Alveolata;
                                                   SEQUENCE 360 AA;
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                                                                             Query Match
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falciparum in clinical isolates from the Kilombero District,
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                        Tanzania.";
Acta Trop. 74:51-61(2000).
EMBL; AF061142; AAC69741.1;
NON_TER 352
                                                                                                                                                                                                    Matches 308; Conservative
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                                                                                                              SEQUENCE
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Best Local :
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Q9TZV4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 DAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYK 171
                                                                                                                                                                                                                                                                                                                                                                     "Sequence diversity of the merozoite surface protein 1 of Plasmodium falciparum in clinical isolates from the Kilombero District, Tanzania.";
Acta Trop. 74:51-61(2000).
BMB. AF061132, AAC69731.1:
SEQUENCE 347 AA, 39603 MW; 5E155E74DB6CDDCB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 VLEKRIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKE 347
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                                                                                                                                                                                                    Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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NCBL_TaxID=5833;
                                                                                                                                                                                                                                                                                                                              Daubenberger C., Huber W., Matile H., Tanner M.,
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Pluschke G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 18.3%; Score 1544.5; DB 5; Length Best Local Similarity 86.2%; Pred. No. 1.7e-41; Matches 307; Conservative 11; Mismatches 29; Indels
                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Merozoite surface protein 1 (Fragment).
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Last annotation update)
                        347 AA.
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                           PRT;
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01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                        PRELIMINARY;
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Eukaryota; Alveolata;
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                                                                                                                                                                                           Eukaryota; Alveo.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                              Jiang G., Dar
Pluschke G.;
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                      O9TZV5
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61 AVTTSTPGSKGSVASGGSVASGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDS 120
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                                                                                                                                                                                                                                                                                                61 AVITSTPGSGGSVTSGGSGGSVA---SVASGG---SGGSVASGGSGNSRRINPSDNSSDS 114
                                                                                                                                                                                                                                                                                                                                                                           DAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYK 180
                                                                                                                                                                                                                                                                                                                                                                                                       241 YIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLIS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 YIKKNYTTIANINELIEGSKKTIDQNKNADNEEGKKKLYQAQYNLFIYNKQLQEAHNLIS 294
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Acta Trop. 74:51-61(2000).
ACTA Trop. 74:51-61(2000).
NON_TER 347 347 347
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                                                       Length 352;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20106724; PubMed-10643908;
Jiang G., Daubenberger C., Huber W., Matile H., Tanner M.,
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352 AA; 39477 MW; 1C62B4ED3025175B CRC64;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Merozoite surface protein 1 (Fragment).
                                                    18.3%; Score 1544; DB 5; 86.0%; Pred. No. 1.8e-41; tive 19; Mismatches 23;
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PRELIMINARY;
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                                                                                                                            Eukaryota; Alveo.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                          SEQUENCE
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                          241 YIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLIS 300
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                                                                            229 YIKKNKTITANINESIEGSKKIIDQNKNADNEEGKKKLYQAQYDLSIYNKQLEEAHNLIS
            DAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYK
                                                              LNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMED
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                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Merozoite surface protein 1 (Fragment).
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MEDLINE-20106724; PubMed-10643908;
Jiang G., Daubenberger C., Huber W., Matile H.,
Pluschke G.;
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Pred. No. 9e-40;
                                                                                                                                                                                                                                                         AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence diversity of the merozoite falciparum in clinical isolates from Tanzania.";
Acta Trop. 74:51-61(2000).
EMBL: AF061150; AAC69749.1; ...
NON_TER 344 344
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82.68;
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01-DEC-2001
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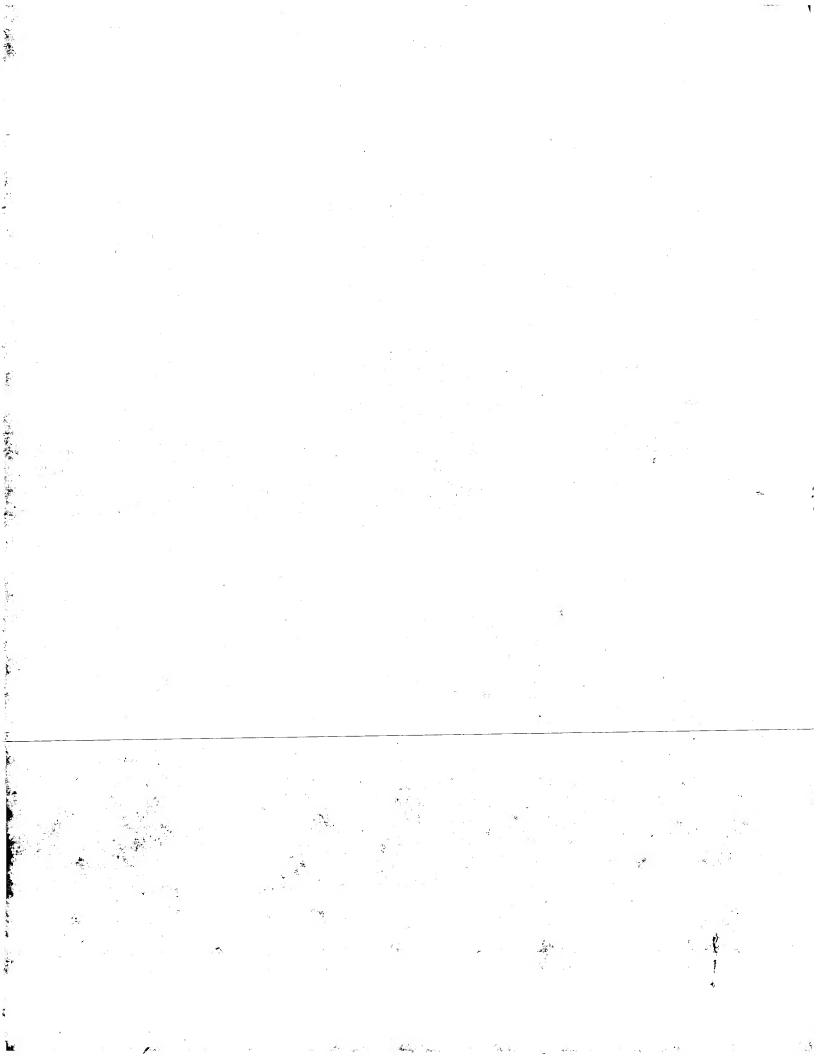
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NCBI_TaxID=5833;
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Merozoite surface protein 1 (Fragment)
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[2]
*SEQUENCE_FROM N.A.
MEDLINE-95107347; Pubmed-7808474;
Kerr P.J., Ranford-Cartwright L.C., Walliker D.;
*Proof of intragenic recombination in Plasmodium falciparum.";
MOI. Blochem. Parasitol. 66:241-248(1994).
                                                                                                                                                                                       Query Match 17.4%; Score 1467.5; DB 5; Length 363; Best Local Similarity 81.6%; Pred. No. 4.4e-39; Matches 298; Conservative 10; Mismatches 38; Indels 19;
                                                                                              Ranford-Cartwright L.C.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; X52963; CAA37136.1; -
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SEQUENCE 363 AA; 40336 MW; A86C08A93DE5AF9B CRC64;
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A., Lockyer M.J., Odink R.G., Sandhu J.S., Riveros-Moreno V.,
S.C., Hillman Y., Davey L.S., Tizard M.L.V., Schwarz R.T.,
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= surface protein 1 precursor (Merozoite surface antigens)
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ilarity 100.0%; Pred. No. 2.9e-267;
Conservative 0; Mismatches 0;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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MEDLINE-86136024; PubMed=3004972;
Mackay M., Goman M., Bone N., Hyde J.E., Scaife J., Certa U.,
Stunnenberg H., Bujard H.;
Polymorphism of the precursor for the major surface antigens of
Plassmodium falciparum merozoites: studies at the genetic level.";
EMBO J. 4:3823-3829(1985).
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Pan M., TOlle R., Bujard H.;
Submitted (JUN.1995) to the EMBL/GenBank/DDBJ database
-i- SUBCELLULAR LOCATION: Attached to the membrane by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-AUG-1987 (Rel. 05, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite (PMMSA) (P190).
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Haemosporida;
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Apicomplexa;
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Eukaryota; Alveolata;
NCBI_TaxID=5839;
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Db 532 EKLTKALKYMEDYSLRNIVVEKELKYY QY 601 ENKPDEKILEVSDIVKVQVQKVLLMNP	Qy 661 PYYLIVLKKEIDKLKVFMPKVESLINE Db 652 PYYLIVLKKEIDKLKVFMPKVESLINI Qy 721 AGSALEGDSVQAQAQEQKQAQPPVVVE Db 712 AGSALEGDSVQAQAQEQKQAQPPVVVE Db 712 AGSALEGDSVQAQAQAQEQKQAQPPVVVE	781 772 772 841	DD 832 DSLNNSLSQLFMEIYEKEMVCNLYKLF QY 901 PQDKPEVSANDDTSHSTNLNNSLKLFF DD 892 PQDKPEVSANDDTSHSTNLNNSLKLFF QY 961 TFYNESFTNFVKSKADDINSLNDESKE DD 952 TFYNESFTNFVKSKADDINSLNDESKE	QY 1021 KKKTVGKYKMQIKKLTLLKEQLESKLA DD 1012 KKKTVGKYKMQIKKLTLLKEQLESKLA QY 1081 TKILLKHYKGLVKYYNGESSPLKTLSE QY 1081 TKILLKHYKGLVKYYNGESSPLKTLSE DD 1072 TKILLKHYKGLVKYNGESSPLKTLSE	1141 1132 1201 1192	QY 1261 TGEAVTPSVIDNILSKIENEYEVLYLK	OY 1381 DVLGYYKILSEKYKSDLDSIKKYINDK Db 1372 DVLGYYKILSEKYKSDLDSIKKYINDK OY 1441 AKVLNYTYEKSNVEVKIKELNYLKTIC Db 1432 AKVLNYTYEKSNVEVKIKELNYLKTIC	OY 1501 TGMVFENLAKTVLSNLLDGNLQGMLN1
CC the European Bioinformatics Institute. There are no restrictions on its CC use by non-profit institutions as long as its content is in no way CC modified and this statement is not removed. Usage by and for commercial CC entitles requires a license agreement (See http://www.isb-sib.ch/announce/CC or send an email to license@isb-sib.ch).	EMBL; X03371; CAA; PIR; A25120; SAZ01 InterPro; IPR00056 Pfam; PF00008; EGI Malaria; Merozoite Transmembrane; GPI SIGNAL	CHAIN 20 1630 MEROZOITE SURFACE PROT DOMAIN 67 84 TRIPEPTIDE SG(TP) REPE TRANSMEM 1614 1630 MEMBRANE ANCHOR. CARBOHYD 259 259 N.LINKED (GLCNAC) CARBOHYD 755 755 N.LINKED (GLCNAC) CARBOHYD 755 759 N.LINKED (GLCNAC)	GLCNAC:) (POTENTIAL) GLCNAC:) (POTENTIAL) GLCNAC:) (POTENTIAL) GLCNAC:) (POTENTIAL) GLCNAC:) (POTENTIAL) GLCNAC:) (POTENTIAL) GLCNAC:) (POTENTIAL) GLCNAC:) (POTENTIAL) GLCNAC:) (POTENTIAL) GLCNAC:) (POTENTIAL)	SEQUENCE 1630 AA; 187289 Duery Match Best Local Similarity 97.1%; Matches 1591; Conservative 1 MKIFFLGSFLFFIINTQCVTHE	1 MKITFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFHKEKMILNEEEITT 61 AVTTSTPGSKGSVASGGSVASGGSVASGGSVASGGSGNSRTNPSDNSSDS :	112 DAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYK 181 LNFYFDLLRAKLNDVCANDYCQIPFNIKIRANELDVIKKLYFGYRKPLDNIKDNYGKMED 172 LNFYFDLLRAKLNDVCANDYCQIPFNIKIRANELDVIKKLYFGYRKPLDNIKDNYGKMED 241 YIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEBAHNLIS 111	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	1 NELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKEKITEKKKIESDKKSYEDRSKS

1140 1200 1440 1251 1431 KRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFD 1020 IITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVV 1260 NISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYK 1560 780 840 999 720 771 FENILSLGKNKNIYQELIGQKSSENFYEKILKDSD 960 951 651 711 831 591 FENILSLGKNKNIYQELIGQKSSENFYEKILKDSD YYKNLISKIENEIETLVENIKKDEEQLFEKKITKD *VPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYE* **2YKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMF** YTGNSPSENNTDVNNALESYKKFLPEGTDVATVVS **LODKLADFKKNNNFVGIADLSTDYNHNNLLTKFLS** NEEKKNIKTEGOSDNSEPSTEGEITGOATTKPGQQ SEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEK OKQGENEKY LPFLNNIETLY KTVNDK IDLFV IHLE

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PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, 4 kDa AND 19 kDa ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1104-1726 FROM N.A.
MEDLINE=88143999; PubMed=3278296;
Weber J.L., Sim B.K.L., Lyon J.A., Wolff R.;
Wherozoite surface protein sequence from the Camp strain of the hum malaria parasite Plasmodium falciparum.";
Nucleic Acids Res. 16:1206-1206(1988).
-:- SUBCELLUIAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                surface antigens)
                                                                                                                                                                                                                                                                                                                                                                           Weber J.L., Leininger W.M., Lyon J.A.; $^{\circ}$
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InterPro; IPR000561; EGF-like.
Pfam; PF00008; EGF: 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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Haemosporida; Plasmodium
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                                                                                                                                                                                                                                                                                                                                                                                                                          the human malaria parasite Plasmodium falciparum.'
Nucleic Acids Res. 14:3311-3323(1986).
                                                                                                                              01-0CT-1996 (Rel. 34, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite (PMMSA) (P195).
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ilarity 60.1%; Pred. No. 2.5e-160;
Conservative 221; Mismatches 342;
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Eukaryota; Alveolata; Apicomplexa;
NCBI_TaxID=5835;
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P04934;
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RESULT 3
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                                                                                                    NHMLTLCDNIHGFKYLIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRA
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1064 NKKKEAEIAETENTLENTKILLKHYKGLVKYNGESSPLKTLSEESIOTEDNYASLENFK 11120 NKKKEAEIAETENTLENTKILLKHYKGLVKYNGESSPLKTLSEESIOTEDNYASLENFK 1121 VLSKLEGKLENTLENTKILLKHYKGLVKYNGESSPLKTLSEVSIOTEDNYANLEKFFR 1124 VLSKLEGKLKDLNLEKKKLSYLSGCHHLIAELKEVIKNYTONSPSENNTDVNNALE 1180 VLSKIDGKLNDNLHLGKKKLSFLSSGLHHLITELKEVIKNKNYTONSPSENNKKVNBALK 1184 SYKKET DEGENNAMHLGKKKLSFLSSGLHHLITELKEVIKNKNYTONSPSENNKKVNBALK	STATE LPECTUALITYSE STATE LITTER AND ALVOSE SYNDDEV DDV I VETER SEEDYDDLGQV SQNVDDEVDDV I VITTER SEEDYDDLGQV TOWNDEDACTIVITY DIFFERENDALITY I LITTER SEEDYDDLGGV TOWNDEDACTIVITY DIFFERENDALITY I LITTER SEEDNDLGGV TOWNDEDACTIVITY DIFFERENDALITY SEEDNDLGGV TOWNDEDACTIVITY SEEDNDLGGV TOWNDEDACTIVITY SEEDNDLGGV TOWNDEDACTIVITY SEEDNDLGGV TOWNDEDACTIVITY SEEDNDLGGV TOWNDEDACTIVITY SEEDNDLGGV TOWNDEDACTIVITY SEEDNDLGGV TOWN		:	1450 KSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLSTDYNHNNLLTKFLSTGMVFENLA 1	1510 KTVLSNLLDGNLQGMLNISQHOCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVEN 1::	1570 PNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSSNFLGISFLL 	1630 ILMLILYSFI 1639 	T 4 PLABA MSD1 PLAEP STANDARD - DRT- 1726 AA	6 (Rel. 34, Created) 6 (Rel. 34, Last sequence 6 (Rel. 34, Last annotatio surface protein 1 precurso	(PMMSA) (GP195). MSP-1. Plasmodium falciparum (isolate Palo Alto / Uganda) Eukaryota; Alveolata; Apicomplexa; Haemosporida; P. NCBI TastD=57270;	[1] SEQUENCE FROM N.A. MEDILINE-89005525; PubMed=3049134; Chang S.P., Kramer K.J., Yamaga K.M., Kato A.	W.A.; um falciparum: gene structure and ozoite surface antigen (gp195) of	Exp: Parasitol. 67:1-11(1988). 1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (Potential). 1- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, kDa AND 19 kDa ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
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IDRORO0561; EGF-11ke.
Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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            QVQKVLLMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVF
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               1657 PNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSSNFLGISFLL 1716
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Merczoite surface protein 1 precursor (Merczoite surface antigens)
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-i- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
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1570 PNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSSNFLGISFLL
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Plasmodium.
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
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MEDLINE-88011243; PubMed=3079521;
Mackay M., Goman M.; Scaife J.G.;
"Allelic dimorphism in a surface antigen gene
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39, Last sequence update)
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Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat;
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Stunnenberg H., Bujard H.;
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J. Mol. Biol. 195:273-287(1987).
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                                                                               MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGT
         . .) (POTENTIAL). . . . (POTENTIAL). . . . (POTENTIAL). . . .
.) (POTENTIAL)
                                                      Best Local Similarity 60.1%; Pred. No. 3.8e-158;
Matches 1042; Conservative 226; Mismatches 339; Indels 126;
                                              Length 1701;
N-LINKED (GLCNAC: ..)
N-LINKED (GLCNAC: ..)
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MW, 3FC2EC59AF96EA98 CI
                                               Score 5069; DB 1;
Pred. No. 3.8e-158;
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                                                                                                      antigens)
                                                                                                                                                                                       KKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVS
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  AND---DTSHS----TNLNNSLKLFENILSLGKNKNIYQEL-IGQKSSENFYEKILKDSD
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Apicomplexa; Haemosporida; Plasmodium
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01-JAN-1990 (Rel. 13, Last sequence update)
01-OT-1996 (Rel. 34, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite
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Eukaryota; Alveolata;
NCBL_TaxID=5837;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                       OF
Plasmodium falciparum.";
. Biochem. Parasitol. 27:291-302(1988).
. SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
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N-LINKED (GLCNAC...)
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Malaria; Merozoite; Polyprotein; Repeat;
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|||||:::||||||||:|:||
1291 GESEDNDEYLDQVVTGEAISVT-MDNILSGFENEYDVIYLKPLAGVYRSLKKQIEKNIIT
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                                ---ESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKL
                                                THHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEIETLVEN
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                         SEQUENCE OF 1-1061 FROM N.A.
MEDILINE-88156657; PubMed-3127688;
Cetta U., Rotmann D., Matile H., Reber-Liske R.;
"A naturally occurring gene encoding the major surface antigen precursor p190 of Plasmodium falciparum lacks tripeptide repeats.";
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N.LINKED (GLCNAC. ) (POTENTIAL).

N.LINKED (GLCNAC. ) (POTENTIAL).

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                                                     C-terminal region of
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          QDKLADFKKNNNFVGIADLSTDYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLN
                                                                                                                                                                                                                                        surface antigens)
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                                                                                                 EMBL; M35727; AAA29715.1; -.
EMBL; V00087; CAA68280.1; -.
EMBL; 235326; CAA84555.1; -.
PIR; S06286; S06286; S06286;
InterPro; IPR000561; EGF-like.
Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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                                                                                                                                                                                         P19588; Q25921;
01-FEB-1991 (Rel. 17, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite (PMMSA) (P190).
                                                                                                                                                                                                                                                                         Plasmodium falciparum (isolate ro-33 / Ghana).
Eukaryota; Alveolata; Apicomplexa; Haemosporida;
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1032-1682 FROM N.A.
MEDLINE-95354793; PubMed-7628566;
MOLIDE R., Bujard H., Cooper J.A.

"Plasmodium falciparum: variations within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                 merozoite surface antigen-1.";
Exp. Parasitol. 81:47-54(1995).
-!- SUBCELLULAR LOCATION: Attached to the
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N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
MW; C82A1E159948CAD6 CRC64;
                                                                                                                                           DB 1; Length 1682;
                                                                                                                                        57.6%; Score 4854.5; DB 1; Length 58.4%; Pred. No. 3.6e-151; ive 223; Mismatches 368; Indels
                                                                                                                                        Query Match 57.6%; Sco
Best Local Similarity 58.4%; Pre
Matches 1007; Conservative 223;
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                               924 HDPLTVLSISNDLKGIVSLLNLGNKTKVPNPLTISTTEMEKFYENILKIMIPIFNDDIKQ
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HS----TNLNNSLKLFENILSLGKNKNIYQEL-IGQKSSENFYEKILKDSDTFYNESFTN
                                                                                                                                                                                                                                                                                                                           GLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLDEKKKLSYLSSG
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                                                                                                         FVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGKYK
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NCBL_TaxID=5862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKITCECTKPDSYPLFDGIFCSSSNFLGISFLLILMLILYSFI 1639
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                                                             Burns J.M. Jr., Daly T.M., Vaidya A.B., Long C.A.; The 3' portion of the gene for a Plasmodium yoeili merozoite suri antigen encodes the epitope recognized by a protective monoclonal antibody.";
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                                                   MEDLINE=88124889; PubMed=2448778;
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Mol. Biochem. Parasitol. 39:285
[2]
SEQUENCE OF 1093-1772 FROM N.A.
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-!- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, 4 kDa AND 19 kDa ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
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01-JAN-1990 (Rel. 13, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
(PMMSA) (Glycoprotein 185) (GP185) (Fragment).
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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6150B76E0F21B299 CRC64;

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This SWISS-PROT entry is copyright. It is produced through a collaboration
 281 AA;
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                                                                                                                                         AVTTSTPGSKGSVASGGSGSVASGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDS 120
                                                                                                                                                     121 DAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYK 180
                                                                                                                                                                                                  LNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMED 240
                                                                                                                                                                                                                                             (Potential).
MISCELLANEOUS: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF
                                                                      Gaps
                                                                                                     Peterson M.G., Coppel R.L., McIntyre P., Langford C.J., Woodrow G., Brown G.V., Anders R.F., Kemp D.J.; "Variation in the precursor to the major merozoite surface antigens of Plasmodium falciparum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83K, 42K & 19K ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF
MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . Biochem. Parasitol. 27:291-302(1988).
SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                             MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
MERCOLITE SURFACE PROTEIN 1.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
 . .) (POTENTIAL).
                                                                      12;
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                                               Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                      0; Indels
                        26050 MW; 1DE4D31ACAEEE965 CRC64;
                                              Score 1187; DB 1;
Pred. No. 7.4e-33;
0; Mismatches 0;
  N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                               281 AA.
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                                               14.1%;
95.1%;
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                                                                     Conservative
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109
248
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                     233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   (PMMSA) (Fragment)
                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Modod V., Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A.,

Modod V., Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A.,

Squuros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

R. Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

R. Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

Andre K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

R. Monorey P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

R. Andrefford K., Rutter S., Saunders D., Stewens K.,

R. Skelton J., Simmonds M., Squares R., Squares S., Stewens K.,

R. Skelton J., Simmonds M., Squares R., Squares S., Stewens K.,

R. Skelton J., Volkaert G., Aert R., Robben J., Grymonprez B.,

Woodward J., Volkaert G., Aert R., Robben J., Grymonprez B.,

Weltjens I., Vanstreels E., Rieger M., Moeller H.,

R. Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

R. Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

R. Goffeau A., Cadleu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

R. Loras M., Rochet M., Gaillardin C., Tallada V.A., Gaizon A., Thode G.,

R. Loras M., Rochet M., Gaillardin C., Tallada V.A., Gaizon A., Thode G.,

R. Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

R. Shakovski G.V., Ussery D., Barrell B.G., Nurse P.;

R. The genome sequence of Schizosaccharomyces pombe.";

R. Dature 415:871-880(2002).
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                                                                                                                                                                                                                                                                                                                                                57 EITT-----KG--ASAQSGASAQSGASAQSGASAQSGTSGPSGTSPSSRSNTLPRSN 109
                                                                     Gaps
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                                                                                                                                       1 MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGT '60
                                                                                                                                                                           1 MXIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNE----E
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DB 1; Length 281;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                Pred. No. 8e-30;
; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last sendation update)
Hypothetical protein CIF3.06c in chromosome I
SPACIF3.06C.
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Score 1096.5;
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(Rel. 34, Last seq
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                                        Similarity
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1221 GAESNTITTSQNVDDEVDDV-----11VPIFGESEEDYDDLGQVVTG------1262
                                                                                                                                                                                                                                                                                                    1435 FVIHLEA------KVLNYTYEKSNV-EVKIKELNYLKTIODKLADFKKNNNFVGIADL 1485
                                                                                                   984 KSSKLEADIEHLKNKVSEVEVERNALLASNERLMDDLKNNGENIASLQTEIEKKRAENDD 1043
                                                                                                                                                                                1102 LKTLSEESIQTEDNYASL-ENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEV 1160
                                                                                                                                                                                                                                   1161 IKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHV 1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :| | || : :: ::| || || 130 QRQKESSLLDAKNELEHMLDDTSRKNSS---LMEKIESINSSLDDKSFELASAVEKLGAL 1486
                                                                          986 KRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGK----YKMQIKKLTLLKEQ 1041
                                                                                                                              1042 LESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENTLENTKILLKHYKGLVKYYNGESSP 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1487 OKLHSESLSLMENIKSOLOEAKEKIOVDESTIOELDHEITASKNNYEGKLNDKDSIIRDL 1546
880 NDQILTQLAELSKNYDSLEQESAQLNSGLKSLEAEKQLLHTENEELHIRLDKLTGKLKIE 939
                                       1390 -SEKYKSDLDS---IKKYINDKQGENEKYLPFLNNIETLYKTVNDKI-----DL
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                                                                                                                                                                                                 1321 KRE-NFKNVL------BSD--LIPYKDLTSSNYVVKDPYK-FLNKE------
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01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Intracellular protein transport protein USO1.
USO1 OR INTI OR YDL058W.
Eacharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetais; Saccharomycetes.
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P25386;
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USO1_YEAST
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1390 KYLEL--QKESSEKIKEEL--DAKTTELKIQLEKITNLSKAKEKSESELSRLKKTSSEERK 1345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTH 1219
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                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: CYTOPLASMIC, ASSOCIATED WITH INTRACELLULAR MEMBRANES. PROBABLY PRESENT ON VESICLES OPERATIONAL BETWEEN THE ER AND THE GOLGI COMPLEX.
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DISPENSABLE FOR THE PROTEIN FUNCTION.
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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: REQUIRED FOR PROTEIN TRANSPORT FROM THE ER
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6CE2B216E9FD4818 CRC64;
                        SEQUENCE OF 782-1790 FROM N.A.
Hogtetter M.K., Herman D.J., Bendel C.M., McClellan M.,
                                                                                                                    Submitted (FEB-1993) to the EMBL/GenBank/DDBJ databases
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ilarity 20.6%; Pred. No. 4.4e-09;
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SEQUENCE OF 1-8 FROM N.A.
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                                                              OKIN------EIKNPPPANSGNTPNTLLDKNKK-IEEHEKEIKEI- 357
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2052 VREALKRLSQVEGIRCHFENFHRLLDNTEELENLKKMVTIYRDKKSERESGLQEMENEMN 2111
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Bou G., Esteban P.F., Baladron V., Gonzalez G.A., Cantalejo J.G.,
Remacha M., Jimenez A., del Rey F., Ballesta J.P.G., Revuelta J.L.;
"The complete sequence of a 15,820 bp segment of Saccharomyces
cerevisiae chromosome XI contains the UBI2 and MPL1 genes and three
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 new open reading frames.";
Yeast 9:1349-1354(1993).
-!- FUNCTION: MYOSIN-LIKE PROTEIN THAT IS PROBABLY INVOLVED IN DNA
                         DVI-- 7. - - - - IVPIFGESEEDYDDL---GQVVTGEAVTPSVIDNILSKIENEYEVLY--
                                        2112 TYSNSITQLEGIVVSAGESKEDIEKLERSNEEMRNISEKISTIDSKVIEMNSTIDELYKL
                                                                                         GRNCQAHWISLISYTANMKTSKLIMINKEKENTEKCVDY-IKDNSSSTDGYVETLKGFY
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Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-S288C;
MEDLINE-93247549; PubMed-8483450;
KGelling R., Nguyen T., Chen E.Y., Botstein D.;
KA new yeast gene With a myosin-like heptad repeat structure.";
Mol. Gen. Genet. 237:359-369(1993).
                                                                                                                                                                                                                                                                                    ----LKTIQDKLADFKKNNNFVGIADLSTDYNH-
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-i- CAUTION: REF.2 MISQUOTES THE GENE NAME AS "MPL1".
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----NVTIKOLTETKRDLES------QVQDLQTRISQI----
                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 1875;
and
                                                                                                                                                                                                                                                                                                                                                                                                                              1.1e-08;
thes 545; Indels
                                                                                                                                                                                                                                                   COILED COIL (POTENTIAL).
78 COILED COIL (POTENTIAL).
66 COILED COIL (POTENTIAL).
01 R -> A (IN REF. 1).
218455 MW; 683A0D34C9066867 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              289; Mismatches
removed
                                                                                                                                                                                                                                                                                                                                                                                                           5.6%; Score 474.5; 20.7%; Pred. No. 1.1k
                     entities requires a license agreement (
or send an email to license@isb-sib.ch)
not
                                                                                          EMBL; L01992; AAA34783.1; -.
EMBL; X73541; CAA51948.1; -.
EMBL; Z28320; CAA82174.1; -.
PIR; S38173; S38173.
SGD; S0001803; MLP1.
Coiled coil; DNA repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                        487
1678
1866
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1875 AA;
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SEQUENCE MEDLINE=9 Galinski "A reticu merozoite	-I - FUNCT HUMAN -I - SUBCE	This SWIS between the Europ	modified entities or send a	EMBL; M88 Malaria; NON_TER NON_TER	Ouery Match Best Local S	272 EEER	1 EFDE	42 385 NIDI		138 QDI- 496 YDSM	186 IAKE 556 RNIV		250 QINF 676 VFME 1 1 295 KFKE	725 LEGE : 352 KESE	785 SYIC	844 NNSI 412 NNDF	903 ркрв
RY RY RT RY RT RT RT RT RT RT RT RT RT RT RT RT RT	8888	8888	8888	DR KW FT	O # ;	6 VO 1	Qy	oy oy	do Qy	Oy Oy	qa VQ	δο ο γ	a v	QQ QD	da Op	qa ov	0y
	903 DKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIY-QELIGQKSSENFYEKI 955 1124 IQIYTAADKEVNNSTNGFGLNNILITLRRERDILÖJTKVTVARRDAKMLRQKISL 1177	956LKDSDTFYNESFTNFVKSKADDINSLNDESKR 987 1178 MDVELQDARTKLDNSRVEKENHSSIIQQHDDIMEKLNQLNLLRESNITLRNELENNNNKK 1237	988 KKLEEDINKLKKTLQLSFDLYNK-YKLKLERLFDKKKTVGKYKMQIKKLTLL 1038 : ::: :: :: :: :: :: ::	1039 KEQLESKLNS-LNNPKHVLQNFSVFFNK-KRAEIAE 1073 	1074 TENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEG 1130	1131KLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPS 1172 	1173 ENNTDVNNALESYKKFLPEGTDVATVVSESGSDTLEQSOPKKPASTHVGAESNTITT 1229	1230 SQNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVĮDNILSKIENEYEVLYLKPL 1289	1290 AGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFKNVLESDLIPYKDLTSSN 1343 ::	1344 YVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYYKILSEKYKSDLDSIKKY 1403 15.	HLEAKVLNYTYEKSNVEVKIKELNYL 146	1464 KTIQDKLADFKKNNNFVGIADLSTDYNHNNLLTKFLSTGM/FENLAKTVLSNLLDGNLQG 1523 ::: :: :	1524 MLNISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGÖKCVENPNP 1572 : : : :	RESULT 15 RBP2_PLAVB ID RBP2_PLAVB STANDARD; PRT; 1251 AA.	01-APR-1993 (Rel. 25, Created) 01-APR-1993 (Rel. 25, Last sequence update) 01-APR-1996 (Rel. 34, Last annotation update) Reficulocyte binding nortein 2, Fragment)	Plasmodium vivax (strain Belem). Eukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium.	NCB1_TaxID=312/3;
qa da	oy G	oy Oy	oy Op	Oy Dp	Oy Dp	Qy Dp	Qy Dp	Oy Dp	yo da	Qy	Qy Db	Qy Dp	ογ Op	2,53	2555	OS OS	N.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71;
                                                                                         1213-1226(1992).
CTION: INVOLVED IN RETICULOCYTE ADHESION. SPECIFICALLY BINDS TO AN RETICULOCYTE CELLS.
CELLULAR LOCATION: Membrane-bound (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4PKVES-----LINEEKKNIKTEGQ-----SDNSEPSTEGEITGQATTKPGQQAGSA 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLDKINEIKNPPPA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3DSVQAQAQEQKQAQPPVPVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNT 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNID---SLFTDPLELEYYLREK----NK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JISAKVETKESTEPNEYPNGVT----YPLSYNDINNALNELNSFGDLINPFDYTKEPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IYTDNERKKFINEIKEKIKIEKKKIESDKKSYEDRSK---SLNDITKEYEKLLN--EI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYMEDYSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V OK V LLMNK I DELKKTOLILK NVELKHNIHVPNSYKQENK OEPYYLIVLKKEI DKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WRE---IMNKKDEIKSYLSEIKEYKDKCTTEISNSKRGKDK------IEFLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPNEESNSNKVNINEINENIRNSEQYLKDIEDAEKQASTKVELFHKHET---TISNIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMY-SMFDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILSQLFMEIYEKEMVCNLYKLKDN-DKIKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----QNALGFRENAKTKLNKTDELLQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1251;
                      i M.R., Medina C.C., Ingravallo P., Barnwell J.W.; culocyte-binding protein complex of Plasmodium vivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1251 1251
1251 AA; 143741 MW; 54BA51C7404AC572 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.4%; Score 457.5; DB 1;
Similarity 21.1%; Pred. No. 2.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06; Conservative 228; Mismatches 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        =92315338; PubMed=1617731;
                                                                                                                                                                                                                                                                                                                                                                                                             38098; AAA29744.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor; Membrane.
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                                                                                                                                                                                                                                                                                                             Chan G.K.T., Schar B.T., Yen T.J.;

"Characterization of the kinetochore binding domain of CENP-E reveals interactions with the kinetochore proteins CENP-F and hBUBRI.";

Gell Biol. 143:49-63(198).

-I- FUNCTION: MINUS-END DIRECTED MICROTUBULE MOTOR. PROBABLE KINETOCHORE MOTOR. ACCUMULATES JUST BEFORE MITOSIS AT THE G2 PHASE OF THE CELL CYCLE. PROBABLY IMPORTANT FOR CHROMOSOME MOVEMENT AND/OR SPINDLE ELONGATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              534 LDEFEALERKTKKDQEMQLIHEISNLKNLVKHREVYNQDLENELSSKVELLREKEDQIKK 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 ADLKHRVRNYLLTIKELK---YPQLFDLTNHMLT-----------LCDNIHGFKY 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'CENP-E is a putative kinetochore motor that accumulates just before
                                                                                                                                          Phrower D.A., Jordan M.A., Schaar B.T., Yen T.J., Wilson L.;
Witotic HeLa cells contain a CENP-E-associated minus end-directed
nicrotubule motor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 LIDGYEEI-----PFNLKINFYFDL--LRAKLNDVCANDYCQI-----PFNLKIR-ANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----IKKLVFG---YRKPLDN------IKDNVGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001752; kinesin_motor.
Pfam: PF00225; kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMARTY; SM00129; KISC; 1.
PROSITE; PS0041; KINESIN_MOTOR_DOWAIN1; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOWAIN2; 1.
MOTOR protein; Cell division; ATP-binding; Coiled coil; Mitosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: INTERACTS WITH CENP-F AND BUBRI KINASE.
SUBCELLULAR LOCATION: ASSOCIATES WITH KINETOCHORES DURING
CONGRESSION, RELOCATES TO THE SPINDLE MIDZONE AT ANAPHASE,
QUANTITATIVELY DISCARDED AT THE END OF THE CELL DIVISION.
SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71. COILED COIL (POTENTIAL).
53 GLOBULAR (POTENTIAL).
53 TAP (ST SIMILARITY).
312087 MW; CEFC13880C8C8CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No. 1.6e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 1.6e
349; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KINESIN-MOTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 443.5;
                                                                                                                        PubMed=7889940;
                                                                                                                                                                                                                                                                      CHARACTERIZATION.
MEDLINE-98437347; Pubmed-9763420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 215005; CAA78727.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                        EMBO J. 14:918-926(1995).
                                                Nature 359:536-539(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew; HGNC:1856; CENPE.
MIM; 117143; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell cycle; Centromere.
DOMAIN 1 335
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HSSP; P17119; 3KAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2663 AA;
                                                                                                                           MEDLINE-95196755;
                                                                                                                                                                                                 microtubule motor,
                                                                                               CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2472
86
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SEQUENCE
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                            mitosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1485 LSTDYNHNNLLTKFLSTGMVFENLAKTVLSNL------LDGNLQGMLNISQH- 1530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1115 MKSNAD-----KYIDVSKIFNTVLDTQKSNIVTNQHSINNVKDKLKGKLQELIDADSSF 1168
                                                                                                                                                                    988 ----KKLEEDINKLKKTLQLSFDL---YNKYK-LKLE-----RLFDKKKTVGKYKMQIK 1033
                                                                                                                                                                                                                                                                      1034 KLTL-----LKEQLESKLNSL------NNPKHVLQNFSVFFNKKKEAEIAE-- 1073
                                                                                                                                                                                                                                                                                                                                                                     -----TENTLEN-TKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENF 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1123 KVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVN-NA 1181
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MEDLINE-93024922; PubMed-1406971;
Yen T.J., Li G., Schaar B.T., Szilak I., Cleveland D.W.;
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Mammalla; Eutheria; Primates;
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Qy Dp	Οy	Q À	q _Q	Qy Db	oy Oy	ති ති	qa	Š 20	Oy Dp	op Op	RES!	TOTAL	OS	OX RN RP	RA RA	RA RA RA	RI RN RP	RX RT RT
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1136 LNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDV 1195
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AIN-AICC 33530 / G-37;
DINE-96026346; PubMed-756993;
DINE-96026346; PubMed-756993;
Sizer C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
Sischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
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tence 270:397-403(1995).
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AIN-ATCC 33530 / G-37;
AINE-94075230; PubMed=8253680;
AINE-94075230; Dubmed=8253680;
SUN, HU P.-C., Bott K.F., Hutchison C.A. III;
Survey of the Mycoplasma genitalium genome by using random
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                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                          RNYLLTI------GFKYL 167
                                                                                                                                                                                                                                                                                                                    Gaps
Bacteriol. 175:7918-7930(1993).
FUNCTION: COMPONENT OF THE CYTOSKELETON-LIKE STRUCTURE WHICH STABILIZES THE SHAPE OF THE WALL-LESS MYCOPLASMA. THIS CYTOSKELETON-LIKE NETWORK OF ACCESSORY PROTEINS CONTAINING HAW PROTEINS 1 TO 5 ALLOWS THE PROPER ANCHORING OF CYTADHESIN PROTEIN THE MYCOPLASMAL MEMBRANE AT THE ATTACHMENT ORGANELLE (BY
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TOYKGGNLYHTDVSLFGEPTEFEYLRKVLFEY -> HLTKV
ALTTRMSHBLENLPNLSICEKCFLSI (IN ISOFORM
2).
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-i- DISEASE: ANTIGEN IN THE AUTOIMMUNE DISEASE SJOEGREN'S SYNDROME AND IN HEPATITIS B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: ASSOCIATED WITH THE CYTOPLASMIC FACE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thesís (1994), Instituto municipal de investigacion medica, Spain.
-!- FUNCTION: MAY PLAY A ROLE IN VESICULAR TRANSPORT FROM THE TRANS-
                                                                                                                                                                                                                                                                                                                                                                          Erlich R., Gleeson P.A., Campbell P., Dietzsch E., Toh B.-H.;
"Molecular characterization of trans-Golgi p230: a human peripheral
membrane protein encoded by a gene on chromosome 6p12-22 contains
extensive coiled-coil alpha-helical domains and a granin motif.";
J. Biol. Chem. 271:8328-8337(1996).
                                                                GGG4_HUMAN STANDARD; PRT; 2230 AA. 013439; 014436; 013270; 013654; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 15-0TN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 60191 autoantigen, golgin subfamily A 4 (Trans-Golgi p230) (256 kDa GOLGA4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Placenta;
MEDIINE=96125112; PubMed=8537393;
Fritzler M.J., Lung C.-C., Hamel J.C., Griffith K.J., Chan E.K.L.;
"Molecular characterization of golgin-245, a hovel Golgi complex protein containing a granin signature.";
J. Biol. Chem. 270:31262-31268(1995).
                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seelig H.P.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=96215236; PubMed=8626529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | InterPro; | IPR000237; GRIP_domain. | Pfam; PF01465; GRIP; 1. | Golds stack; Antigen; Coiled coil; | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower | Lower |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 131-2230 FROM N.A.
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                                                                                                                                                                                                                                                       Homo sapiens (Human)
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MIM; 602509;
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-----QSQDKSLRIAELREELQMD 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                       EQLIQRLRRMERSLSSYRGKYSELVTAYQMLQREKKKL--------QGILS- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGSGGSVASGGSVASGGSVASGGSGASRRTNPSDNSSDSDAKSYADLKHRVRNY 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QGEELREQKEKSERAAFEELEKALSTAQKTEEARRKLKAEMDEQIKTIEKTSEEERISLQ 456
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                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    377 YYL-REKNKNIDISAK--------VETKESTEPNEYPNGVTYPLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  598 KNKHNKEITVMVEKHKTE--LESLKHQQD-ALWTEKLQVLKQQYQTEMEKLREKCEQEKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    344 LI--TOLRDAKNLIEOLEODKGMVIAETKROMHETLEMKEEEIAQLKSKIKOM----TT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    471 KKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTH----
                                                SWLRSSS (IN ISOFORM 4).
                                                                                                                                                                                                                                                                                          Length 2230;
                                                                Y -> K (IN REF. 3).

Y -> H (IN REF. 3).

T -> A (IN REF. 3).

T -> A (IN REF. 3).

T -> A (IN REF. 3).

K -> E (IN REF. 3).

K -> E (IN REF. 3).

K -> N (IN REF. 3).

W, 3BB733DB1EA86134 CRC64;
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(IN ISOFORM 2).
(IN ISOFORM 3).
                    MISSING (IN ISOFORM FTSPRSGIF -> SWLRSSS
                                                                                                                                                                                                                                                                                            Score 424; DB 1;
Pred. No. 5.8e-07;
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Matches 343; Conservative 303; Mismatches
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::: : :	LKQY.TIKEEESKLSSCDPLDLLFNIQNNIPVMYSMPDSLNNSLSQLFMBIYEKEMV 860 ::	KLKDNDKIKNLLEBAKKVSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTSH- 915 : : : : : :	STNLNNSLKLFENILSLGKNKNIYOELIGQKSSENFY 952 	EKILKDSDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTL-QLSFDLY 1008 : :: :: : :	NKYKLKLERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVLQ 1057 	NESVFEN	ESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLK 1133 	KKLSYLSSGLHH	-DVNNALESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTIT 1228 	TSQNVDDEVDDVIIV-PIFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIENEYEVLYLK 1287 	VYRSLKKQLENNVMTENVNV	DLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVL 1383	ILSEKYKSDLDS	LNNIETLYKTVNDKIDLFVIHLEAKVLNYTYE-KSNVEVKIKELNY 1462 ::	LKTIQDKLADFKK 1475 :: :: : EBELKALEDRLESSBAAKLAELKR 1642	STANDARD; PRT: 1679 AA. Rel. 31, Created) Rel. 31, Last sequence update) 131, Last annotation update) 195.1 kDa protein in DNA43-UBI1 intergenic region.
	LKQYKITKEEESK ::: LLTKQVAEVEAQK	CNLYKLKDNDK : : KLEDGNKEQ	STNLNNSI LNEEYETKFKNQE	EKILKDSDTF : AKMLEMAQANSAG	NKYKLKLERLFDK :::: : EIHEIQLQEK	NFSVFFN QKSAHVNSLAQDE	ESSPLKTLSEE : -TSKLKTTDEEFQ	DNLNLEKKKLSYLS ::: : :: ELINISSSKTNAIL	ENNTDVNNALESYK : : 1 : 1 QOATHQLEEKENQIKSMK	TSQNVDDEVDDVI : : : : LKKELSENINAVT	PLAGVYRSLKKQLENNV : : KQYDEEKCELLDQV	۱ ب۵	GYYKILSEKYKSDLDS : : : KSKMEKKESNLET	LPFLNNIETLYKT : : : VQKLQHFQEL	LKTIQD :: EEELKALEDRLES	(Re (Re 119
818	804	861 (916	953 1	1009 1	1058 1	1098 1	1134 1	1173 1	1229 1	1288 F	1324 1	1384 (1415 I	1463 ·	KESULT 19 YIO9_YEAST AC P40457; DT 01-FEB-199; DT 01-FEB-199; DT 01-FEB-199; DT 01-FEB-199; DT 01-FEB-199; DT NI-FEB-199; DT NI-FEB-199; DT NI-FEB-199; DT NI-FEB-199;
QO	Oy Db	Oy Dp	Oy Dp	Qy	Qy Db	Qy Db	oy P	ç g	oy Ob	oy Dp	Oy Db	oy da	Oy Db	Qy Db	Qy Dp	RESULT YIO9_Y ID Y AC P DT 0 DT 0 DT 0 DT 0

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         527 HNTFASYEN-SKHNLEKLTKALKYMEDYSLRN-----IVVEKELKYYKNLISKIENEIET 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252 INELIEESKKTIDKNKNATKEE-----EKKKLYQAQYDLSIYNKQLEEAHNLISVL 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-S288GC / AB972;
Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,
Louis E., Lye G., Moule T., Odell C., Pearson D.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Walsh S.V., Whitehead S.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::||::|| : || || || || || : || : | | || : || : || : || : || : || : || : || : || : || : || : || ERQLLDES----SEQKNTAKEELNGLKDQLNEERSRYRREID--ALKKQLHVSHEAMREV
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Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.0%; Score 423; DB 1; Length 1679; Best Local Similarity 19.7%; Pred. No. 4.6e-07; Matches 335; Conservative 296; Mismatches 583; Indels 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 1679 AA; 195141 MW; 298950CC52202D8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; 238059; CAA86129.1; -.
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SGD; S0001411; MLP2
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---ILKNVELKHNIHVPNS 652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sweeney F.P., Watts F.Z., Pocklington M.J., Orr E.; "The MYOl gene from Saccharomyces cerevisiae: its complete nucleotide
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                                                                                                                                                                                                                                                                                                               MYOI OR YHR023W. The state (Baker's yeast). Saccharomyce cerevisiae (Baker's yeast). Bukaryota: Fungi; Ascomycota; Saccharomycetiae; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetaeea; Saccharomyces.
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01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                      1928 AA
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PIR; 512323; 512323.

PIR; 546773; 546773.

HSSP, P087799; 1MND.

SGD; 50001065; MYO1.

InterPro; IPR001048; IQ_region.

InterPro; IPR001609; myosin,head.
                                           PRT;
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STRAIN=S288c / AB972;
MEDLINE=94378003; PubMed=8091229;
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I -> T (IN REF. 1 AND 3).

V -> S (IN REF. 1 AND 3).

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N -> S (IN REF. 1).

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N -> MISSING (IN REF. 1).

N -> A (IN REF. 1).

R -> A (IN REF. 1).

H -> D (IN REF. 1).

ETYVEGMLSKN -> NTLWKAGYPKT (IN REF. 1).

MISSING (IN REF. 1).

EYNYDGMLSKN -> NTLWKAGYPKT (IN REF. 1).

MISSING (IN REF. 1).

EYSSA -> GKNLLVC (IN REF. 1).

N -> K (IN REF. 1 AND 3).

E -> R (IN REF. 1 AND 3).

E -> R (IN REF. 1).

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N -> NGITKINTNITTETPQSTYIGERPKRVICGN (IN REF. 1).

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NELRLREHIHALKQAEEDVKNMASIIEKLKTONKQKEKLIW
EREMERNDSDMQLQETLLE -> P (IN REF. 1).
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EBAH -> KKLD (IN REF. 1).

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LE -> WK (IN REF. 1).
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P -> S (IN REF. 1).
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E -> Q (IN REF. 1).
PDKESDINKLMLE -> LTKSLILTNGNAS (IN
                                      Myosin; Actin-binding; ATP-binding; Coiled coil; Alkylation.

DOMAIN 794 823 IQ.

DOMAIN 856 1911 COILED COIL (POTENTIAL).

DOMAIN 866 1911 COILED COIL (POTENTIAL).

MP. BIND 180 187 ATP (BY SIMILARITY).

DOMAIN 460 529 ACTINI BINDING (BY SIMILARITY).

CONFLICT 36 36 K -> I (IN REF. 1).
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DDLVSE -> MTLFL (IN REF. 1).
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73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   036 DKL-----SSSEEDLDIKLVTLE--------KNCNIAMSRLQSLVTEN 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 RNSLVESLNDSKIKELEARLSQEISLNQYLNKRISGNSVETNISSTRRS-----TS 1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESKRKK---LEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGKYKMQIK----- 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1324 VDYLKROLDIETRAHYDAENAISALHS-----KFRKI--QGESSLSSSDIYKLKFEAS 1374
                                                                                                                                                                                                                                        121 DAKSYADLKHRVRNYLLTIK-----ELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEIN 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : : | |:| : | ||:| 923 KTSSETLQKQFDDLVSEKDEISREKLEVAQNLEEAHQKIQGLQETIREREATLEKLHSKN 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312 NENIKELLDKINEIKNPPPANSGNTPNTLLDKNK-KIEEHEKEIKEIAKTIKFNIDSLFT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                371 DPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSF---- 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDLINPFDYTKEPSKNIYTDNERKKFINEIKEK ----IKIEKKKIESDKKSYEDRSKSLN 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSKHNLEK 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        543 LTKALKYMEDYSLRNIV--VEKELKYYKNLISKIE-NEIETLVENIKKDEEQLFEKKITK 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                600 DENKPDEKILEVSDIVKVQVQKVLLAMKIDELKKTQLILKNVELKHNIHVPNSYKQENKQ 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                660 EPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGOSDNSEPSTEGEITGOATTKPGO 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QAGSALEGDSVQAQAQEQKQ----AQPPVPVPVPEAKAQVPTPPAPVNNKTENVSKL--- 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            773 -DYLEKLYEF-LNTSYICHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLFNI- 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DKIKNLLEEAK-KVSTSVKTLSSSSMQPLSLTPQ-DKPEVSANDDTSHSTNLNNSLK--- 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   925 -LFENILSLGKNKNIYQELIGQKSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLND 983
                                                                                                                                                                                                                                                                               176 ELLYKLNFYFDLLRAKLNDVCANDY------CQIP-FNLKIR-----ANELDVLKKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 VFGYRKPLDNIKDNVGKMEDYIK----KNKKTI---ENINELIEESKKTIDKNKN-ATKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---FNEQINKLKNDLQEMESKKKFLEEKNQKTVNELENTQDLLNQEKENLRKNESLLNRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEKKKLYQAQYDLSIYNK------QLEEAHNLISVLEKRI----DTLKK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....QNNIPVMYSMFDSLNN--SLSQLFMEIYEKEMVCNLYKLKDN
                                                                                            Query Match 5.0%; Score 421.5; DB 1; Length 1928; Best Local Similarity 20.8%; Pred. No. 6e-07; Matches 304; Conservative 246; Mismatches 487; Indels 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 YSDDP----LDKEDIIK------KYYDLQLAFTEITRN-----
1902 1904 FWK -> NSGKRLDADDL (IN REF. 1).
1928 AA; 223634 MW; 6F54C7611F43DC9F CRC64;
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59;
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                                                                                                                                                                                                                                                                                                                                                                                                                203 IPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMEDYIKKNKKTIENINELIEESKKT 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 IDKNKNATK--EEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLD 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       378 YLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSFGDLINPFDYTK 437
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------DEIRKMRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            879 INKYRAELEKLESDKDDLEKRIIG-------LODELNEKDRDTDRLNAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---RDNHQKKIDSMN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321 KINEIKNPPPANSGNTPNTLLD-KNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLE--LEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          651 RDEIIKQKDKLAKELADLENKLNNETKMRGDAEKLNQRHLDEIDNFKKQINEYITEVTII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----YKVEKLTHHNTFASYENS----KHNLEKLTKALKYMEDYSLRNIVVEKELKYYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLISKIENEIETLVENIKKDEEQLFE-KKITKDENKPDEKILEVSDIVKVQVQKVLLMNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                628 IDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKKNIKTEGOSDNSEPSTEGEITGOATTKPGQOAGSALEGDSVQAQAQEQKQAQPPVPVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          966 ALIDELRSKLN--DAERAMADLQNRDSILERENNDWKEKSDALNMELDRLRDEL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1018 --LSVRRDAEK-----EINRYNTDLQTAARNEIKLLTPTNNEMKSQLNAAEDKINSLNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -NDITKEYEKLLNEIYD--SKFNNNI-------DLTNFEKMMGKRYS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                748 VPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       808 KITKEEESKLSSCDPLDLLFNIQNNIPVM-----YSMFDSLNNSLSQLFMEIYEKEMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --- LNNSLKLFE-NILSLGKNKNIYQE---LIGQK--SSENFYEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPSKNIYTDNERKKFINEIKE-KIKIEKKKIESD--KKSYEDRSKSL-----
                                                                                                                                                                                                                                                                                                                          Indels 418;
                                                                                                                                                                                                                                                                     DB 1; Length 2022;
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                                                                                                       COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                Query Match
4.8%; Score 405; DB 1; L
Best Local Similarity 18.0%; Pred. No. 2.2e-06;
Matches 281; Conservative 308; Mismatches 553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :: | :: | | :| | :| | :| | 921 IDDLKRKLQTEIEKVRKETTTVQERYHIEWDEE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           474 LDDAKHTVKDLEDRLKSLEQEKASIDSARHHLE-----
                                                                                                                                                                                                                      237341
EMBL; U12681; AAA80009.1;
EMBL; J03995; AAA29412.1;
                                                                                                                                                                                       1879
                                                                                                                                251
384
                                                  PIR; A54513; A54513.
Antigen; Coiled coil
DOMAIN 74 13
                                                                                                                                  151 25
327 38
417 187
2022 AA;
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|::| :|::| :|: | : || : || : ||.:| ||:| || DALDKLRPEYDRLONYREKIKOAENLTOAVODLESRLNOSRRELRDATDKLIASEGDRN 1233
                                                                                              SLNNPKHVLQNFSVFFNKK-----KEAEIAETENTLENTKILLKHYKGLVKY-YN 1096
                                                                                                                                                                                                                                                          ESMDEKKETVLQTQKSPDGKSKERFDISDL------DTNIQKLIGRIEKLELERNE 1398
                                                                                                                                                                                                                                                                                                                                                                                                                        1307 FNV------NVKD-----ILNSRFNKRENFKNVLESDLIPYKDLT 1340
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----EKRDKFLSSYNYIKDSIDT---DINFAN 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1568 ESKNADMKEDNDRLKKDLIKASTNEAELRRTIDQNSRVVSDNQILKDQLESAQNDLSNAN 1627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1482 IADLSTDYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQNS 1541
 --NDMLKTAKESNEAEIDRLKQKLQRSIENAKKYS 1173
                                                                                                                             1234 ALRSEVEKLOHEVOFMREOLLRKTDEYQAALSDLVNAHRTAEDGRVNAVQALEARKYEIN 1293
                                                                                                                                                                                                                          HLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSESGSDTLEQSQ 1211
                                                                                                                                                                                                                                                                                          -----PKKPASTHVGA-ESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLG-QVVT 1261
                                                                                                                                                                                                                                                                                                                       1399 YRDALDRIKKKSIESHIKINKQETIFT--NIEDQLVDV------EEEKRTLEMRLAS 1447
                                                                                                                                                                                                                                                                                                                                                         1262 GEAVTPSVIDNI------LSKIENEY--EVLYLKPLAGVYRSLKKQLENNVMT 1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TVNDKIDLFVIHLEAKVLNYTYEKSNVEVKIKE-----LNYLKTIQDKLADFKKNNNFVG 1481
                                                                                                                                                                                                                                                                                                                                                                             TVS-----QQRTIETEIRQQLSLALNERNTLQNDLRDLQRR----
                                                                                                                                                             GESSPLKTLSEESIQTEDNYASLEN----FKVLSKLEGKLKDNLNLEKKKLSYLSSGLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D------VKYINDKQGENEKYLPFLNNIETLYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGVLHDHEERWYAHKFHLESKLKDQESESQQIRLLVANFETERNSLNEKVRDLASRLQQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-87092266; PubMed-3540939; Warrick H.M., de Lozanne A., Leinwand L.A., Spudich J.A. "Conserved protein domains in a myosin heavy chain gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grabatin B., Wippler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 83:9433-9437(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                LKLERL - - - FDKKKTVGKYKM - QIKKLTLLKEQLESKL - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 2116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida;
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-90353583; PubMed=2387408;
Lueck-Vielmeter D., Schleicher M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myosin II heavy chain, non muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -SSNYVVKDPYKFLNK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 09, Created)
(Rel. 12, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dictyostellum discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION SITES,
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1130 IKGDIDSLFGE-
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MYS2_DICDI
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"Replacement of threonine residues by serine and alanine in

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PTM: PHOSPHORYLATION INHIBITS THICK FILAMENT FORMATION AND REDUCES
THE ACTIN-ACTIVATED ATPASE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HAM). IT CAN BE FURTHER SPLIT INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
                                                                                                                                                                                                                                               Fisher A.J., Smith C.A., Thoden J.B., Smith R., Sutoh K., Holden H.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dictyostellum discoldeum myosin motor domain.";
J. Mol. Biol. 274:394-407(1997).
-!- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN & HAS ATPASE
-!- SUBGUNT: MYOSIN IS ACTIVATED BY ACTIN.
-!- SUBGUNT: MYOSIN II HEAVY CHAIN IS TWO-HEADED. IT SELE-ASSEMBLES
INTO FILAMENTS. HEXAMER OF 2 HEAVY CHAIN SUBGUNTS (MHC), 2 ALKALI
LIGHT CHAIN SUBGUNTS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "X-ray structure of the magnesium(II) ADP.vanadate complex of the Dictyostelium discoideum myosin motor domain to 1.9-A resolution."; Biochemistry 35:5404-5417(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MgAMPPNP complexes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 characterization
phosphorylatable heavy chain fragment of Dictyostelium myosin II.", FEBS Lett. 269\colon 239-243(1990).
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95345067; PubMed=7619796;
Smith C.A., Rayment I.;
"X-ray structure of the magnesium(II)-pyrophosphate complex of the
truncated head of Dictyostelium discoideum myosin to 2.7-A
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                                                                                                                             the
                                                            PHOSPHORYLATION SITES.
MEDLINE-88112226; PubMed-2828113;
Wagle G., Noegel A., Scheel J., Gerisch G.;
"Phosphorylation of threonine residues on cloned fragments of
                                                                                                                                                                                                                                                                                          Dictyostelium
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                                                                                                                                                                                                                                                                                    "X-ray structures of the myosin motor domain of Dict; discoideum complexed with MgADP.BeFx and MgADP.AlF4-Biochemistry 34:8960-8972(1995).
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"X-ray structures of the MgADP, MgATPgammaS, and MgAD
of the Dictyostelium discoideum myosin motor domain."
Blochemistry 36:11619-11628(1997).
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MEDLINE=98070605; PubMed=9405148;
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MEDLINE=97452580; PubMed=9305951;
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MEDLINE-96206189; PubMed-8611530;
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                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
                                                                                                                                                Dictyostelium myosin heavy chain. FEBS Lett. 227:71-75(1988).
                                                                                                                                                                                                                              MEDLINE=95345066; PubMed=7619795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochemistry 34:8973-8981(1995).
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966 QSDTISRLEKIKDE-LQKEVEELTESFSEESKDKGVLEKTRVRLQSELDDLTVRL 561 EKELKYKNLISKIENEIETLVENIKKDEEQLFEKKITKDENKPDEKI :	Db 1020 DSETKDKSELLRQKKKLEEEELKQVQEALAAETAAKLAQEAANKKLQGEYTELNEKFNSEV 1079 Qy 609 LEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELKHNIHVPN 651 : : : : :	652	OY 707 GEITGGATT-KPGQQAGSALEGDSVQ-AQAQEQKQAQPPVPVPVPEAKAQVPTPPAPVNN 764 1	2y 765 KTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEE 814	2) 815 SKLSSCDPLDELFNIONNIFVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKDNDKIKN 874 1303 KKQKESNEKRKVDLEKEVSELKDQIEEEVASKKAVTEAKNKKESE 1347	2) 875 LLEEAKKVSTSVKTLSSSSWQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLF 926	2y 927 ENILSLGKNKNIYQELIGQKSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDES- 985 1 1 1 1 1 1 1 1 1	QY 986 -KRKKLEEDINKLKKTLQLSFDLYNK-YKLKLERLFDKKKTVGKYK 1029	QY 1030 MQIKKLTLLKEQLESKLNSLNNPKHVLQNESVFENKKKEAEIAETENTLENTKILLKHYK 1089 1511 ELEVRVAELEESLEDKSGTVNVEFIRKKDAEIDDLRARLDRE 1552	DY 1090 GLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLS 1147	2y 1148 SGLHHLIAELKEVIKNKYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSESGSDTL 1207 	DY 1208 EQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTP 1267 : :: D	29 1268 SVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKR 1322 : :::::	2y 1323 ENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDV 1382 	29 1383 LGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLFVIHLEAK 1442 1	29 1443 VLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLSTDYNH 1491 	2y 1492NULLTKFLSTGMVFENLAKTVLSNLLDGMLNIS 1528 : :
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CC use by non-profit institutions as long as its content is in no way CC modified and this statement is not removed. Usage by and for commercial CC entities requires a license agreement (See http://www.isb-sib.ch/announce/CC or send an email to license@isb-sib.ch).	, M146 A2665 S0025 IMMA;	PDB; PDB; PDB;	PDB; IMNE; 17-AUG-96. PDB; IVOM; 23-DEC-96. PDB; ILVK; 28-JAN-98. DictyDb; DD01008; mhc	Interl Interl Interl Pfam;		SMART; SMART; PROSITE MYOSIN;		NP_BIND 179 186 DOMAIN 638 660 DOMAIN 738 752 MOD_RES 130 130	Ž.	Ouery Match Best Local Similarity 20.4%; Pred Marches 319: Conservative 266: M	CQIPFNEKIRANELDVLKKLVFGYRRPLDNIKDNVGKME	245 NKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNL	299 ISVLEKRIDTLKK	~ m ac	387 DISAKVETKESTEPNEYPNGVTYPLSYNDINNALNELN-SFGDLINPFDYTKEPSK	ON OLY DEGREE LEARNING TO THE TOTAL OF THE T	502 NNIDLINFEKMAGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKALK-YMEDYSLRNIVV : :: :: :: :: :: :: ::

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RA Wood V., Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A.,

RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Collins M., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Honsby T., Howarth S., McDonald S., McLean J.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA James K., Jones L., Jones M., Leather S., McDonald S.,

RA Mooney P., Woule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Nitherford K., Thutter S., Saunders D., Quali M.A., Rabbinowitsch E.,

RA Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Skelton J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Wedtjens I., Vanstreels E., Rieger M., Schaefer M., Meeller H., Ribbert H.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Daga R.R., Cruzado L., Jamenez J., Sanchez M., del Rey F., Benito J.,

RA Daga R.R., Cruzado L., Jamenez J., Sanchez M., del Rey F., Benito J.,

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RA Daga R.R., Cruzado L., Jamenez J., Sanchez M., del Rey F., Benito J.,

RA Daga R.R., Cruzado L., Jamenez J., Sanchez M., del Rey F., Benito J.,

RA Daga R.R., Persun R. Schizosaccharomyces pombe.";
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-!- FUNCTION: AFTER THE ONSET OF MITOSIS, AT MID- TO LATE ANAPHASE, CO-LOCALIZES WITH THE MEDIAL ACTIN RING. MAY PLAY A ROLE IN
                1529 QHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCT 1588
                                                1908 -RETVEEAEDSKS-----BAEQSKRLVELELEDAR------RNLQKEIDAKEI 1948
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"The alm1+ gene from Schizosaccharomyces pombe encodes a coiled-coil protein that associates with the medial region during mitosis.";
Mol. Gen. Genet. 262:921-930(2000).
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Schizosaccharomycetales; Schizosaccharomycetaceae;
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16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update
Abnormal long morphology protein 1 (Sp8).
                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces pombe (Fission yeast).
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MEDLINE-20223868; PubMed-10759889;
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MEDLINE-21848401; PubMed-11859360;
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Q9UTK5; 013313; Q9UTT8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 AGLAQONTE-LNEKIQLFEQKRSNYSSDGNISKILETDPTSIKELEEEVE--TQKRLTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       533 YENSKHNLEKLTKAL---KYMEDYSLRNIVVE-----KELKYYKNLISKIENEIETLVEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1727;
                                                                                                                                                                                                                                                                                                                                                                     361 COILED COIL (POTENTIAL).
463 COILED COIL (POTENTIAL).
740 COILED COIL (POTENTIAL).
1106 COILED COIL (POTENTIAL).
1427 COILED COIL (POTENTIAL).
1555 COILED COIL (POTENTIAL).
1654 COILED COIL (POTENTIAL).
1664 COILED COIL (POTENTIAL).
AA: 197858 MW; F820BF8D9C132644 CRC64;
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SUBCELLULAR LOCATION: Cytoplasmic.
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EMBL; AF010473; AAB65416.1; ALT_INIT.
EMBL; AB028012; BAA87316.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1183 QLLFLENKKLKRTVE-----SSNRVIAD----LQRGITEKDVSS---TSESVGER 1225
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                                                                                                                                                                                                                                                                967 FINFVKSKADDINSLNDESKRKKLEEDINKLKKTLQ-LSFÖLYNKYKLKLERLFDKKKTV 1025
                                                                                                                                                                                                                                                                                                                                                                                                           EAEIAETENTLEN--TKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYA--SLENFK 1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1376 INFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFL-NNIETLYKTVNDKIDL 1434
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847 IEYSSRIKTLMLEKQSLSEDNRKLLDNQDAMEIKLQELNGVIELEKQRESTLEAKFTQQK
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RSSILSHNSSAGNI----
                                                   ----LEMEIYEKEMVCN
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                                                                                                                        863 LYKLK-DNDKIKNLLEEAKKVSTSVKTLSS--SSMQPLSLTPQDKPEVSANDDTSHSTNL
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                                                     ITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQ
|: :| :| :| || || 584 TLSEQIKNLESELNSSKIKNESLLNERNLLKEMLATS---
                                                                                                                                                                                              920 NNSLKLFENILSLGK---NKNIYQELIGQKSSENFYEKIL
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P12753;
01-OCT-1989 (Rel. 12, Created)
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EQLNKPSATP 1432
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                         containing a
                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence analysis of the 33 kb long region between ORC5 and SUII from the left arm of chromosome XIV from Saccharomyces cerevisiae."; Yeast 13:49-860(1997).

-i- FUNCTION: INVOLVED IN DNA DOUBLE-STRAND BREAK REPAIR (DSBR). THE RADSO/AMREII COMPLEX POSSESSES SINGLE-STRAND ENDONUCLEASE ACTIVITY AND ATP-DEPENDENT DOUBLE-STRAND-SPECIFIC EXONUCLEASE ACTIVITY. RADSO PROVIDES AN ATP-DEPENDENT CONTROL OF MREII BY UNWINDING AND/OR REPOSITIONING DAN BEDOSITIONING BADDS INTO THE MREII ACTIVE SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMEDYIKKNKKTIENINELIEESKKTI 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSNLKKKFDEIFQAMK----FTKALDNLKSIKKDMSVDIKLLKQSVEHLK------L 214
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01-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA repair protein RAD50 (153 kDa protein).
RAD50 OR YNL250W OR N0872.
Saccharomyces cerevisiae (Baker's yeast).
Saccharomyces cerevisiae (Baker's Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    376;
                                                                                                                                                                                                     MEDLINE-89276917; PubMed-2659437;
Alani E., Subbiah S., Kleckner N.;
"The yeast RAD50 gene encodes a predicted 153-kD protein cont
purine nucleotide-binding domain and two large heptad-repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1312;
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STAIN-S288C / FY1679; MEDLINE-2888C / FY1679; MEDLINE-9737792; PubMed-9234673; Sen-Gupta M., Gueldener U., Beinhauer J.D., Fiedler T.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative 251; Mismatches 443; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA repair; Hydrolase; ATP-binding; Coiled coil; Meiosis.
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COLLED COIL (POTENTIAL).
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Pred. No. 3.3e-06;
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EMBL; Z71256; CAA96157.1; -
PIR; S05808; BWRYPL.
SGD; S0005194; RAD50.
INCEPTO: IPR004349; ABC_transportr.
InterPro: IPR004584; Rad50.
TIGRPAMS; TIGR00606; rad50; 1.
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                                                                                                                                                                                                                                                                                           Genetics 122:47-57(1989).
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1108
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                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                   NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                 Hegemann J.H.;
                                                                                                                                                                                        STRAIN-RE821
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DOMAIN
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Tentry is copyright. It is produced through a collaboration wiss Institute of Bioinformatics and the EMBL outstation-loinformatics Institute. There are no restrictions on its cofit institutions as long as its content is in no way his statement is not removed. Usage by and for commercial res a license agreement (See http://www.isb-sib.ch/announce/iltolicense@isb-sib.ch).
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|--VITHDEKFLGH 1279
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CONTAINS I PH DOMAIN.

IS UNCERTAIN WHETHER MET-1 IS THE INITIATOR.
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CONTROLS NUCLEAR MIGRATION. NUM1 SPECIFICALLY CONTROLS TYRON OF THE BUD NECK CYTOSRELETON WITH THE PRETYON OF THE BUD NECK CYTOSRELETON WITH THE PRETY OF THE BUD NECK CAPOSRELETON WITH THE PRETY OF THE NUCLEUR CAPOSINIZING G2-SPECIFIC MICROTUBULI OR OTHER COMPONENTS OF THE NUCLEAR
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ji; Ascomycota; Saccharomycotina; Saccharomycetes;
les; Saccharomycetaceae; Saccharomyces.
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77: PubMed-1745235;
shaaff-Gerstenschlaeger I., Zimmermann F.K.,
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                                                                                                                                                                              125 IDDLLTQASLEYEQORRTNQVLKEKHRQVQQHFQNLVHAKKKLDQKRHYLAEQKRIDEEQ 484
                                                                                                                                                                                                                                                       LFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELKHNIHVPN 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              695 KFKEKELEAAQKQLSLDN--NNNAGLKLQLDKLSESLKTERLELEASKERILDFYD-ESS
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                                                                                                                                                                                                                                                                                                                                 185 IFK---LKEKIATERRELEKLYLVKKOKO------DOKENDLLIFEKOLR---OYOA
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STOSKELENOL-LIKE NETWORK OF ACCESSORY PROTEINS CONTAINING HAW
PROTEINS 1 TO 5 ALLOWS THE PROPER ANCHORING OF CYTADHESIN PROTEINS
IN THE MYCOPLASMAL MEMBRANG AT THE ATTACHMENT ORGANELLE (BY
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J. Bacteriol. 179:2668-2677(1997).
-i- FUNCTION: COMPONENT OF THE CYTOSKELETON-LIKE STRUCTURE WHICH
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                              Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
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                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-9725247; PubMed-9088066;
Krause D.C., Proft T., Hedreyda C.T., Hilbert H.,
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                                                                                                                                                                                  Nucleic Acids Res. 24:4420-4449(1996)
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EMBL; U59896; AAB52527.1; -.
PhosSite; P75471; -.
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Query Match
                Best_Local
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 N-----KFDQRRKEAVSSILNSHKK-LKQKEGELQGILQKLSLKKTQIEQEFSKLYQQ- 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE-96337999; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Sutton G.G., Rinkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
Compact genome sequence of the methanogenic archaeon, Methanococcus
                                                                                           ---FVGIADLSTDYNHNNLLTKFLSTGMVFENLAK---TVLSNLLDGNLQGMLNISQHQC 1532
                                                                                                                        1453 FEYFRKI-----RNEIEKKEAHIKTVLEETQKKRHLVETEAVKLHLQKQSIISKGQE 1504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       jannaschii.";
Science 273:1058-1073(1996).
-!- FUNCTION: Involved in DNA double-strand break repair (DSBR). The
rad50/mre11 complex possesses single-strand endonuclease activity
and ATP-dependent double-strand-specific exonuclease activity.
Rad50 provides an ATP-dependent control of mre11 by unwinding
and/or repositioning DNA ends into the mre11 active site (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probom; PD000006; ABC_transportr; 1.
DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete proteome. NP_BIND 32 39 ATP (BN SIMILARITY).
DOMAIN 158 849 COILED COIL (POTENTAL).
SEQUENCE 1005 AA: 119387 MW; 9BBB48173E78883 CRC64;
                                                1429 NDKID-----LFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQ----DKLADFKKNNN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i-SUBUNIT: Forms a complex with mrell (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                         Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA double-strand break repair rad50 ATPase.
                                                                                                                                                                                                                                                                   1005 AA
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                                                                                                                                                       1533 VKKQCPQNSGCFRHLD-EREECKCLLN 1558
                                                                                                                                                                                    LKEIKERVSRDISHTNKQREELNSLLH 1531
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InterPro; IPR003405; SMC_C.
InterPro; IPR003395; SMC_N.
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16-OCT-2001 (Rel. 40, Last sequ
16-OCT-2001 (Rel. 40, Last anno
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Methanococcus jannaschii.
                                                                                                                                                                                                                                                                   STANDARD;
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Pfam; PF02483; SMC_C;
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                                                                                                                                 363 FNIDSLFTDP-----LELEYYLREKNKNIDISAKVETKESTEPNE--YPNGVTYPLSYND 415
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DE--FEKCYQKMGEIVKEYEKRLERI-EGELNYK---ENYEKELKNKMSQLEEKNKKLME
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                                                                                                                                                                                                                                                                  116 INNALNEL----NSFGDLINPFDYTKEPSKNIYTDNERKKFIN-EIKEKIKIEKKKIES
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   Length 1005;
4.4%; Score 372; DB 1;
Similarity 20.9%; Pred. No. 1.2e-05;
'2; Conservative, 204; Mismatches 364
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EMBL;
  Witczak O., Skaalhegg B.S., Keryer G., Bornens M., Tasken K.,
Jahnsen T., Oerstavik S.;
"Cloning and characterization of a cDNA encoding an A-kinase anchoring
protein located in the centrosome, AKAP450.";
                                                     SIDTDINFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVND 1430
                                                                                                                                  1431 KIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQ----DKLADFKKNNNFVGIADLS 1486
                                                                                                                                                                                                                 1487 TDYN-----HNNLLT-KFLSTGMVFENLA-----KTVLSNLLDGNL------QGMLNIS 1528
                                                                                                                                                                                                                                                                                                                                                                                                                            AKA9_HUWAN STANDARD; PRT; 3911 AA.

099996, 09U004; Q9U0H3; Q9Y6Y2; 014869; 043355; 094895; Q9Y6B8;

16-0CT-2001 (Rel. 40, Last sequence update)

16-0CT-2001 (Rel. 40, Last annotation update)

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16-0CT-2001 (Rel. 40
843 KLTKFVEYLDK--VRRIFGRNGFQAYLRE-KYVPLIQKYLNEAFSEFDLPYSFV---ELT 896
                                                                                                                                                                                                                                    TISSUE-Brain;
MEDLINE-99151389; PubMed-9482789;
Lin J.W., Wyszynski M., Madhavan R., Sealock R., Kim J.U., Sheng M.;
Lin J.W., Wyszynski M., Madhavan R., Sealock R., Kim J.U., Sheng M.;
Lin J.W., anovel protein of neuromuscular junction and brain that
interacts with specific splice variants of NMDA receptor subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takahashi M., Shibata H., Shimakawa M., Miyamoto M., Mukai H., Ono Y. "Characterization of a novel giant scaffolding protein, CG-NAP, that anchors multiple signaling enzymes to centrosome and the golgi
                                                                                             812 EIETGI-----MSNLE----KEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Gastric parietal cell;
MEDLINE-99115654; PubMed-9915845;
Schmidt P.H., Dransfield D.T., Claudio J.O., Hawley R.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 2), AND VARIANT GLN-1347 INS. MEDLINE-99219864; Pubmed-10202149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                            QHQCVK------KQCPQNSGCFRHLDEREECKCLLNYKQEGD 1564
                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 323-3911 FROM N.A. (ISOFORM 2)
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Kemmner W.A., Deiss S., Schwarz U.;
"Cloning of Hyperion.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-99287934; PubMed-10358086;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 4).
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REQUENCE OF 17-1800 FROM N.A.

A WU X., Graves T., Bradshaw H.;

Lundited (SEP-1998) to the Embl./Genbank/DDBJ databases.

Lundited (SEP-1998) to the Embl./Genbank/DDBJ databases.

Lundited (SEP-1998) to the Embl./Genbank/DDBJ databases.

SUBSTRATASES ON CENTROSOME AND GOLGI APPRARTUS WHERE PHYSTOLOGICAL EVENTS CAN BE REGULATED BY PHOSPHORYLATION STATE OF PROTEIN KINASE AND SAPARATES. ISOFORM 4/YOTIAO IS ASSOCIATED WITH THE N-METHYL-D-CASPARATES RECEPTOR AND IS SPECIFICALLY FOUND IN THE NEUROMUSCULAR JUNCTION (NMJ) AS WELL AS IN NEURONAL SYNAPSES EXPLAINING THAT ITS ROLE MAY BE TO ORGANIZE POSTSYNAPTIC SPECIALIZATIONS.

C. -I- SUBUNT: INTERACY WITH THE REGULATORY REGION OF PROTEIN KINASE N (PKN), PROTEIN PHOSPHATASE 2 (PPZA), PROTEIN PHOSPHATASE 1 (PPL)

C. -I- SUBUNT: NUERANCY WITH THE REGULATORY REGION OF PROTEIN CONTON.

C. -I- SUBUNT: NUERANCY WITH THE REGULATORY REGION OF PROTEIN CONTONING THAT ITS SUBCELLAR LOCATION: CENTROSOMAL IN MANY CELL TYPES AND CYTOPLASMIC IN PARIETAL CELLS.

C. -I- ALTERNATIVE PRODUCTS: 6 ISOFORMS; 1 (SHOWN HERE), 2, 3/CG-CANTANCY CONTONING THAT CELLS.

C. -I- ALTERNATIVE PRODUCTS: 6 ISOFORMS; 1 (SHOWN HERE), 2, 3/CG-CANTANCY.

C. -I- ALTERNATIVE PRODUCTS: 6 ISOFORMS; 1 (SHOWN HERE), 2, 3/CG-CANTANCY.

C. -I- ALTERNATIVE PRODUCTS: 6 ISOFORMS; 1 (SHOWN HERE), 2, 3/CG-CANTANCY.

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C. -I- ALTERNATIVE PRODUCTS: 6 IS
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the Buropean Bioinformatics Institute. There are no restrictions on
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modified and this statement is not removed. Usage by and for commerc
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-!- DOMAIN: RIL BINDING SITE, PREDICTED TO FORM AN AMPHIPATHIC HELIX, COULD PARTICIPATE IN PROTEIN INTERACTIONS WITH A COMPLEMENTARY SURRACE ON THE R-SUBUNIT DIMER.

-!- CAUTION: REF. 6 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO TWO FRAMESHIFTS IN POSITIONS 3782 AND 3811.

-!- CAUTION: REF. 9 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FOUR FRAMESHIFTS IN POSITIONS 29, 1653, 1699 AND 1735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; Prediction of the coding sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Milgram S.L., Goldenring J.R., Schmidt P.H.;
"AKAP350: A multiply spliced family of proteins with centrosomal
association.";
Trotter K.W., Milgram S.L., Goldenring J.R.; "AKAP350, a multiply spliced protein kinase A-anchoring protein associated with centrosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                 databases
                                                                                                                                                                                                                                                                                                                                              Hinds K., Sutterer C., Becker M., Hawkins M.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ
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9
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EMBL; AC004013; AAB96867.1; ALT_FRAME.
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                                                                                                                                               Biol. Chem. 274:3055-3066(1999).
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MEDLINE=99087487; PubMed=9872452;
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BAA34523.1;
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                                                                                                                                                                                          1164 KNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAE 1223
                                                        -----TEQNYEAE--IHCLOKRL-----QAVSES-----TVPPSLPVDSVVITE 1405
                                                                                                                              IENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFKNVLESDLIPY 1336
                                                                                                                                                    SDLDSIKKYINDKQGENEKYLPFLNN-----IETLYKTVNDKIDLFVIHLEAKV 1443
                                                                                                                                                                              KDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGY--YKILSEKYK 1394
                                                                                                                                                                                                                                                   1524 EEFKPLSKEL----GEHGKEILLSNSDPHDIPESKDCVLTISEEMFSKDKTFIVR---- 1574
                                                                                                                                                                                                                                                                           1444 LNYTYEKSNVEVKIKELNYLKTI -- - QDKLADFKKNNNFVGIADLSTDYNHNNLLTKFL 1499
                                                                                                                                                                                                                                                                                          ----QSIHDEISVSSMDASRQLMENNEEQLEDMRQ------QSIHDEISVSSMDASRQLMENNEEQLEDMRQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lemaire C., Heilig R., Mandel J.L.; "The chicken dystrophin cDNA: striking conservation of the C-terminal coding and 3' untranslated regions between man and chicken."; EMBO J. 7:4157-4162(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLASMA MEMBRANE.

-!- FUNCTION: MAY PLAY A ROLE IN ANCHORING THE CYTOSKELETON TO THE PLASMA MEMBRANE.
-!- SIMILARITY: THE ACTIN-BINDING DOMAIN IS OF A TYPE FOUND IN MANY ACTIN-BINDING PROFIEINS (SUCH AS ACTININ, DYSTROPHIN, FIMBRIN, ABP-120, ABP-180, OR BETA-FODRIN).
-!- SIMILARITY: CONTAINS 2 CALPONIN-HOWOLOGY (CH) DOMAINS.
-!- SIMILARITY: CONTAINS 1 WM DOMAIN.
-!- SIMILARITY: CONTAINS 1 WM DOMAIN.
-!- SIMILARITY: CONTAINS 1 Z2-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lemaire C., Heilig R., Mandel J.L.;
"Nucleotide sequence of chicken dystrophin cDNA.";
Nucleic Acids Res. 16:11815-11815(1988).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                              3660 AA
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MEDLINE-89210800; PubMed=3072195;
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MEDLINE-89098331; PubMed=3062582;
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01-0CT-1989 (Rel. 12, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Dystrophin.
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DMD_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 YRKPLDNIKDNVGKMEDYIKKNKKTIENINELIEE------SKKTIDKNKNA 269
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                                                                                                                                                                                                                                                                                                                                                                                                      Structural protein; Actin-binding; Calcium-binding; Cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               %; Score 361; DB 1; Length 3660;
%; Pred. No. 0.00011;
297; Mismatches 592; Indels 588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> H.
-> R.
85493DAF6D5B6D4A CRC64;
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SPECTRIN 5.
SPECTRIN 6.
SPECTRIN 7.
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SPECTRIN 2.
SPECTRIN 3.
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SPECTRIN 19
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SPECTRIN 7
SPECTRIN 8
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SPECTRIN 1
SPECTRIN 1
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MISSING.
                           InterPro; IPR001589; Actbind_actnin.
InterPro; IPR001715; Calponin-like.
InterPro; IPR002017; Spectrin.
InterPro; IPR0020349; WW.
InterPro; IPR001202; WW_RSp5_WWP.
InterPro; IPR001433; Znf_Zz.
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SMARY; SM00291; ZNF_ZZ; 1.
PROSITE; PS00019; ACTININ_1; 1.
PROSITE; PS00020; ACTININ_2; 1.
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Pfam; PF00569; 22; 1.
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PROSITE; PS50135; ZF_ZZ_2;
                                                                                                                                                                                                  PRINTS; PR00403; WWDOMAIN.
                                                                                                                                                                                                              SMART; SM00033; CH; 2.
SMART; SM00150; SPEC; 21.
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3351
1171
1869
1885
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137	TREEERRELYONGYDESIYNRULEARINLISVLEKRIDIEKK- 311 	NENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEHEKEIKEIAKTIKFNIDSL 368 	FTDPLELEYYLREKNKNIDISAKVET	PLSYNDINNAL	YTKEPSKNIYTDNERKKFINEIKEKKIESDKKSYEDRSKSLNDITK 486 :	EYEKLINEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSK 537 : : : : : : : :	HNLEKLTKALKXMEDYSLRNIVVE	KELKYYKNLISKIENEIETLVENIKKDEEQ ^L FEKKITKDENKPDEKILEV 611 : : : : :: KPFIPLKELEQFDFDIQKLLEPLEVEIQQGV-NLKEEDFNKDMSEDDESTVKELLQR 1832	SDIVKVQVQKVLLMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPXYLIVL 667 :: :: :: : :	KKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAG 722 ::	SALEGDSVOAQAQEQKQAQPPVPVPVFAKAQVPTPPAPVNNKTENVSKLDYLEKL 778 :	YEFLNTSYICHKYILUSHSTMNEKILKQYKITKEEËSKLSSCDPL 823 	BLLENIQNNIPVMXS-MFDSLNNSLSQLFMEIYEKEMVCNLYKLK 867	DNDKIKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNS 922	LKLFENILSLGKNKNIYQELIGQKSSENFYEKİLKDSDTFYNESFTNFVKSK 974	ADDINSLNDESKRKKLEEDINKLKKTLQLS 1004 :: : : : LGNLNTRWQEICRQLYEKRRIEEEKNILSEFQEDLNKLILMLEETENVIAIPLEPGNED 2247	FDLYNKYKLKLERLFDKKKTVGKYKMQ KKLTLLKEQLESKLNSLNN 1051 	-AETENTLENTKILLKHYKGLVKYYNGESSP-LKTL 1105
									SDIVKVQVQKVLL :: :: GDTLQKRI									PKHVLQNFSVFFNKKKEAEI
1	uy 270 Db 1374	Oy 312 Db 1433	Qy 369 Db 1491	Qy 410 Db 1551	Qy 435 Db 1611	Qy 487 Db 1668	Qy 538 Db 1717	Qy 562 Db 1777	Oy 612 Db 1833	Qy 668 Db 1885	Oy 723 Db 1945	Oy 779 Db 1978	Qy 824 Db 2038	Qy 868 Db 2098	Oy 923 Db 2143	Oy 975 Db 2188	Qy 1005 Db 2248	у 1052
	B 5	Qy Dp	Oy Dp	Q B	ç, G	Qy Dp	Qy Gp	Qy Dp	Qy Dp	O D	Q D	Q D	Q Dp	oy G	oy B	oy Op	69 Op	οy

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1 : | | | : | | | : | | | 2418 EKPTFGEPALTSPGVLTSGQTVAVDTQARVTKETTSFTPEMPSSVLLEV-PALADFNKAW 2476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2800 STDQWKRLHISLQELLAWLQLKEDELKQQAPIG-GDIPTVQKQNDVHRTFKRELKTKEPV 2858
                                                                      SEESIQTEDNYASLENFKVLSKLEG----KLKDNLNLEKKKLSYLSS---GLHHLIAELK 1158
                                                                                                                 1362 KETEAAVQAKQPINE--EVLSK--GCHLYKEKPATHPVKKKLEDLINADHKAINHLILQLK 2417
                                                                                                                                                                                                                       ------VIKNKNYTGNSPSENNTDVNNALESYKKFL 1189
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2303 -RRLLKVSRDLPEKQKEIEILLKDFIELNQQINQLTLWITPVKNQLELYNQVGQPGAFDI 2361
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MEDLINE-95096166; PubMed=7798308;

MEDLINE-95096166; PubMed=7798308;

Byrd D.A., Sweet D.J., Pante N., Konstantinov K.N., Guan T.,

Saphire A.C.S., Mitchell P.J., Cooper C.S., Aebi U., Gerace L.;

"Tpr, a large coiled coil protein whose amino terminus is involved in activation of oncogenic kinases, is localized to the cytoplasmic surface of the nuclear pore complex.";

J. Cell Biol. 127:1515-1526(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                          2528 ITAAQNLKNKTSNQEARTIITDRIEKIQSQWDDVHGYLQNRRQQLHEMQKDSTQWLEAKQ
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-0cT-1996 (Rel. 34, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Nucleoprotein TPR.
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SEQUENCE FROM N.A.
MEDLINE=93064711; Pubmed=1437155;
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P12270;
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TPR_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :99
                                                                                                                -:- FUNCTION: COMPONENT OF THE CYTOPIASMIC FIBRILS OF THE NUCLEAR PORE IN TINVOLVED IN ACTIVATION OF ONCOCRONIC MARSES.
-:- SUBCELLULAR LOCATION: CYTOPIASMIC SURRACE OF THE NUCLEAR PORE COMPLEX. THE ASSEMBLY OF THE NPC IS A STEPWISE PROCESS IN WHICH TRP-CONTAINING PERIPHERAL STRUCTURES ASSEMBLE AFTER OTHER
                                                                                                                                                                                                                                                                     COMPONENTS, INCLUDING P62.

TISSUE SPECIFICITY: HIGHEST IN TESTIS, LUNG, THYMUS, SPLEEN AND BRAIN, LOWER LEVELS IN HEART, LIVER, AND KIDNEY.

DISEASE: INVOLVED IN TUMORIGENIC REARRANGEMENTS WITH THE MET, TRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNHMLTLCDNIHGFKYLIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIR 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MNGLKTSNEHLQKHVEDLLTKLKEAKEQQASMEEKFHNELNAHIKLSNLYKSAADDSEAK 299
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SEQUENCE OF 1-142 FROM N.A.
MEDLINE-88262257; PubMed=3387099;
King H.W.S., Tempest P.R., Merrifield K.R., Rance A.J.;
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ilarity 18.5%; Pred. No. 8.3e-05;
Conservative 317; Mismatches 659;
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                                                                                                   Oncogene 2:617-619(1988)
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Genew; HGNC:12017; TPR.
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                                                                            ----VAKIVKPGMKLTELYNAYVETQDQLLLEKLENKRINKYLDEIVKEVEAKAPILK 438
                                                                                                                                                                                                                                                                                                                                THHNTFASYE----NSKHNL--EKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEI 578
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-YKSDLDSIKKYINDKOGENEKYLPFLNN 1420
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"Characterization of the kinetochore binding domain of CENP-E reveals interactions with the kinetochore proteins CENP-F and hBUBRI.";
J. Cell Biol. 143:49-63(1998).
-I- FUNCTION: PROBABLY REQUIRED FOR KINETOCHORE FUNCTION, INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhu X., Chang K.-H., He D., Mancini M.A., Brinkley W.R., Lee W.-H.; "The C terminus of mitosin is essential for its nuclear localization, centromere/Kinetochore targeting, and dimerization."; J. Biol. Chem. 270:19545-19550(1995).
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SEQUENCE OF 2194-3210 FROM N.A.
MEDLINE-95336446; PubMed-7612011;
Li Q., Ke Y., Kapp J.A., Fertig N., Medsger T.A. Jr., Joshi H.C.;
Li Q., ke Y., Kapp J.A., Fertig Solving Model of the protein: C-terminal
"A novel cell-cycle-dependent 350-kba nuclear protein: C-terminal
                                                                                                                   ::: | :: | | :: | HEQHVSVQEMQELKETLNQAETKSKSLESQV--ENLQKTLSEKETEARNLQEQTVQLQS
                                                                                                                                                                   FKKNNNFV-GIADLSTDYNHNNLLTKFLSTGMVFENLAKTV-----LSNLLDGNLQGML
                                               IETLYKTVNDKIDLFVIHLEAKVLNYT-----YEKSNVEVKIKELNYLKTIQDKLAD
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TISSUE=Breast carcinoma;
MEDILINE-95348175; Pubmed-7542657;
Liao H., Winkfein R.J., Mack G., Rattner J.B., Yen T.J.;
"CENP-F is a protein of the nuclear matrix that assembles onto
Kinetochores at late 62 and is rapidly degraded after mitosis.";
J. Cell Biol. 130:507-518(1995).
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                                                                                                                                                                                                                                                                                                                                                         F) (Mitosin) (AH
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                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                        (Centromere protein
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NFANDVLGYYKILSEK
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[2]
SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
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                                                               -i- SUBCELLUIAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE NUCLEOLUS), REORGANIZATION TO THE KINETOCHORE/CENTROMENE (CORONAL SURFACE OF THE OUTER PLATE) AND THE SPINDLE DURING MITOSIS.

-i- DEVELOPMENTAL STAGE: GRADUALLY ACCUMULATES DURING THE CELL CYCLE.
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CHROMOSOME SEGREGATION DURING MITOSIS. INTERACTS WITH RETINOBLASTOMA PROTEIN (RB), CENP-E AND BUBRI. SUBUNIT: HOMO- OR HETERODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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        Mitosis;
        Phosphorylation;
        Antigen;
        Cell Cycle;
        Repeat.

        DOMAIN
        273
        769
        COLLED COLL (POTENTAL).

        DOMAIN
        273
        1328
        COLLED COLL (POTENTIAL).

        DOMAIN
        1642
        1746
        COLLED COLL (POTENTIAL).

        DOMAIN
        1862
        2987
        COLLED COLL (POTENTIAL).

        DOMAIN
        2007
        2568
        2 x 177 AA TANDEM REPEATS

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L -> O (IN REF. 2).
G -> D (IN REF. 2).
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V -> L (IN REF. 2).
V -> L (IN REF. 2).
ER -> DG (IN REF. 3).
L -> O (IN REF. 3).
D -> N (IN REF. 3).
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llarity 18.8%; Pred. No. 0.00015;
Conservative 305; Mismatches 631;
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Chromosomal protein; Nuclear prot
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tock K.G., Merrick J.M., Glodek A.,
dman J.F., Fuhrmann J.L., Nguyen D.,
rson J.D., Sadow P.W., Hanna M.C.,
M.A., Kaine B.P., Borodovsky M.,
I.O., Woese C.R., Venter J.C.,
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dman J.F., Fuhrmann J.L., Nguyen D.,

rson J.D., Sadow P.W., Hanna M.C.,

M.A., Kalne B.P., Borodovsky M.,

O., Woese C.R., Venter J.C.;

GenBank/DDBJ databases.

ROLE IN CHROMOSOME STRUCTURE AND

HROMOSOME PARTITION (BY SIMILARITY).

C FAMILY.
                                                                                                                           ENNVMTFNVNYKDILNSRFNKRENFKNVLE 1330
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                                       VT-----GEAVTPS----VIDNILSKIE 1278
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ASIEHE-----ALYLEADLEVVQTEKL 2029
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TISSUE-Heart;
MEDLINE-90016823; PubMed-2798112;
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                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smitth D.R.;

"Genome sequence and comparative analysis of the solvent-producing Dacterium Clostridium accetobutylicum.";

"Genome sequence and comparative analysis of the solvent-producing Dacterium Clostridium accetobutylicum.";

"Bacteriol. 183:4823-4838(2001).

"I Bacteriol. 183:4823-4838(2001).

"I FUNCTION: SDCCD cleaves DNA hairpin structures. These structures can inhibit DNA replication and are intermediates in certain DNA recombination reactions. The complex acts as a 3->5 double strand exonuclease that can open hairpins. It also has a 5' single-strand endonuclease activity (By similarity).

"SUBUNIT: Heterodimer of sbcC and sbcD (By similarity).

"SUBUNIT: BELONGS TO THE SMC FAMILY. SBCC SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNE 313
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                                                                                                                                                                                                                                                                                                                                             Interpro; IPR003439; ABC_transportr.
Hydroclase; Nuclease; Exonuclease; Endonuclease; DNA replication;
DNA recombination; ATP-binding; Coiled coil; Complete proteome.
NP_BIND
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 1163;
                                                                                                                                                                                                                                                                                                                                                                                                                                     CE5F0BD2215D7A92 CRC64;
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Matches 274; Conservative 212; Mismatches 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.2%; Score 352.5;
                                                                                                                                                                                                                                                                                                                                                                                                                     446 1003 COI
1163 AA; 135507 MW;
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197
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DINKLK-KTLQLSFDL--YNKYKLKLERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNSL 1049
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                              464
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01-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, cardiac muscle beta isoform (MyHC-beta).
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1784
1851
1858
1935
   Myosin; Muscle
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                                                                                                                                                                                                                                                                                                                                                                                                THE TATACTATION WISCLE CONTRACTION.

- 1- FUNCTION: MUSCLE CONTRACTION.

- 1- SUBGUIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

- 1- SUBGUIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

- 2- BEGULATORY LIGHT CHAIN SUBGNITS (MLC-2).

- 3- BEGULATORY LIGHT CHAIN SUBGNITS (MLC-2).

- 1- SUBGELLULAR LOCATION: THICK filaments of the myofibrils.

- 1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING

CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,

CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,

CHARACTERISTIC FOR ALPHA-HELICAL COILED COILE.

- 1- PTM: TWO CYSTEINE RESQUIRED FOR MYOSIN ATPASE ACTIVITY.

- 1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO I LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (AMM). IT CAN LATER BE

SPLIT FURTHER TINTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                    SEQUENCE OF 1524-1935 FROM N.A.
MEDILINE-82220065; Pubbed-7045682;
Mandavi V., Periasamy M., Nadal-Ginard B.;
"Molecular characterization of two myosin heavy chain genes expressed
                                                                                          MEDLINE-90133919; PubMed-2614840; MCN31ly E.M., Kraft R., Bravo-Zehnder M., Taylor D., Leinwand L.A.; "Full-length rat alpha and beta cardiac myosin heavy chain sequences. "Comparisons suggest a molecular basis for functional differences."; J. Mol. Biol. 210:665-671(1989).
                                                                                                                                                                                                                                                                                                                                           Mahdavi V., Lompre A.M., Chambers A.P., Nadal-Ginard B.; "Cardiac myosin heavy chain isozymic transitions during development and under pathological conditions are regulated at the level of mRNI availability.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBFRAGMENT (S2).

MISCELLANEOUS: THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATPASE MYOSIN, WHILE THE BETA ISOFORM IS A 'SLOW' ATPASE.

SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
craft R., Bravo-Zehnder M., Taylor D., Leinwand L.A.;
Complete nucleotide sequence of full length cDNA for rat beta
                                              Nucleic Acids Res. 17:7529-7530(1989).
                                                                                                                                                                                                                                                                                                           STRAIN-Wistar; TISSUE-Heart;
MEDLINE-85179510; PubMed-6241892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0193; MYOSINHRAVY.
PRODOM; PD000355; MYOSINI-head; 1.
SMART; SM00195; TQ: 1.
SMART; SM00242; MYSC; 1.
PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro: IPR000048; IQ_region.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                               SEQUENCE OF 1871-1935 FROM N.A.
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Pfam; PF00612; IQ; 2.
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                                 cardiac myosin heavy chain.";
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                                                                                                                                                                                                                                                                 Nature 297:659-664(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF02736; Myosin_N;
                                                                             DISCUSSION OF SEQUENCE.
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024 KVKLEQQVDD--LEGSLDQDKKVRMDLERAKRKLEGDLKLT-QESIMDLENDKQQLDERL 1080
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protein; Coiled coil; Thick filament; Actin-binding;
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METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
IRK -> VRR (IN REF. 3).
N -> K (IN REF. 3).
N -> K (IN REF. 3).
R -> K (IN REF. 3).
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Matches 286; Conservative 265; Mismatches 589;
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ACTIN-BINDING.
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                                                                            LEKMCRTLEDOMNEHRSKAEETQRSVNDLTRQRAKLQTENGELSRQLDEKEALISQLTR- 1303
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  ALRKKHADSVAELGEQIDNLQ----RVKQKLEKEKSEFKLE--LDDVTSNMEQIIKAKAN 1244
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                                     ----TKPGQQAGSALEGDSVQAQAQEQKQAQPPVPVPEAKAQVPTPPAPVNNKTEN
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                                                                                                                  VSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLFN
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Catarrhini; Hominidae;
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MEDLINE-91065634; PubMed=2249844;
Medlicke T. Diederich K.W., Haas W.,
Pfordt M., Bach A., Vosberg H.P.;
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Mammalla; Eutheria; Primates;
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"Molecular cloning and characterization of human cardiac alpha- and
beta-form myosin heavy chain complementary DNA clones. Regulation of
expression during development and pressure overload in human
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Y., Joh-O K., Kawana M., Takao A.,
     chain gene
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Sci. U.S.A. 86:7416-7417(1989).
     beta-myosin heavy
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MEDLINE-88299163; Pubmed-2969919;
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                                                           1081 KKKDFELNALNARIEDEQALGSQLQKKLKELQARIEELEEELES--ERTARAKVEKLRSD 1138
                                                                                                                                                                                                                                                                                                                                                                                1191 ALRKKHADSVAELGEQIDNLQ----RVKQKLEKEKSEFKLE--LDDVTSNMEQIIKAKAN 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1245 LEKMCRTLEDOMNEHRSKAEETQRSVNDLTSORAKLOTENGELSROLDEKEALISOLTR- 1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KTIHELEKVRKQLEAEKMELQSALEEAEASLEHEEGKILRAQLEF---NQIKAEIERKLA 1577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDV-----NNALESYKKFL-PE 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1674 VERRNNLLQAELEELRAVVEQTERSRKLAEQELIETSERVQLLHSQNTSLINQKKKMDAD 1733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1833 NAESVKGMRKSERRIKELTYQTEEDRKNLLR----LQDLVDKLQLKVKAYKRQAEEAEE 1887
-- NKVKNLTEEMAGLD 986
                                                                                                                                                                                                                                                                                                                                            655 QENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEPSTEGEITGQAT 714
                                                                                                                                                                                                                                                                                                                                                                                                                          ----TKPGQQAGSALEGDSVQAQAQEQKQAQPPVPVPVPEAKAQVPTPPAPVNNKTEN 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   769 VSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLFN 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLSSSSMQPLSLTPQDKPE---VSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQELIG 944
                                   DLIMPFDYTKEPSKNIYTDNERKKFINEIKEKIKIEKKKIESDKKSYEDRSKSLNDITKE 487
                                                                                                                                                                                                                                                                597 ITKDENKPDEKILEVSDIVKVQVQKVLLMNK--IDELKKTQLILKNVELKHNIHVPNSYK
                                                                                                           YEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYKVE---KLTHHNTFASYENSKHNLEKLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKD-NDKIKNLLEEAKKVSTSVK
                                                                                                                                                                                         KALKY - - - - - - - MEDYSLRNIVVEKELKYYKNLISKIENEIETLVENIKKDEEQLFEKK
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-AKVEKEKHATE-
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1888 QANTNLSKFRKVQHELD 1904
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 SIYNKQLEEAHNLISVLEKRIDTLK-----KNENIKELLDKINEIKNPPPANSGNTPNT 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 SDAKSYADLKHRVRNYLLTIKELKYPQL-----FDLTNHMLTLCDNIHGFKYLIDGYEE 173
                                                                                                                                                                                                                                                                                                                Coulson A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEAKTFNNVLSR-WEYLLKLLALKWRQLEKEIESIEFKNK----CDSI-----VDWILK 114
                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                         Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hiller L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen F
Sims M., Smaldon N., Smith A., Sonhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ن
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 INELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRA---NELDVLKKLVFGYRKPLDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 IKESDESGKEIFDEIRK-----CSMVWN-EISATFQQMLDPTATDTSNYEK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 IKDNVGKMEDYIKK-NKKTIENINELIEESKKTIDKNKNATK--EEEKKKLYQ--AQYDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 VHETWSNFQEYIDSLHKKLSEN----ERFQKFVDNAEDLIKWMDDKEKEICEKYSKMDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2198;
                                                     01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical 256.3 kDa protein C50C3.2 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD1B2C1092C5EDC8 CRC64;
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Ā
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                                                                                                                                                                                                                                                    STRAIN=Bristol N2;
MEDLINE=94150718; PubMed=7906398;
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                                    (Rel. 28, Created)
(Rel. 28, Last seq
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InterPro; IPR002048; EF-hand.
InterPro; IPR002017; Spectrin.
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Hypothetical protein; Calcium
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Pfam; PF00435; spectrin; 10.
ProDom; PD000012; EF-hand; 1.
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STANDARD;
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                                                                                                                                  Caenorhabditis elegans.
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                                    01-FEB-1994
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SEQUENCE
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Oy 1284 LYLKPL Qy 1284 LYLKPL Db 1159 CDA/TLI Qy 1344 YVVKDP :: 1 Db 1207BNK Qy 1401 KKYIND Qy 1401 KKYIND Qy 1461 NYLKTI Db 1236 SQILID Qy 1461 NYLKTI Db 1267KTK	RESULT 37 WYH6_MESAU ID WYH6_MESAU ID WYH6_MESAU AC P13539; Q60 DT 01-JAN-1990 DT 15-DEC-1998 DT 16-OCT-2001 DE Myosin heav GN WRH6.		RT Syrian hams RL Proc. Natl. CC -!- SUBNIT CC - HEAVY C CC - SUBNIT CC -!- SUBNIT CC -!- SUBLIL CC -!- DOMAIN CC -!- PTW. TW CC -!- PTW. TW CC -!- PTW. TW CC -!- PTW. TW CC -!- PTW. TW CC -!- PTW. TW CC -!- PTW. TW CC -!- PTW. TW CC -!- PTW. TW CC -!- SUBFROMYO CC -!- MISCELL CC -!- MISCELL CC -!- MISCELL CC -!- MISCELL CC -!- MISCELL CC -!- MISCELL CC -!- SIMILAR CC -!- SIMILA
			7
115 EVMMKYRTVEIEMKSVEORIKOLKEOPVGMENDNLENIPDPKNH 259 340 LLDKNKKIEEHEKEIKEIARTIKFNIDSLETDPLELEYYLREKNKNIDISAKVETKES 397 11	LUNKIDELKKTQLILKNVEIKHNIHVPNSYKQENKQEYKTTVNSRKAILQRILLDVTYF LMMKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYLLTVKKEIDKLKVFMPK	797 STMNEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVWYSMFDSLNNSLSQ 849 633ICASYKKSIDSKLEELANVYTDNDPRCLLEGIQ	1001 LQLSFDLYNKYKLERLEPDKKKTVGKYKMQIKKITLLKEQLESKLN 1047 8 1
		64 64 65 65 65 65 65 65 65 65 65 65 65 65 65	

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|DEQ-----FDTIRQWIKERTEA----LEADV-----EVSN------1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "I. Acad. Sci. U.S.A. 83:3175-3179(1986).

ION: MUSCLE CONTRACTION.

IT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

THE MUSCLE MYOSIN IS A LEKALI LIGHT CHAIN SUBUNITS (MLC.)

REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

LEULAR LOCATION: Thick filaments of the myofibrils.

LEULAR LOCATION: Thick filaments of the myofibrils.

SOF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CTERISTIC FOR ALPHA-HELICAL COLLED COLLS.

CTERISTIC FOR ALPHA-HELICAL COLLED COLLS.

TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ATED. AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY (BY
RETIDIKQDDLCRFADILG-AERDCERLYSWASGKR------HQLETEATM 1158
                                                                   LAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFKNVLESDLIPYKDLTSSN 1343
                                                                                                           LVRRMNEVEKMMMSRIGEVD-QLRDFL-----DNLKASKTSDTFQTTEL---- 1206
                                                                                                                                                                                                           PYKFLNKEKRDKFLSSYNYIKDSI---DTDINFANDVLGYYKILSEKYKSDLDSI 1400
                                                                                                                                                                                                                                                                                                                                               DKQGENEKYLPFLNNIETLYKTVNDKIDLFVIHLEAKVLNYTYEKSNVEVKIKEL 1460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IQDKLADFKKNNNFVGIADLSTDYN-HNNLLTKFLSTGMVFENLAKTV---LSNL 1516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115033; PubMed=7815459;
Sole M.J., Cukerman E., Liew C.-C.;
traction and nucleotide sequence of the cardiac alpha-myosin in gene from Syrian hamster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0F 1630-1939 FROM N.A.
;205859; PubMed=3458174;
, Jandreski M.A.;
ino and characterization of the alpha form of a cardiac
ivy chain cDNA clone and its developmental expression in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NRITY).

LAMBOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT COSIN (LAM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGMENT (S2).
LANDEOUS: THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATPASE
A, WHILE THE BETA ISOFORM IS A 'SLOW' ATPASE.
MARITY: CONTAINS I MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
ARITY: CONTAINS I 1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               00 (Rel. 13, Created)
88 (Rel. 37, Last sequence update)
11 (Rel. 40, Last annotation update)
NVy chain, cardiac muscle alpha isoform (MyHC-alpha).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QGMLNISQHQCVKKQCPQNSGCFRHLD 1548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TROKSLAQ-----EC-QKSRLFELLD 1343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VASGGSVASGGSVASGGSG----NSRRTNPSDNSSDSDAKSYADLKHRVRNYLLTIKELK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRKGAEKLLSSLDIDHNQYKFGHTKVFFKAGLLGLLEEMRDERLSRIITRIQAQARGQLM 799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50096; IQ; 1.
Myosin; Muscle protein; Colled coil; Thick filament; Actin-binding;
ATP-binding; Methylation; Alkylation; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGTAVTTSTPGSKGSVASGGSGGSVASGGS
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ACTIN-BINDING.
METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
ALKYLATION (SH-2).
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COILED COIL (POTENTIAL).
POLY-ALA.
ATP (POTENTIAL).
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19.4%; Pred. No. 0
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InterPro; IPR00409; Myosin_N.
InterPro; IPR004099; Myosin_Lail.
InterPro; IPR001509; Myosin_head.
Pfam; PF00612; Myosin_head; 1.
Pfam; PF01576; Myosin_Lail; 1.
Pfam; PF01576; Myosin_Lail; 1.
PrinrS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
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SMART; SM00242; MYSC; 1.
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                                                                                                                                                                                                                                                                                                                                                           DLLREQYEEEMEAKAELQRVLSKANSEVAQWRTKYETDAIORTEELEEAKKKLAQRLQDA 1402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1232 ---nvddevddviivpifgeseedyddlggv-vtgeavtpsvidnilskieneyevlylk 1287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     777 KLYEFLNTSYICHKYILVSHSTMNE----KILKQYKITKEEESKLSS------C 820
                                                                                                                                                                                                                                                                                                                                                                                                                                     482 NDITKEYEKL---LNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSKH 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  539 NLEKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEIETLVENIKKDEEQLFEKKIT 598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKVSTSVKTLSSSSMQPLSLTPQDKPE---VSANDDTSHSTNLNNSLKLFENILSLGKNK 936
256 IEESKKTIDKNKNATKEEEKK--KLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNE 313
                                                                                                                                                                                                                                                                                                                           DLINPFDYTKEPSKNIY-----TDNERKKFINEIKEKIKIEKKKIESDKKSYEDRSKSL 481
                                                FGRVKESLEKSEARRKELEEKMVSLLQEKNDLQF---QVQAEQDNLNDAEERCDQLIKNK 914
                                                                                                                                                                                                                 FTDPLELEYYLREKNKNIDISAKVE-TKESTEPNEYPNGVTYPLSYNDINNALNELNSFG 427
                                                                                                                                                                                                                                                                     --DDLELTL-----AKVEKEKHATE------NKVKNLTEEMAGLD
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                                                                                                       ----NIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNIDSL
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                                                                         1288 PLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVK 1347
                                                                                                        1830 -----AEQKRNAESVKGMRKSERRIKELTYQTEEDKKN-----LVRLQDLVDKLQLKV 1877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: MUSCLE MYOSIN IS A HEAAMERIC PROTEIN THAT CONSISTS OF 2 BEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC.2).

SUBCELLULAR LOCATION: Thick flaments of the myofibrils.

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAR PATHEN COMPOSED OF 4 HEPTAPERITIDES, CHARACTERISTIC FOR ALLHA-HELICAL COLLED COLLS.

PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLAFED AND ARE REQUIRED FOR MYOSIN ATOMIN AND I LIGHT MEROMYOSIN (LAM) AND I HEAVY CHAIN CAN BE SPLIT INTO I LIGHT MEROMYOSIN (LAM) AND I HEAVY MEROMYOSIN (HAM). IT CAN LATER BE SPLIT FURTHER LAND SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-83161144; PubMed-6833296; MEDLINE-83161144; PubMed-6833296; Meximsky C.J., Umeda P.K., Sinha A.M., Blzinga M., Tong S.W., Zak R., Jakovcic S., Rabinowitz M.; "Cloned mRNA sequences for two types of embryonic myosin heavy chains from chick skeletal muscle. I. DNA and derived amino acid sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molina M.I., Kropp K.E., Gulick J., Robbins J.;
The sequence of an embryonic myosin heavy chain gene and isolation
of its corresponding only ".
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SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, fast skeletal muscle, embryonic.
                                                                                                                                                                                                                                                                                                                                                        1940 AA
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                                                                                                                                                                                                         1348 DPYKFLNKEKRDKF---LSSYNYIKDSID 1373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     its corresponding cDNA.";
Biol. Chem. 262:6478-6488(1987).
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MEDLINE-87194881; PubMed-3571266;
                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 01, Created)
(Rel. 33, Last sequ
(Rel. 40, Last anno
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                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A02990; A02990.
PIR; A29320; A29320.
HSSP; P13538; 2MYS.
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P02565;
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InterPro; IPR000048; IQ_region

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 GGSVASGGS------GNSRRTNPSDNSSDSDAKSYADLKHRVRNYLLTIKELKYPQ 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            435 YTKEPSKNIYTDNERKKFINEIKEKIKIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNE 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   495 IYDSKFNNNIDLTNFEKMMGKRYSYKVE---KLTHHNTFASYENSKHNLEKLTKALKY-- 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVFGYRKPLDNIKDNVG-------KMEDYIK--KNKKTIENINELIEESKKT 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    316 KELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLEL 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 DAVLTGYSLFQKEKMVLNEGTSGTAVTTSTPGSKGSVASGGSGGSVASGGSVASGGSVAS 96
                                                                                                                                                                                                                                                                                                          Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
Calmodulin-binding; ATP-binding; Methylation; Alkylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            925 KELTERAEDEEE---MNA----ELTAKKRKLED---ECSELKKDI------DDLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              808 KMMERRESIFCIQYNVRAFMNVKHWPWMKLFFKIKPLLKSAESEKEMANMKEEFEKTKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 IDKNKNATKEEEKK--KLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNE----NI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 LF--DLTNHMLTLCDNIHGFKYLIDG------YEEINELLYKLNFYFDLLRA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTIN-BINDING.
ACTIN-BINDING.
METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          776 ACTIN-BINDIAMO.
130 METHYLATION (FRI-) (POTENTIAL).
700 ALKYLATION (SH-1).
710 ALKYLATION (SH-2).
379 G -> D. II-2).
1547 T -> A (IN REF. 2).
1915 ERA -> GRT (IN REF. 2).
AR; 222816 MW; C34833D75B04DFF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -KLNDVCANDYCQIPF ----NLKIRANELDVLK ------
                                                                                                                                                                                                                                                                                                                                                                                                                                          COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; DB 1;
0.00015;
                                                                                                                                                                                                                                                                                                                                                                                          MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 19.1%; Pred. No. 0.000
Matches 299; Conservative 262; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.1%; Score 348;
                                                                                                                     Pram; PP01576; Myosin_tail; 1.
Pfam; PF02736; Myosin_N; 1.
PRINTS; PR00193; MYOSINHEAVY.
Pr00bm; PD000355; myosin_head; 1.
SMART; SM0015; IQ; 1.
SMART; SM00242; MYSC; 1.
PROSITE; PS50096; IQ; 1.
IPR004009; Myosin_N.
IPR002928; Myosin_tail
IPR001609; myosin_head
                                                  InterPro; IPR001609; myosin_
Pfam; PF00063; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1940 AA;
                                                                                                                                                                                                                                                                                                                                                                  Multigene family.
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01-OCT-1993

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                                       SQIQSKIEDEQALGMQLQKKIKELQARIEELEEEEE--AERTSRAKAEKHRADLSRELEE
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-----MEDYSLRNIVVEKELKYYKNLISKIENEIETLVENIKKDEEQLFEKKITKDENK
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1225 AA.

PRT;

STANDARD;

SMC1_YEAST P32908;

SMC1_YEAST ID SMC1_YI AC P32908;

RESULT 39

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69;
                                                                                                                                                                                         MEDLINE-94103320; PubMed-8276886; Strunnikov A.V., Larionov V.L., Koshland D.; Strunnikov A.V., Larionov V.L., Koshland D.; SMCI: an essential yeast gene encoding a putative head-rod-tail protein is required for nuclear division and defines a new ubiquitous protein family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 IPFNLKIRANEL--DVLKKLVFGYRKPLDNIK----DNVGKMED----YIK----KNKK 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
ALA/ASP-RICH (DA-BOX).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAT. Genet. 10:261-266(1995).

-!- FUNCTION: INVOLVED IN CHROMOSOME SEGREGATION IN MITOSIS. COULD PART OF A CHROMOSOME CONDENSATION MOTOR.

-!- SUBUNIT: HOMODIMER OR HETERODIMER WITH SMC2 OR OLIGOMERS.

-!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.

-!- DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COLLED-COIL REGIONS FLANKED BY PUTATIVE GLOBULAR REGISONS AT THE N- AND C-TERMINUS.

-!- SIMILARITY: BELONGS TO THE SMC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                          Χ.
                                                                                                        Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
4.1%; Score 347; DB 1; Length 1225;
Best Local Similarity 20.3%; Pred. No. 9.6e-05;
Matches 284; Conservative 248; Mismatches 505; Indels 364;
                                                                                                                                                                                                                                                                                                                                                                    Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M., Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama Yamazaki M., Tashiro H., Eki T.; "Analysis of the nucleotide sequence of chromosome VI from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S->L: IN TS MUTANT SMC1-2.
N->D: IN TS MUTANT SMC1-1.
W; B504017AA0ECCA8C CRC64;
                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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COILED COIL (POTENTIAL).
                                 15-JUN-2002 (Rel. 41, Last annotation update)
Chromosome segregation protein SMC1 (DA-box protein
SMC1 OR CHL10 OR YFL008W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coil; Nuclear protein.
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                      Last sequence update)
                                                                                                                                                                                                                                                                                 . Cell Biol. 123:1635-1648(1993).
                                                                                                                                                                                                                                                                                                                                   STRAIN=S288c / AB972;
MEDLINE=95400292; PubMed=7670463;
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PIR; S41804; S41804.
SGD; S0001886; SMC1.
InterPro; IPR003405; SMC_C.
InterPro; IPR003395; SMC_N.
Pfam; PP02463; SMC_N.
Pfam; PP02463; SMC_N.
I.
Mitosis; ATP-binding; Coiled co
DOMAIN
173 489
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DOMAIN
679 1063
CO
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489
1063
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(Rel. 27, (Rel. 27, 1
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1225
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SEQUENCE
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RUEDITECTURETKNEPPANSCHTPHTLLDKNKKIEREHKEIKEIAKTIKFRIND AOSPY-ELSRMFEEYSSS	DTLKKNENIKELLDKINEIKNPPPANSGNTPNT SUSTADPLELEYTLREKNKNIDISAKVETKESTE NRRIHGELKTYREGINKNEEFYRKOLDKK GDLINPFDYTKEPSKNIYTDNERKKFINEIK ALLOYLEQUEELTOKKUSDLKLSALNSEISSIK KSKLDYIFKDKEKLVSDLRILKVP FASYENSKHNLEKLTRALKYMEDYSLRNI- I
KNENIKELLDKINEIKNPPPANSGNTPNTLLDKNK	DTLKKNENIKELLDKINEIKNPPPANSGNTPNT :
MUSTERETERNITERNE AQSPV-ELSRMFEEV DPLELEYLRERNENIDI	

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                                                                                                                                                             |: | : | | : | | : | | 1063 LFEKTFDYVSDHLDAIYRELTKNPNSNVELAGGNASLTIE----DEDEPFNAGIKYHATPP 1119
                                                                                       1120 LKRFKDM-------EYLSGGEKTVAALALLFAINSYQPSPFFVLDEVDAALDITN- 1167
1284 LYLKP-----LAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFKNVLESDLIP- 1335
                                                                   ---YKDLTSSNYVVKDPYKFLNKEKR-------DKFLSSYNYIKDSIDTDINFAND 1381
                                                                                                                                         1382 VLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLFVIHLEA 1441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 392.353-358(1998).

-I- FUNCTION: Involved in DNA double-strand break repair (DSBR). The rad50/mrell complex possesses single-strand endonuclease activity and ATP-dependent double-strand-specific exonuclease activity. Rad50 provides an ATP-dependent control of mrell by unwinding and/or repositioning DNA ends into the mrell active site (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 4.1%; Score 344.5; DB 1; Length 978; Best Local Similarity 19.2%; Pred. No. 9e-05; Matches 228; Conservative 232; Mismatches 353; Indels 377; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98196666; PubMed-9537320;
Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
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COILED COIL (POTENTIAL).
A; 9B0F2BF51ADD1151 CRC64;
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Probable DNA double-strand break repair rad50 AFPase.
RAD50 OR AQ_1006.
                                                                                                                                                                                                                                                                                                                                      PRT;
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SEQUENCE FROM N.A.
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RA50_AQUAE
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31 KLEALEDAVLTGYSLFOKEKMVLNEGTSGTAVTTSTPGSKGSVASGGSGGSVASGGSVAS 90

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ີ &	-LFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQI 203
ц	KTIENINEL :: : VLEKTLKNLEEE
256	IEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKN 31'2 :: : :
313	ENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKTI 361
	KFNIDSLFTDPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALN 421 SFAQEELNRIEAEKEKFKEEKELEHRLKKLQEIKEILK 353
	ELNSFGDLINPFDYTKEPSKNIYTD-NERKKFINEIKEKI-KIEKKKIESDKKSYE 475 : : : : : : : : ELSQLSSSLKEKEREYEGQARQEFEDLSERVEKGKKLVAETEEKLEKIKELFSEEETTSLK 413
	DRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYEN 535 ::
536	SKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEIETLVEN 584
585 501	IKKDEBQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQL 636 : : : : : : : : VDAEGISELKHAKELKEKEEREIDTTLKLYAQKINSLKEEMEKLRNEVEELRK 553
	ILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEG 696 : : : : : : : : : : :
	QSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQAQPPVPVPPVPEAKAQVP 756
	TPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEESK 816 :
	LSSCDPLDLLFUQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKDNDK 871 1 1 1 1 1 1 1 1 1
872 652	IKNLLEEBAKKVSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFENI 929 ::: : : :: :: LQEIEEKEKKLRKHFEELSSRKSKLEGELSALNESINSLEEERKEKLKELANI 704
930	LSLGKN-KNIYQELJGQKSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDESKRK 988 : : : : : : : : : :
989	KLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNS 1048 :: ::
049	LNNPKHVLQNFSVFFNKKKEAEIAETENTLENTKILLKHYKG-LVKYYNGESSPLKTL 1105 ::: : :::: : : - EELQKEISELEKKLEVYRVISNDFRGDRFQKYVSEIMLQKVVDR 842

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STRIN-FIB.
STRIN-FIB.
MEDLINE-95115033; PubMed-7815459;
Wang R., Sole M.J., Cukerman E., Liew C.-C.;
Wang R., Sole M.J., Cukerman E., Liew C.-C.;
Wang R., Sole M.J., Cukerman Baster.";
J. Mol. Cell. Cardiol. 26:1155-1165(1994).
[12]
SEQUENCE OF 962-1935 FROM N.A.
MEDLINE-88247788; PubMed-3380703;
Jandreski M.A., Sole M.J., Liew C.-C.;
"Sequence of cDNA encoding the Syrian hamster cardiac beta-myosin heavy chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
1106 -SEESIQTEDNYASLENFKVLSKLEGKLKDNLNLE----KKKLSYLSSG 1149
                                                                                                                                                                                                                                                                             P13540, 060540;
01-JAN-1990 (Rel. 13, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, cardiac muscle beta isoform (MyHC-beta).
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                                         PRT; 1934 AA
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Interpro; IPR004009; Myosin_N.
Interpro; IPR0012928; Myosin_tail.
Interpro; IPR001609; myosin_head.
Pfam; PF00063; myosin_head; I.
Pfam; PF00612; IQ; 2.
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Pfam; PF02736; Myosin_N; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; MYOSIN_head; 1.
SMART; SM00015; 10; 1.
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EMBL; X07273; CAA30256.1; -.
PIR; A28298; A38298.
HSSP; P08799; 1MND.
                                                                                                                                                                                                                                                      STANDARD;
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SEQUENCE FROM N.A.
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MYH7_MESAU
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TL-----QLSFDLYNKYKLKLER-LFDKKKTVGKYKM-QIKKLTLLKE 1040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOSELKDTQIQLDDAVRANDD-----LKENIAIVERRNNLLQAELEELRAVVEQT 1694
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IE----MNKKREAEFQKMRRDLEEATLQHEA----TAAALRKKHADSVAELGEQIDNLQ- 1210
                                                                                                                                                                                                                                                                                        1211 ---RVKOKLEKEKSEFKLE--LDDVTSNMEQIIKAKANLEKMCRTLEDQMNEHRSKAEET 1265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----KROLEEEVKAKNTLAHALQSARHDCDLLREQYEEETEAKAELQCVLSKANSEVAQ 1369
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01-MAR-1989 (Rel. 10, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical 259 kDa protein ycf2 (ORF 2136).
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Marchantia polymorpha (Liverwort).
Chloroplast.
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                                                    Coiled coil; Thick filament; Actin-binding;
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                                                                                                                                                                                                                                                          ACTIN-BINDING.
METHYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
D -> E (IN REF. 2).
E -> Q (IN REF. 2).
E -> Q (IN REF. 2).
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K (IN REF. 2).
FDBAC58310B0B57D CRC64;
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                                                                                                                                                           IQ.
COILED COIL (POTENTIAL).
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19.4%; Pred. No. 0.00019;
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Marchantiopsida; Marchantiidae; Marchantiales; Marchantiineae;
Marchantáaceae; Marchantia.
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                                                                                             Ohyama K., Fukuzawa H., Kohchi T., Shirai H., Sano T., Sano S.,
Umesono K., Shiki Y., Takeuchi M., Chang Z., Aota S., Inokuchi H.,
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                                                                                                                                          "Chloroplast gene organization deduced from complete sequence of liverwort Marchantia polymorpha chloroplast DNA."; Nature 322:572-574(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.1%; Score 344; DB 1; Length 21.
ilarity 19.8%; Pred. No. 0.00022;
Conservative 243; Mismatches 541; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Chloroplast; Hypothetical protein.
SEQUENCE 2136 AA; 259911 MW; 5BD170C9CCF61197 CRC64;
                                                                                                                                                                                        SIMILARITY: BELONGS TO THE YCF2 FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROȚEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
--- SUBCELLULAR LOCATION: THICK filaments of the myofibrils.
--- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
--- PTM: TWO CYSTEINE RESIDUES IN THE SI DOWAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR WYOSIN ATPASE ACTIVITY.
--- MISCELLANBOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                        gene and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kurabayashi M., Tsuchimochi H., Komuro I., Takaku F., Yazaki Y.; "Modecular cloning and characterization of human cardiac alpha- and beta-form myosin heavy chain complementary DNA clones. Regulation of expression during development and pressure overload in human
                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                             [2]
SEQUENCE FROM N.A.
MEDLINE-94140346; PubMed-8307559;
Epp T.A., Dixon I.M., Wang H.Y., Sole M.J., Liew C.-C.;
"Structural organization of the human cardiac alpha-myosin heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATPASE
                                                                                                                                                                                                                                                                                                    Matsuoka R., Beisel K.W., Furutani M., Arai S., Takao A.; "Complete sequence of human cardiac alpha-myosin heavy chain gramino acid comparison to other myosins based on structural and functional differences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [3]
SEQUENCE OF 1-177 AND 1551-1939 FROM N.A.
MEDLINE-89264452; PubMed-2726733;
Yamauchi-Takihara K., Sole M.J., Liew J., Ing|D., Liew C.-C.;
"Characterization of human cardiac myosin heavy chain genes.";
Proc. Natl. Acad. Sci. U.S.A. 86:3504-3508(1989).
                                                                                                       P13533; Q13943; Q14906; Q14907; Q1-JAN-1990 (Rel. 13, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, cardiac muscle alpha isoform (MyHC-alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBFRAGMENT ($2).
MISCELLANEOUS: THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATP MYOSIN, WHILE THE BETA ISOFORM IS A 'SLOW' ATPASE.
SIMILARITY: COUPLINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
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Proc. Natl. Acad. Sci. U.S.A. 86:7416-7417(1989).
                                                                                                                                                                                                                   Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
                                                                                                    PRT; 1939 AA
                1638 IVIYKVGKTIIQNILIKSSSMNLLNI 1663
MVFENLAKTVLSN-LLDGNLQGMLNI 1527
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SEQUENCE FROM N.A.
MEDLINE-92133665; PubMed-1776652;
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                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                    STANDARD;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50096; IQ; 1.
Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                          METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
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ECB87E7CE8768B6F CRC64;
                                                                                                                                                                                                                                                                                                                                                        ATP-binding; Methylation; Alkylation; Multigene family;
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Pfam; PF000612; i0; 2.
Ffam; PF001612; i0; 2.
Pfam; PF01576; Myosin_tail; 1.
Pfam; PF01576; Myosin_Lail; 1.
PRINTS; PR00193; MYOSINHEAVY.
PYDDOM; PD000195; myosin_head; 1.
SWART; SM0015; i0; 1.
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InterPro; IPR002928; Myosin_tail
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- 1- FUNCTION: WUSCLE CONTRACTION.
- 1- FUNCTION: WUSCLE CONTRACTION.
- 1- SUBUNIT: WUSCLE CONTRACTION.
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- 1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
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CYCLES OF A 28-RESIDUES IN THE SI DOMAIN ARE SELECTIVELY
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- I- MISCELLANBOUS: EACH MYOSIN HEAVY MEROMYOSIN (HMM). IT CAN LIGHT
MEROMYOSIN (LMM) AND I HEAVY MEROMYOSIN (HMM). IT CAN LAFER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND I ROD-SHAPED
SDLTEQLGEGGKNVHELEKVRKQLEVEKLELQSALEEAEASLEHEEGKILRAQLEF---N 1568
                                                                                                28 LEGKLKDNLNLEKKKLSYLSSGLHHLIAEL------KEVIKNKNYTGNSPSENNT 1176
                                                                                                                                                                                                                                                                                                                                                              DVN---------NALESYKKFLPEGTDVATVVSESGSDTLEQSQP 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKPASTHV-GAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVID 1271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 KYKLKLER-LFDKKKTVGKYKMQIKKLT-LLKEQLESKLNSLNNPKHVLQNFSVFFNKKK 1067
                                                                                                                                                                                          58 EAEIAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSK 1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFKNVLES 1331
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3I_TaxID=10090;
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haracterization of the allelic differences in the mouse cardiac
pha-myosin heavy chain coding sequence.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12566; 064258; 064258; Created)
-JUL-1998 (Rel. 36, Last sequence update)
-JUL-1998 (Rel. 36, Last sequence update)
-OCT-2001 (Rel. 40, Last annotation update)
-OSIN heavy chain, cardiac muscle alpha isoform (MyHC-alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 DLIPYKDLTSSNYVVKDPYKFLNKEKRDKF---LSSYNYIKDSID 1373
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RAIN=BALB/C, A/J, C57BL/6J, and DBA/2J;
DLINE=92250040; Pubmed=1577481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem. 266:9180-9185(1991).
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1122 EELE--AERTARAKVEKLRSDLSRELEEISERLEEAGGATSVQIE----MNKKREAEFQK 1175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IKRQLEEEGKAKNALAHALQSSRHDCDLIREQYEEEMEAKAELQRVLSKANSEVAQWRTK 1376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1045 KLNSLNNPKHVLQNFSVFFNKKKEAEIAETENTLENTKILL----KHYKGLVKYYNGESS 1100
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                                                          1014 AEEDK------VNTLTKSKVKLEQQVDD--LEGSLEQEKKVRMDLERAKRKLEGDLK 1062
                                                                                                                             1228 LE--LDDVTSNMEQIIKAKANLEKVSR-----TLEDQANEYR-----VKLEEAQR 1270
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                                                                                                    LTHHNTFASYENSKHNLEKLTKALKY - - - - - - MEDYSLRNIVVEKELKYYKNLISKIE
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                    467 IESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYKVE---K
                                                                                                                                                                                  576 NEIETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNK--IDELKK
                                                                                                                                                                                                                                                               TQLILKNVELKHNIHVPNSYKQENKQEPYXLIVLKKEIDKLKVFMPKVESLINEEKKNIK
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                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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METHIAPION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
SUBFRAGMENT (S2).
MISCELLANEOUS: THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATPASE MYOSIN, WHILE THE BETA ISOFORM IS A 'SLOW' ATPASE.
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY)
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COILED COIL (POTENTIAL).
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CALMODULIN-BINDING
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ACTIN-BINDING.
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InterPro; IPR000048; IQ_region.
InterPro; IPR00409; Myosin_n.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
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PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                    K-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 1-818, AND REVISIONS 204-215
                                                                                                                                                                                                                                                                                                                                                         Dominguez R., Freyzon Y., Trybus K.M., Cohen C.; "Crystal structure of a vertebrate smooth muscle myosin motor domain and its complex with the essential light chain: visualization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                            Complete primary structure of vertebrate smooth muscle myosin heavy
                                                                                                                                                                     chain deduced from its complementary DNA sequence. Implications on topography and function of myosin.";
J. Mol. Biol. 198:143-157(1987).
                                                                                                                SEQUENCE FROM N.A.
MEDLINE-88118918; Pubmed-2892941;
Yanagisawa M., Hamada Y., Katsuragawa Y., Imamura M., Mikawa T.,
                                                                                                                                                                                                                                                                                Malta T., Onishi H., Yajima E., Matsuda G.;
"Aniho acid sequence of the amino-terminal 24 kDa fragment of
"Aniho f chicken gizzard myosin.";
J. Biochem. 102:133-145(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBFRAGMENT (S2).
-!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-!- SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                     Submitted (FEB-1989) to the EMBL/GenBank/DDBJ databases
      01-JUL-1989 (Rel. 11, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, gizzard smooth muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-88032919; PubMed-3312184;
                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98412652; PubMed-9741621;
                                                                                                                                                                                                                                                                                                                                                                                        pre-power stroke state.";
Cell 94:559-571(1998).
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                                                                                                                                                                                                                                                           SEQUENCE OF 1-203.
                                                                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                 REVISIONS
                                                                                                                                                                                                                             Masaki T
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1019 NLAEEEERAKNLTKLKNKHESMISELEVRLKKEEKSRQELEKIKRKLEGESSDLHEQIAE 1078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----- QNLERHISTLTIQLSDSKKKLQEFTATV---- 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1139 RNKA----EKOKRDLSEELEALKTELEDTLDTTATQOELR-----AKREQEV-TVLKRA 1187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       791 YILVSHSTMNE---KILKQYK-ITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNS 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELKH 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257 EESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIK 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLELE 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ITKEYEKL---LNEIYDSKFNNNIDLTNFEKMMGK----RYSYKVEKLT 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           906 ELYAEAEEMRVRLAAKKOELEEILHEMEARIEEEEERSQQLQAEKK----KMQQQMLDLE 961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            377 YYLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSF-----GDLIN 431
                                                                                                                                                                                                                       Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; ATP-binding; Methylation; Alkylation; Calmodulin-binding;
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                                                                                                                                                                                                                                                                                                                                                   IQ.
RODLIKE TAIL (S2 AND LMM DOMAINS).
COILED COIL (POTENTIAL).
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16 ALKYLATION (SH-2).
27 MISSING (IN REF. 3).
15 KDTSITGGPSFS -> RTPASLKVHLFP (IN 1).
228663 MW; B7BGC923E5273D93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.1%; Score 341.5; DB 1; Length 1978;
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                                                                                                                                                                                                                                                                                                                        MYOSIN HEAD-LIKE
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ACTIN-BINDING.
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                                                                                                                        myosin_head; 1.
                                                                                                                                                                                                                                                                      Multigene family; 3D-structure.
INIT_MET 0 0 0
DOMAIN 1 790 MY
                     Pfam; PF00612; IQ; 1.
Pfam; PF01576; Myosin_tail; 1.
Pfam; PF02736; Myosin_N; 1.
PRIWTS; PR01193; MYOSINIEAVY.
ProDom; PD000355; myosin_head;
PF00063; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.0%;
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SMART; SM00242; MYSc; 1.
PROSITE; PS50096; 1Q; 1.
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706 70
716 71
127 12
204 21
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CONFLICT
CONFLICT
SEQUENCE
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1433 889 1491 921 1551	981 1610 1015 1666 1050 1726 1106	1161 1839 1218 1892		M., M.,
1393 847 1434 890	922 SIKILFENILSLGKNKNIYQELIGQKSSENFYEKILKDSDTFYNESFTNEVKSKADDINSL	11 12 11 11 11 11 11 11 11 11 11 11 11 1	70.50 20.00	STRAIN-ATCC 35210 / B31; MEDLINE-98065943; MEDLINE-98065943; Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwin Dougherty B., Tomb JF., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson van Vugt R., Palmer N., Adams M.D., Goodyne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujil C., Cotton M.D., Horst K., Roberts K., Hatch B. Smith H.O., Venter J.C.; "Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferl."; Nature 390;580-586(1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR004586; RecB.
InterPro; IPR00212; UvrD-helicase.
Pfam; PF00580; UvrD-helicase; 1.
TIGRPAMS; TIGR06609; recB; L.
Hydrolase; Nuclease; Exonuclease; Endonuclease; Helicase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286 NIKHEKYKSEDNRNKNRNNLKQYVILKVEYKILKYIEKELKKTIKSTNTIDQNYIISNLK 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 379 LRE------KNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSFGD 428
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ATP) in either 5'- to 3'-or 3'- to 5'-direction to yield 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
4.0%; Score 338; DB 1; Length 1169;
Best Local Similarity 19.6%; Pred. No. 0.00018;
Matches 288; Conservative 237; Mismatches 455; Indels 490;
                                                                                       (BY SIMILARITY).
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                              phosphooligonucleotides.
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W; B61D63C1C959B91F CRC64;
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NP_BIND 18 25 ATF
SEQUENCE 1169 AA; 137828 MW;
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE001164; AAC66981.1; -.
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TNYLGRNKEDYNITNLENTIKKEYYD---LQYKIYALGIKKILFKNKKEY--NQKFGGII 1122
                                                                                                                                                                                                                           ----TVGKYKMQIKKLTLLKEQL--ESKLNSLNNPKHVLQNFSVF-----FNKKKEA 1069
                                                                                                                                                                                                                                                                                                             1130 GKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTG-NSPSENNTDVNNALESYKKF 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1368 IKDSIDTDINFANDVLGYYK-ILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYK 1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1427 T---VNDKIDLEVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIA 1483
                                                                                                                                                                                ---TNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKK- 1023
                                                                                                                                                                                                                                                                    EIAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLE 1129
                                                                                                                                                                                                                                                                                                                                                       1189 LPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGE 1248
                                                                                                                                                                                                                                                                                                                                                                                                  1249 SEEDYDDLGQVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFN 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                             1309 VNVKDILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKE-KRDKFLSSYNY 1367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRA---INTRLCDIEELQKEME----FLIK----INPEFQKQKYL---F 1031
                                                                                                                                                  --EIEEKINNINNDNESIE-LMTHKSKGLGMNIV------FLLNTTPIENSNFF 766
                                                                                                                                                                                             1032 DKHFEDLHIKLSD---GYLKGIVDLIFKA---NNKIYILD--------YK 1067
                                                                   663 WAKNKINYKGLLIKEGKLENLKTYETTLEIISKIYHKEQNIQSLISTLESLIINEEPE-- 720
                                                                                                                                                                                                                                        807 FYVGATRAKFALFIIKINSITSKLLEIAKIFTIDDIKH---DFNIHEFIGQKRFNKKK-- 861
                                                                                                                                                                                                                                                                                          887
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Sciurognathi; Muridae; Murinae; Rattus.
                             565 -----KTKEFSEIFYIIKCLDRKQSFKTLNYILSSKILNVPWNLQRILIKQDKICLIEE
                                                                                            ------SSSMQPL----SLTPQDKPEVS
                                                   SKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKDNDKI--
          PAPVNNKTENVSKLDY - - - - LEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEE
                                                                                                                                                                                                                                                                                         ----YNTNVNTKLI---------PPKPIIKNMFKKE--YTS-----
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21-JUL-1986 (Rel. 01, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, cardiac muscle alpha isoform (MyHC-alpha).
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
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-I. FUNCTION: MUSCLE CONTRACTION.

-I. SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2.

-I. SUBUNITS (HAL), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

-I. SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

-I. DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING

CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,

CYCLES OF A 28-RESIDUES IN THE SI DOMAIN ARE SELECTIVELY

ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

-I. MISCELLANBOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1512-1938 FROM N.A.
MEDLINE=82220036; PubMed=7045682;
Mahdavi V., Periasamy M., Nadal-Ginard B.;
"Molecular characterization of two myosin heavy chain genes expressed
                                                                                                                                                                                                                                                                                           MEDLINE=90133919; PubMed=2614840; MCMAILY E.M., Kraft R., Bravo-Zehnder M., Taylor D., Leinwand L.A.; "Full-length rat alpha and beta cardiac myosin heavy chain sequences." Comparisons suggest a molecular basis for functional differences."; J. Mol. Biol. 210:665-671(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mahdavi V., Lompre A.M., Chambers A.P., Nadal-Ginard B.; "Cardiac myosin heavy chain isozymic transitions during development and under pathological conditions are regulated at the level of mRNA availability.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS ($1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-167 FROM N.A. MEDLINE-84194059; PubMed-6585819; Mahdavi V., Chambers A.P., Nadal-Ginard B.; "Cardiac alpha- and beta-myosin heavy chain genes are organized in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANDONS: THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATPASE MYOSIN, WHILE THE BETA ISOFORM IS A 'SLOW' ATPASE. SIMILARITY: CONTAINS I MYOSIN-LIKE GLOBULAR HEAD DOMAIN. SIMILARITY: CONTAINS I 1Q DOMAIN.
                                                                      Proc. Natl. Acad. Sci. U.S.A. 81:2626-2630(1984).
                                                                                                                                                     cardiac myosin heavy chain.";
Nucleic Acids Res. 17;7527-7528(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Wistar; TISSUE-Heart;
MEDLINE-85179510; PubMed-6241892;
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InterPro; IPR002928; Myosin_tail.
                                       PubMed=2798111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1872-1938 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in the adult heart.";
Nature 297:659-664(1982).
                                                                                                                                                                                                                                                                SEQUENCE.
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PIR; A02988; A02988.
HSSP; P08799; IMND.
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TISSUE=Heart;
MEDLINE=90016822;
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DISCUSSION OF
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Dp	1862	LVRLQDLVDKLQLKVKAYKRQAEEAEEGANTNLSKFRKVQHELD 1905

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"Comparison of molecularly cloned bullous pemphigoid antigen to desmoplakin I confirms that they define a new family of cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stanley J.R., Tanaka T., Mueller S., Klaus-Kovtun V., Roop D.; "Isolation of complementary DNA for bullous pemphigoid antigen by use of patients' autoantibodies."; J. Clin. Invest. 82:1864-1870(1988).
                                                                                                                                                                                                                                   Elgart G.W., Stanley J.R.; "Cloning of the 5' mRNA for the 230 kD bullous pemphigoid antigen by rapid amplification of cDNA ends."; "Invest. Dermatol. 101:244-246(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The hemidesmosomal plague. I. Characterization of a major constituent protein as a differentiation marker for certain forms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang H.-Y., Chaffotte A.-F., Thacher S.M.;
"Structural analysis of the predicted coiled-coil rod domain of the cytoplasmic bullous pemphigoid antigen (BPAGI). Empirical Jocalization of the N. terminal globular domain-rod boundary.";
J. Biol. Chem. 271:9716-9722(1996).
-!- PUNCTION: COMPONENT OF HEMIDESMOSOME PLAQUE. THE PROTEINS PROBABLY SELF-AGGREGATE TO FORM FILAMENTS OR A TWO-DIMENSIONAL MESHWORK. POTENTIAL INTERACTION WITH KERATIN INTERMEDIATE FILAMENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                     Hopkinson S.B., Jones J.C.; "Identification of a second protein product of the gene encoding a human epidermal autoantigen."; Blochem. J. 300:851-857(1994).
                           003001; 013775; Q9UGDB; Q9UGD7; Corrected) (1-007-1996 (Rel. 34, Created) (1-007-2001 (Rel. 40, Last sequence update) (1-007-2001 (Rel. 40, Last annotation update) (BPA) (Hemidesmosomal plaque protein).
                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1650-2257 FROM N.A.
MEDLINE-91216368; Pubmed-2090522;
Owaribe K., Kartenbeck J., Stumpp S., Magin T.M., Krieg T.,
                                                                                                                                                                                                                                                                                                                        fanaka T., Parry D.A.D., Klaus-Kovtun V., Steinert P.M.,
                                                                                                                                                                               Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1777-2704 FROM N.A. (ISOFORM 4).
                    2704 AA
                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
                                                                                                                                                                                                                                                                                                                                                                   unction plague proteins.";
f. Biol. Chem. 266:12555-12559(1991),
                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Keratinocytes;
MEDLINE=89067122; PubMed=2461961;
                                                                                                                                                                                                                TISSUE=Keratinocytes;
MEDLINE=93346806; PubMed=8345227;
                                                                                                                                                                                                                                                                                                   TISSUE=Keratinocytes;
MEDLINE=91286285; PubMed=1712022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       epithelia."; Differentiation 45:207-220(1990).
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MEDLINE=94280413; PubMed=8010969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-96199235; PubMed-8621649;
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 2)
                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Franke W.W.
                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                  Stanley J.R.;
                    BPA1_HUMAN
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                                                                                                                                                                       Laird
        BPA1_HUMAN
RESULT 48
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MHSSSYSYRSSDSVFSNTTSTRILDSNENLLLVHCGPTLI
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VAVQSNLANLEHAFYVAEKIGVIRLLDPEDVDVSSPDEKSV
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TEKSKIKRLYKLLEKVFCFLKIWIEFGRIKLLQGYHPNDIE
KEWGKLIIAMLEREKALRPEVE (IN ISOFORM 1).
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ALTERNATIVE PRODUCTS: 4 ISOFORMS; 1, 2, 3 (SHOWN HERE) AND 4; MAY BE PRODUCED BY ALTERNATIVE SPLICING.
DISBASE: INVOLVED IN THE SUBEPIDERMAL BLISTERING DISEASE BULLOUS PEMPHIGOID, AN AUTOIMMUNE DISEASE.
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                                                                                                                                                                             --- SIMILARITY: CONTAINS 10 PLECTIN REPEATS.
--- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
--- SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.
--- SIMILARITY: BELONGS TO THE PLAKIN OR CYTOLINKER FAMILY.
--- CAUTION: ISOFORMS 2 AND 4 ARE FRAGENTS AT THE N-TERMINUS.
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InterPro; IPR002017; Spectrin.

Pfam; PF00018; SH3: 1.

R Pfam; PF00018; SH3: 1.

R Pfam; PF000681; Plectin; 3.

R SMART; SM00150; SPEC; 11.

R SMART; SM00150; SPEC; 3.

R PROSITE; P550002; SH3; FALSE_NEG.

W Antigen; Colled coll, Repeat; SH3 domain; Structural protein (ytoskeleton; Cell adhesion; Alternative splicing.

KT DOMAIN 1 1199 GLOBULAR I.

FT DOMAIN 1200 ? COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUMN COLUM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISSING (IN ISOFORM 2).
MISSING (IN ISOFORM 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISOFORM 4).
MISSING (IN ISOFORM 4).
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SPECTRIN 2.
SPECTRIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001101; Plectin_repeat.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL096710; CAB63786.1; -. EMBL; AL096710; CAB63787.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, L11690, AAA52288.1; EMBL, M83618, AAA3566.1; EMBL, M03459, AAA57184.1; EMBL, X58677; CAA41528.1; GENEY, HCWN:1090; BPAGI. MIM; 113810.
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1544 RITRAHAVAEKNIQHLNSQIHSFRDEKELERLQICQRKSDHLKEQFEKS----HEQLLQ 1598
                                                                                                                                                                                                                          NTK-----ILLKHYKGLVKYYNGE---SSPLKTLSEESIQTEDNYASLENFKVLSKLE 1129
                                                                                                                                                                                                                                                                                                                     1130 GKL-----KDNLNLEKKKLSYLSSGLHHLIAE-----LKEVIKNKNYTGNSPSENNTDVN 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                           1835 VSLQQENSRAQENAKLCETNIKELERQLQQYREQMQQGQHM--EANHYQKCQKLEDE--- 1889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----LIAQKRE-----C 1920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLKKQLENNVMT----FNVNVKDILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPY 1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1717 EFKOKCDOONIIIONTKKEVRNLNAELNASKEEKRRGEOKVOLOOAOVOELNNR-LKKVO 1775
                                                                                                                                                                                                                                                                                                                                                                                                            1180 NALESYKKFLPPGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDD 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro."; DNA Res. 4:141-150(1997).
                                                                    LEKQTIQQRCEALKIQADGFKDQLRSTNEHLHKQTKTEQDFQRKIKCLEEDLAKSQNLVS
                                                                                                                                  KYKMQIKK----KEAEIAETENTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1240 VIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDNILSKI----ENEYEVLYLKPLAGVYR
                                          FVKSKA---DDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVG
                                                                                                                                                                                                                                                                                                                                                             DELHLKTIEEQMTHRKMVLFQEESGKFKQSAEEFRKKMEKLMESKVITENDISGIRLDF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : | | : | | | 1981 QHRVVEQIPKEVQFQPPGAPLEKEKSQQCYSEY-FSQTSTELQITF 2025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KF------1NKEKRDKFLSSYNYIKDSIDTDINF 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D901314E981BF001 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COILED COIL (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical protein KIAA0373.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB002371; BAA20828.1; -.
Hypothetical protein; Coiled coil.
DOMAIN 18 1514 COLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Brain;
MEDLINE-97349984; PubMed-9205841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180065 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y373_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : || || ; ; |
|201 WVAELKKQKSRVEEELPKVREAAENELRKQQRNVEDISLQKIRAESEAKQYRRELETIVR 1260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1360 AEKOLKEKOKIELEAR----RKITEIQYTCRENALPVCPITQATSCRAVTGLQOEHDKOK 1415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1025 TTQRKIQENQPENSKTLATQLNQQKMLVSEIEMK----QSKMDECQKYAEQYSATVKDYE 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1141 RLEEEEVIINSEHPVNIKELEIKRCKETSEHGAYSDLLQRQKATVLENSKLTGKISELER 1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----QIDNRLRDLEGIGKSLKYYRDTYHPLDDWIQQVE 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      485 --TKEYEKLLNEIYDS-----KFNNNIDLTNFEKM-MGKRYSYKVEKLTHHNTFAS---- 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----YENSK-----HNLEK 542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                682 ESLINEEKKNIKTEGQSDNSEPSTEGEITGQATTKPG---QQAGSALEGDSVQAQAQEQK 738
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                                                                                                                                                                                       211 AN------KMEDYIKKLVF-----GYRKPLDNİKDNVG----KMEDYIKKNK 246
                                                                                                                                                                                                                                                                              EAHNLISVLE-KRIDTLKKNENIKELLDKINEIK----NPPPANSGNTPN---TLLDKNK 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                              346 KIEEH-----EKEIKEIAKTIKFNIDSLFTD----PLELEYY-----LREKNKNIDI 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSFG-+----DLINPFD----- 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              435 -----YTKEPSKNIYTD-NERKKFINEIKEKIKIEKKKIESDKKSYEDRSKSLNDI- 484
                                                                                                               Gaps
                                                                                                                                                          166 YLIDGYE-----EINELLYKLN----FYFDLL----RAKLNDVCANDYCQIPFNLKIR 210
                                                                                                                                                                                                                                                                                                                                            247 KT------IENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLE 293
                                                                                                                                                                                                                                                                                                                                                                           ----ENEIE-----TLVENIKKD--EEQLFEKKITKDENKPDEKILEVSDIVKVQVQKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           739 QAQPPVPVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHST
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                                                                                                             Matches 292; Conservative 232; Mismatches 514; Indels 448;
                                                                  Length 2704;
38 G -> R (IN REF. 5).
313084 MW; A7219E687A634A77 CRC64;
                                                                    ; DB 1;
0.00045;
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                                                                  Score 338;
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                       2704 AA;
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CONFLICT
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644 547 686 606 726	Db 767ALRKASSEGKSEMKKLRQQLEAAEKQIKHLEIEKN, Qy 722 GSALEGDSVQAQQQQQQQQPPVPVPVPEAKAQVPTPPA, Db 813ELQGRELK	Db 895 EAKFREKDEREEQLIKAKEKLEND Qy 897 LSLTPQDKPEVSANDDTSHSTNLNNSLKLFENILSLGKNI Db 927GDNSSQLTKMNDELRLKE Qy 954 KILKDSDTFYNESFTNFVKSKADDINSLNDESKRKKLEE Qy 956 KSIEDMTVKAEQSQQEAAKKHEEEKKELERI	OY 1014 KLERLFDKKKTVGKYKMOIKKLTLLKEQLESKLNSLNNPP 	QY 1133 KDNLNLEKKKLSYLSSGLHHLIABLKEVIKNKYTGNSP. : : : : : : : :	QY 1244 PIFGESEDYDDLGQVVTGEAVTPSVIDNILSKIENEYE' ::: :: : Db 1208 KFIKDADEEKASLGKSISITSALLTEKDAELEKLRNEVT' QY 1297 -KKQLENNVMTFNVNVKDILNSRENKRENFKNVLESDLI : : Db 1268 DKVKLELKVKNLELQLKENKRQLSSSGNTDTQ	QY 1356 EKRDKFLSSYNYIKDSIDTDINFAN-DVLGYYKILSE-K : : : : : : : :	RESULT 51 DMD_HUMAN ID DMD_HUMAN STANDARD; PRT; 3685 AA. AC P11532; Q14169; Q14170; DT 01-OCT-1989 (Rel. 12, Created)
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE REED-STERNBERG CELLS CC -1- SIMILARITY: CONTAINS 2 CAP-GLY DOMAINS. CC -1- SIMILARITY: CONTAINS 2 CAP-GLY DOMAINS. CC -1- SIMILARITY: CONTAINS 2 CAP-GLY DOMAINS. CC -1- SIMILARITY: CONTAINS 2 CAP-GLY DOMAINS. CC -1- SIMILARITY: CONTAINS 2 CAP-GLY DOMAINS. CC -1- SIMILARITY: CONTAINS 2 CAP-GLY DOMAINS. CC -1- SIMILARITY: CONTAINS 2 CAP-GLY DOMAINS. CC -1- SIMILARITY: CONTAINS 2 CAP-GLY DOMAINS. CC -1- SIMILARITY: CONTAINS 2 CAP-GLY DOMAINS. CC -1- SIMILARITY: CONTAINS 3 CAP-GLY DOMAINS. CC -1- SIMILARITY: CONTAINS 3 CAP-GLY DOMAINS. CC -1- SIMILARITY: CONTAINS 3 CAP-GLY DOMAINS. CC -1- SIMILARITY: CONTAINS 3 CAP-GLY DOMAINS. CC -1- SIMILARITY: CONTAINS 3 CAP-GLY DOMAINS. CC -1- SIMILARITY: CONTAINS 3 CAP-GLY DOMAINS. CC -1- SIMILARITY: CONTAINS 3 CAP-GLY DOMAINS. CC -1- SIMILARITY: CONTAINS 3 CAP-GLY DOMAINS. CC -1- SIMILARITY: CONTAINS 3 CAP-GLY DOMAINS. CC -1- SIMILARITY: CONTAINS 3 CAP-GLY DOMAINS. CC -1- SIMILARITY: CONTAINS 3 CAP-GLY DOMAINS BL; X64838; CAA46050.1; EMBL; W37501; AAA35693.1; PIR; S22695; S22695. Genew; HGNC:10461; RSN. Genew; HGNC:10461; RSN. Genew; HGNC:1046938; CAP-GL; InterPro; IPRO01938; CAP-GL; InterPro; IPRO01938; CAP-GL; IPRO019302; CAP-GL; 1PRO0193; CAP-GL; 1PROSITE; PS000445; CAP-GLY. PROSITE; PS00445; CAP-GLY.	Cytoskeleton; Microtubules; DOMAIN 78 120 DOMAIN 143 204 DOMAIN 232 274 DOMAIN 350 1342 DOMAIN 1408 1421 VARSPLIC 457 A4; 160989 SEQUENCE 1427 A4; 160989	nery Match 4 0%; lest Local Similarity 19.3%; latches 283; Conservative 2 43 YSLFQKEKMVINEGTSGTAVTT	102 SGGSGNSRRTNPSDNSSDSDAKSYADLKHRVRNYLLTIKELKYPQLFDLTN 1	384 HVGEIEQELALARDGHDQHVLELEAKMDQLKTMVEAADREKVEL 206 NLKIRANELDVLKKLVFGYRRPLDNIKDNVGKMEDYIKKNKKTIENINELIEESKKTIDK 206 NLKIRANELDVLKKLVFGYRRPEESITKGDLETQTKLEHARIKELEGSLLFFKTIDK 226 NKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELL 21	0.00 0.00	QY 435 YTKEPSKNIYTDNERKKFINEIKEKIKIESDKKSYEDRSKSLNDITK 486 DD 603KENSDVIALWKSKLETAIASHQQAMEELKVSFSKGLGTETA 643 QY 487 EYEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKA 546	

QQ	:': :
Oy)Y SLRNIVVEKELKYYKNLISKI
qq	686 AKLMKVIKEKENSLEAIRSKLDKAEDQHLVEMEDTLNKLQ 725
QY	EKILEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEP 66
Dβ	726 EAEIKVKELEVLQAKCNEQTKVIDNFTSQLKATEEKLLDLD 766
Qy	YYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQA 72
QQ (7ALRKASSEGKSEMKKLRQQLEAAEKQIKHLEIEKNAESSKASSITR
δ _ο α	/ll deadle deadl
δλ	778 LYEFLATSYICHKYILVS-HSTMNEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVM 836
QO	841 ELQILKEKFAEASEEAVSVQRSMQETVNKLHQKEEQFNMLSSDLEKLRENLADM 894
QY	ISVKTLSSSSMQP 89
qq	895 EAKFREKDEREEQL 926
Qy	LSLTPQDKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQ-ELIGQKSSENFYE 95
ф	
δλ	4 KILKDSDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKL 101
qq	6 KSIEDMTVKAEQSQQEAAKKHEEEKKELERKLSDLEKKMETSHNQCQELKA 101
Qy	1014 KLERLEDKKTYGKYKMQIKKLTLLKEQLESKLNSLNNPKH-VLONFSVFFNKKEAEIA 1072 :
qq	1017 RYERATSETKTKHEEILQNLOKTLLDTEDKLKGAREENSGLLGELEELRKGADKA 1071
Qγ	1073 ETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKL 1132
qq	1072 KAAQTAEDAMQIMEQ
δλ	LSYLSSGLHHLIAELKEVIKNKNYTGNSPS
qq	1109 QNELDTLKENNLKNVEELNKSKELLTVENQKMEEFRKEIETL 1150
QY	1193 TDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIV 1243
qq	1151 KQAAAQKSQQLS-ALQEENVKLAEELGRSRDEVTSHQKLEEERSVLNNQLLEMKKRES 1207
Qy	1244 PIFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSL 1296
qq	1208 KFIKDADEEKASLQKSISITSALLTEKDAELEKLRNEVTVLRGENASAKSLHSVVQTLES 1267
Qy	ILNSRF
q	1268 DKVKLELKVKNLELQLKEOKRQLSSSSGNTDTQADEDERA
δλ	SSYNYI
qa	1309 ESQIDFLNSVIVDLQRKNQDLKMKVEMMSEAALNGNGDDLNNYDSDDQEKQSK 1361
Οy	1414 YLPFLNNIETLYKTVNDKIDLFVIH 1438
qa	1362 KKPRLFCDICDCFDLH 1377
RESULT DAND HIM	OLT 51 , HIMAN
AC DT	

dystrophy gene.";

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Pearson P.L., van Ommen G.J.B.;
"High resolution deletion breakpoint mapping in the DMD gene by whole cosmid hybridization.";
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Roberts R.G., Gardner R.J., Bobrow M.;
"Searching for the 1 in 2,400,000: a review of dystrophin gene point mutations.";
                                                                                                                                                                                                                                                                                                                                                      'Two human cDNA molecules coding for the Duchenne muscular dystrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Complete cloning of the Duchenne muscular dystrophy (DMD) cDNA and
                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 404-1137 FROM N.A.
MEDILIBE-88111312; PubMed-3428261;
Cross G.S., Speer. Rosenthal A., Forrest S.M., Smith T.J.,
Edwards Y., Flint T., Hill D., Davies K.E.;
"Deletions of fetal and adult muscle cDNA in Duchenne and Becker muscular dystrophy patients.";
EMBO J. 6:3277-3283(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVIEW ON VARIANTS.
MEDLINE-94320940; PubMed=8045556;
Rininsland F., Reiss J.;
"Microlesions and polymorphisms in the Duchenne/Becker muscular
                                                                                                                                                                                                                                                                                                                   Rosenthal A., Speer A., Billowitz H., Cross G.S., Forrest S.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary genomic organization of the DMD gene in normal and affected individuals.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 2147-2204 FROM N.A.
MEDLINE-89345155; Pubmed-2569720;
Blonden L.A.J., den Dunnen J.T., van Paassen H.M.B.,
Wapenaar M.C., Grootscholten P.M., Ginjaar H.B., Bakker E.,
                                                                                                                                                                                         Koenig M., Monaco A.P., Kunkel L.M.;
The complete sequence of dystrophin predicts a rod-shaped cytoskeletal protein.";
Cell 53:219-228(1988).
                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Huth A., Will K., Speer A., Bauer D.;
Submitted (MAR-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 665-722; 2098-2204 AND 2305-2366 FROM N.A. MEDLINE=89083552; PubMed=3205741; Chamberlain J.S., Gibbs R.A., Ranier J.A., Nguyen P.N.,
01-OCT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                      (DMD) locus are highly homologous.";
Nucleic Acids Res. 17:5391-5391(1989).
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                                                                                                                                                                              MEDLINE-88194521; PubMed-3282674;
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-497 FROM N.A.
MEDLINE-87273512; Pubmed-3607877;
                                                                                                                                                                                                                                                                                                 MEDLINE-89345106; PubMed-2668885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 2305-2364 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hum. Mutat. 4:1-11(1994).
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                                                                        Homo sapiens (Human).
                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caskey C.T.:
                                                                                                                                                                                                                                                                                                                                  Davies K.E.;
                                      Dystrophin.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DYSTROPHIN1, 22 AND 3. DYSTROPHIN WARRING AND CALLED DYSTROPHIN1, 22 AND 3. DYSTROPHIN1, 22 AND 3. DYSTROPHIN1, 22 AND 3. DYSTROPHIN1, 32 AND 3. DYSTROPHY (BMD) and Becker muscular dystrophy (BMD). DWD is the most common form of muscular dystrophy; a sex-linked recessive disorder. It typically presents in boys aged 3 to 7 year as proximal muscle weakness causing wadding agit, toe-walking, lordosis, frequent falls, and difficulty in standing up and climbing up stairs. The pelvic girdle is affected first, then the shoulder girdle. Progression is steady and most patients are confined to a wheelchair by age of 10 or 12. Flexion contractures and scoliosis ultimately occur. About 50% of patients have a lower 10 than their genetic expectations would suggest. There is no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treatment. BMD ressembles DMD in hereditary and clinical features but is later in onset and more benign.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feener C.A., Koenig M., Kunkel L.M.; "Alternative splicing of human dystrophin mRNA generates isoforms at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cardiomyopathy (XLCM).

MISCELLANEOUS: THE DMD GENE IS THE LARGEST KNOWN GENE IN HUMANS.

IT IS 2.4 MILLION BASE-PAIRS IN SIZE AND COMPRISES 79 EXONS.

SIMILARITY: THE ACTIN-BINDING DOMAIN IS OF A TYPE FOUND IN MANY ACTIN-BINDING PROTEINS (SUCH AS ACTININ, DYSTROPHIN, FIMBRIN, STMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.

SIMILARITY: CONTAINS 2 SPECTRIN REPEATS.

SIMILARITY: CONTAINS 1 WW DOMAIN.

SIMILARITY: CONTAINS 1 WW DOMAIN.

SIMILARITY: CONTAINS 1 WO DOMAIN.

SIMILARITY: CONTAINS 1 WO DOMAIN.

SIMILARITY: CONTAINS 1 L2—TYPE ZINC FINGER.

DATABASE: NAME—BMD; NOTE—PYSTLOPHIN MUTATION DATABASE;

WWW="http://www.dmd.nl/database.html".
                                                                                                      Prior T.W., Papp A.C., Snyder P.J., Burghes A.H.M., Bartolo C., Sadra M.S., Western L.M., Mendell J.R.;
"A missense mutation in the dystrophin gene in a Duchenne muscular dystrophy patient.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the carboxy terminus.";
Nature 338:509-511(1989).
-!- FUNCTION TAY PLAY A ROLE IN ANCHORING THE CYTOSKELETON TO THE PLASMA MEMBRANE.
                                                                                                                                                                                                                                                                                                                         "Novel small mutations along the DMD/BMD gene associated with different phenotypes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY
                                                                                                                                                                                                                                                       MEDLINE-95152525; PubMed-7849724;
Nigro V., Nigro G., Esposito M.G., Comi L.I., Molinari A.M.,
Puca G.A., Politano L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISEASE: Defects in DMD are a cause of X-linked dilated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS ARE PRODUCED I ALTERNATIVE SPLICING; THE 3 SHORTER VARIANTS ARE CALLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                       VARIANTS DMD HIS-365; TRP-2191 AND ARG-2937
                                                                                                                                                                                                                                                                                                                                                                                                                ALTERNATIVE SPLICING (DYSTROPHIN-1 AND -2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATIVE SPLICING (DYSTROPHIN-3).
                                                                                                                                                                                                                                                                                                                                                                  3:1907-1908(1994).
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EMBL; X06178; CAA29544.1; -.
                                                                             MEDLINE=94004962; PubMed=8401582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-89181947; PubMed-2648158;
                  Hum. Genet. 94:111-116(1994).
                                                                                                                                                                                             Nat. Genet. 4:357-360(1993).
                                                           VARÍANT DMD ARG-54.
                                                                                                                                                                                                                                                                                                                                                                       Hum. Mol. Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Retina;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           White R.A.
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DD 1460 LFOKPANFELRLOBSKMILDEVKMHLPALETKSVEGEVVOSOLNHCVNLYKSLSEVKSEV QY 387 DISAKVETKESTEPNEYPNGVT-YPLSYNDIN	OY 521 VEKLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEI Db 1757 ISELNHRFAAISHRIKTGRASIPLKELEOFNSDIOKLLEPLEBEI QY 579 ETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNK Db 1802 QGCV-NLKEEDFNKDMNEDNEGTVELLQRENLOGRITDERKREIKIKQQLLQTK OY 628 IDELKTOLILKNVELKHNIHVPNSYKOENKOEPYTJULKKKEIDKLKYPMPKVESLI Db 1858 HNALKDLRSQRRKKALEISHQWYQYKRQADDLLKCLDDIEKKLASLPEPR QY 686 NEEKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQA 1908 DERKIKEIDRELQKKKEELNAVRRQAAGGLEGDSVQAQAQEQKQA	OY 741 QPPVPPPPARAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSY 1	State Stat
EMBL; X14298; CAA32479.1; ALT_SEO. EMBL; X15495; CAA3318.1; EMBL; X13045; CAA31451.1; EMBL; X13046; CAA31451.1; EMBL; X13046; CAA31452.1; EMBL; X13048; CAA31453.1; EMBL; X13048; CAA31454.1; EMBL; X13048; CAA31454.1; EMBL; U27203; AAA86115.1; EMBL; U27203; AAA86115.1; EMBL; X15148; CAA31454.1; EMBL; X15148; CAA31455.1; PIR; A27162; A27162. PIR; S05291; S05291. HSSP; P46939; LQAG. Genew; HGNC:2928; DMD. MIM; 300376; MIM; 300	JUZGAS, 1. SPECOLS B9, ACCEDING, PEPCO, IPROGOLTS; Calponing Perco; IPROGOLTS; Calponing Perco; IPROGOLS B9, WM. RSP5, IPROGOLS BPECOLS, WW. RSP5, IPROGOLS BPECOLS, WW. 1. SPECOLS BPECOLS BP	PROSITE; PS00020; ACINNIA_1; 1. PROSITE; PS00021; CH; 2. PROSITE; PS00021; CH; 2. PROSITE; PS00021; CH; 2. PROSITE; PS01159; WW_DOMAIN_1: 1. PROSITE; PS01155; ZF_ZZ_1; 1. PROSITE; PS01155; ZF_ZZ_1; 1. PROSITE; PS01155; ZF_ZZ_1; 1. PROSITE; PS01155; ZF_ZZ_1; 1. PROSITE; PS01155; ZF_ZZ_1; 1. PROSITE; PS01155; ZF_ZZ_1; 1. PROSITE; PS01156; ZF_ZZ_1; 1. PROPAIN 1 240 PROMAIN 134 237 PREPEAT 339 447 SPECTRIN 1. PREPEAT 448 SF6 SPECTRIN 2. PREPEAT 559 667 SPECTRIN 3. PREPEAT 719 828 SPECTRIN 4.	Ch 4.0%; Score 335; DB 1; Length 3685; I Similarity 19.3%; Pred. No. 0.00079; Conservative 281; Mismatches 593; Indels 52 LEFT: Conservative 281; Mismatches 593; Indels 52 LETLTHVOMLTECONING-FYZIDGYEEINELLYKINFYFDLIRAKINDVCAND 1 1 1 1 1 1 1 1 1 1

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LAPGLTTIGASPTQTVTLVTQPVVTKETAISKLEMPSSLMLEVPALADFNRAWTELTDWL 2486
                                                                                                                                                                                                                       2658
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                                                                                                                                                                                                                                                                                                                                                                  -----ATRKERELEDSKGVKELM---KQWQDLQGEIEAHTDVYH 2753
                                                                                                                                                                                                                                                        1388 --ILSEKYKSDLDSIKKYINDKQG-------ENEKYLPFLNNIETLYKTVNDK 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Green K.J., Parry D.A.D., Steinert P.M., Virata M.L.A., Wagner R.M., Angst B.D., Nilles L.A.; "Structure of the human desmoplakins. Implications for function in the desmosomal plaque." J. Biol. Chem. 265:2603-2612(1990).
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Angst B.D., Nilles L.A.;
                                                                                                                                                                                                                                                                                                                                                                                                         1492 NNLLTKFLSTGMVFENLAKTVLS-----NLLDGNLQGM------LNISQH 1530
                                                                                                                                                                                                                                                                                                                                                                                                                                           2754 N-----LDENSQKILRSLEGSDDAVLLQRRLDNMNFKWSLLRKKSLNIRSH 2799
                                                                                                                                 ARAKLESWKEGPYTVDAIQKKITETKQLAKDLRQWQTNVDVANDLALKLLRDYSADDTRK
                                                                                                                                                                                                                                                                                 2659 VHMITENINASWRSIHKRVSEREAALEETHRLLQOFPLDLEKFLAWLTEAETTANVLQD-
                                  -- LGQVVTGEAVTPSVIDNILSKIENEYEVL-----YLKPLAGVYRSLKKQLENNVM
                                                                                                         1306 TFNVNVKDILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLN-KEKRDKFLSS
                                                                     2487 SLLDQVIKSQRVMVGDLEDINEMIIKQKATMQDLEQRRPQLEELITAAQNLKNK----
                                                                                                                                                                                 1365 YN-----YIKDSI-----DTDINFAND----VLGYYK-----
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whittock N.V., Ashton G.H., Dopping-Hepenstal P.J., Gratian M.J.,
Keane F.M., Eady R.A.J., McGrath J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DESP_HUMAN STANDARD; PRT; 2871 AA.
P15924; 014189; 075993; Q9UHN4;
P15924: 014 (Rel. 14, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Desmoplakin (DP) (250/210 kDa paraneoplastic pemphigus antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Virata M.L.A., Wagner R.M., Parry D.A.D., Green K.J.;
"Molecular structure of the human desmoplakin I and II amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phillips S.: Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 89:544-548(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1120-2871 FROM N.A. (ISOFORM DPI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ist B.D., Nilles L.A.;
Biol. Chem. 265:11406-11407(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20062965; PubMed=10594734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Foreskin;
MEDLINE=92115697; PubMed=1731325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Foreskin;
MEDLINE=90153880; PubMed=1689290;
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SEQUENCE FROM N.A. (ISOFORM DPI).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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**MEDINE-98012209; Pubmed-9348233; MEDINE-98012209; Pubmed-9348233; MEDINE-98012209; Pubmed-9348233; MEDINE-98012209; Pubmed-9348233; MEDINE-98012209; Pubmed-9348233; MEDINE-98012209; MEDINE-98012209; MEDINE-98012209; MEDINE-08012209; MEDINE-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DOMAIN: THE N-TERMINAL REGION IS REQUIRED FOR LOCALIZATION TO THE

NOTICE OF THE N-TERMINAL REGION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DESMOSOMAL PLAQUE AND INTERACTS WITH THE N-TERMINAL REGION OF PLAKOPHILIN 1. THE C-TERMINAL REGION INTERACTS WITH INTERMEDIATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Striate palmoplantar keratoderma resulting from desmoplakin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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                                      Invest. Dermatol. 113:940-946(1999)
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Interpro; IPR002017; Spectrin.
Pfam; PF00681; Plectin; 10.
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EMBL, J05211, AAA35766.1, -.
EMBL, AF139065, AAF19785.1, -
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SMART; SM00150; SPEC; 1.
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Genew; HGNC:3052; DSP.
MIM; 125647;
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15.1 1 1 1 1 1 1 1 1 1	Oy 1331 SDLIPYKDLTSSNYVVBDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYYKILS 1390 1	RESULT 53 MYSA_DROME ID MYSA_DROME STANDARD; PRT; 1962 AA. AC P05661; DT 01-NOV-1988 (Rel. 09, Created) DT 15-JUN-2002 (Rel. 41, Last sequence update) DT 15-JUN-2002 (Rel. 41, Last annotation update) DT 15-JUN-2002 (Rel. 41, Last annotation update) DT 15-JUN-2002 (Rel. 41, Last annotation update) DT 15-JUN-2002 (Rel. 41, Last annotation update) DT 15-JUN-2002 (Rel. 41, Last annotation update) DT 15-JUN-2002 (Rel. 41, Last sequence update) DT 1
FT REPEAT 2406 2440 PLECTIN 11. FT REPEAT 2456 2493 PLECTIN 11. FT REPEAT 2610 2644 PLECTIN 12. FT REPEAT 2610 2644 PLECTIN 13. FT REPEAT 2610 2644 PLECTIN 14. FT REPEAT 2724 264 2665 PLECTIN 15. FT REPEAT 2724 2764 PLECTIN 15. FT REPEAT 2764 2764 PLECTIN 17. FT OWAIN 1 584 PLECTIN 17. FT OWAIN 282 2849 2849 PHOSPHORILATION (BY PKA) (POTENTIAL). FT CONFLICT 1020 1120 1120 1120 1120 1120 1120 112	QY 394 TKESTEPNEYPRGVTYPLS-YN-DINNALNELNSFGDLINPFDYTKE-PSKNI 443 Db 1179 QEEGTRKREVENELAKVRNHYNBEMSNLRNKYETEINITKTTIKEISMQKEDDSKNLRNO QY 444	Qy 560 VEKELKYYKNLISKIENEIETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQV 619 1405 LSEEIKRLKNTLTQTTENLRRVEEDLQQQKATGSEVSQRKQOLEVEL 1451 Qy 620 QKVLLMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYLIVLKKEIDKLKVFWP 679 1:: 1:: 1:: 1:: 1:: 1:: 1:: 1:: 1:: 1:: 0y 680 KVESILNEEKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQGEQKO 739 1:: 1:: 1:: 1:: 1:: 1:: 1:: 1:: 1:: 1:: 1:: 1:: 1:: 1:: 1:: 1:: 1:: 1:: 1:: 1:: 1:: 1:: 1:: 1:: 1:: 1:: 0y 740 AQPPVPVPVPERAQVPTPPAPVNNKTENVSKLDYERLYEPINTSYICHKYILVSHTM 799 1:: 1: 1:: 1: 1:: 1: 1:: 1: 1:: 1: 1:: 1:

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                                                                                                                                                                                                                                                                                     DOMAIN: Alternative splicing exons contribute to the specialized contractile activities of different muscle types. Exon 3 encodes the hydrophobic pocket adjacent to the AFP-binding site, exon 9 is adjacent to the actin-binding domain, exon 11 is involved in actin-binding, exon 15 in the S2 hinge and exons 18 and 19 the non-coiled tail region.
                                                                                                           Wassenberg D.R. II, Kronert W.A., O'Donnell P.T., Bernstein S.I.;
"Analysis of the 5' end of the Drosophila muscle myosin heavy chain
gene. Alternatively spliced transcripts initiate at a single site and
intron locations are conserved compared to myosin genes of other
                                                                                                                                                                                                                                                                                                                                                                                                                                         Isoforms containing exon 9a are expressed in indirect flight muscles, exons 9a and 9b are expressed in jump muscles, exons 9b and 9c are expressed in other larval and adult muscles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISCELLANDOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                       Kronert W.A., Edwards K.A., Roche E.S., Wells L., Bernstein S.I.; "Muscle-specific accumulation of Drosophila myosin heavy chains: a splicing mutation in an alternative exon results in an isoform
           MEDLINE-89384556; PubMed-2506434;
George B.L., Ober M.B., Emerson C.P. Jr.;
"Functional domains of the Drosophila melanogaster muscle myosin
heavy-chain gene are encoded by alternatively spliced exons.";
                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: Expressed in larval and adult muscles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBFRAGMENT (S2).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 10 DOMAIN.
                                                                                                                                                                                                               STRAIN-Canton-S; TISSUE-Embryonic muscle; MEDLINE-91330870; PubMed-1907912;
                                                                                                                                                                          Biol. Chem. 262:10741-10747(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -------
                                                           Mol. Cell. Biol. 9:2957-2974(1989)
                                                                                               MEDLINE-87280141; PubMed=3038896;
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InterPro; IPR004009; Myosin_N.
STRAIN-Canton-S; TISSUE-Pupae;
                                                                                                                                                                                                  SEQUENCE OF 333-614 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M61229; AAA28686.1; -.
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PIR; A32491; A32491.
PIR; B32491; B32491.
HSSP; P08799; IMND.
Flybase; Fbgn0002741; Mhc.
                                                                                  SEQUENCE OF 1-264 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X60196; CAA42752.1;
EMBL; X60196; CAA42753.1;
EMBL; X60196; CAA42754.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J02788; AAA28707.1;
                                                                                                                                                                                                                                                                             substitution.",
                                                                                                                                                              organisms
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74;
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YNGFEQLCINFTNEKLQGFFNHIWWWAGEBEYKKEGINWDF IDFGMDLLACIDLIEK -> YNGFEQLCINFTNEKLQGFFN HHWFVLEGEFYKREGIDWAFIDFGMDLLACIDLIEK (IN ISOFORM BDBBA AND ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                              DASVLHNLRQRYYNKLIY (IN ISOFORM 3B,
ISOFORM BDBBA AND ISOFORM BABDB).
DICLLTDNIYDYHIVSQGKVTVASIDDAEEFSLTD -> EY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YQİLNPRGIKDLDCPKKASKVLIESTELNEDLYRLĞHTK
-> YMILAPAIMAAEKVAKNAAĞKCLEAVĞLDPDMYRIĞHT
                                                                                                                                                                                                                                                                                                                                       ATP (BY SIMILARITY).
VRDIKSEKVEKVNPPKFEKIEDMADMTVLNTPCVLHNLRQR
                                                                                                                                                                                                                                                                                                                                                                              YYAKLIY -> TRDLKKDLLQQVNPPKYEKAEDMSNLTYLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DICLLTDNIYDYHIVSQGKVTVASIDDAEEFSLTD -> EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> YQILNPKGIKGIEDPKKCTKVLIESTELNDDQYRLGNT
K (IN ISOFORM 11C).
YQILNPRGIKDLDCPKKASKVLIESTELNEDLYRLGHTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -> YKIMCPKLLQGVEKDKKATEIIIKFIDLPEDQYRLGNT
K (IN ISOFORM 11D AND ISOFORM BABDB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> AEKEKNEYYGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDFGMDLLACIDLIEK -> YNGFEQLCINFTNEKLQQFFN
HHMFVLEQEEYQREGIEWTFIDFGMDLQLCIDLIEK (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YQILNPRGIKDLDCPKKASKVLIESTELNEDLYRLGHTK
-> YQILNPAGIVGVDDPKKCGSIILESTALDPDMYRIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YNGFEQLCINFTNEKLQQFFNHIMFVMEQEEYKKEGINWDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 GGSVASGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDSDAKSYADLKHRVRNYLLT 138
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YQILNPRGIKDLDCPKKASKVLIESTELNEDLYRLGHTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 CVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGTAVTTSTPGSKGSVASGGS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DICLLTDNIYDYHIVSQGKVTVASIDDAEEFSLTD ->
                                                                                                                                                       SMART; SM00015; IQ; 1.
SMART; SM0242; MYSc; 1.
PROSITE; PS50096; IQ; II.
Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; ATP-binding; ATP-binding; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLLSNNIYDYRIVSQGKTTIPSVNDGEEWVAVD (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VFLGQHIGDYPGICQGKTRIPGVNDGEEFELTD (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                585 CVSYNITGWLEKNKDPLNDTVVDQFKKSQNKLLI-----EIFADHAGQSG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F5A888932E414F7F CRC64;
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                                                                                                                                                                                                                                                                                                  IQ.
COILED COIL (POTENTIAL).
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MISSING (IN ISOFORM 18).
EK -> RE (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> K (IN REF. 2)
-> M (IN REF. 2)
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                                                                                                                                                                                                                                                                             MYOSIN HEAD-LIKE.
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                                                                         pfam; PF01576; Myosin_tail; 1.
Ppfam; PF02736; Myosin_N; 1.
Ppfam; PF00193; MYOSINHEAVY.
Probom; PD000355; myosin_head; 4.
                      IPR001609; myosin_head.
InterPro; IPR002928; Myosin_tail
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                                      Pfam; PF00063; myosin_head; 7.
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                      InterPro;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its 1542 ALEEAEAALEQEENKVLRAQLELSQVRQEIDRRIQEKEEEFENTRKNHQRALDSMQASLE 1601 ----NALESYKKFLPEGTDVAT 1197 1198 VVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLG 1257 QVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSL-------KKQLENNV 1304 QADRGR-----RQAEQE-----LADAHEQLNEVSAQNASISAAKRKLESEL 1733 MTFNVNVKDILNSRFNKRENFKNV-----LESDLIPYKDLTSSNYVVKDPYKFLNKEKR 1358 DKFLSSYNYIKD-SIDTDINFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPF 1417 1418 LNNIETLYKTV------NDKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLK 1464 1105 LSEE---SIQTEDN---YASLENFKVLSKLEGKLKDN----LNLEKKKLSYLSSGLHHLI 1154 Euteleostomi; Sus. MISCELLANBOUS: THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATPASE MYOSIN, WHILE THE BETA ISOFORM IS A 'SLOW' ATPASE. SIMILARITY: CONTAINS I MYOSIN'LIKE GLOBULAR HEAD DOMAIN. SIMILARITY: CONTAINS I 10 DOMAIN. 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Myosin heavy chain, cardiac muscle beta isoform (MyHC-beta). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, 1465 TIQDKLADFKKNNNFVGIADLSTDYNHNNLLTKFLSTG 1502 1892 -----LAKFRKAQQELEEAEERADL-AEQAISKFRAKG 1923 PRT; 1935 AA AELK ---EVIKNKNYTGNSPSENNTDVN------STANDARD; SEQUENCE FROM N.A. STRAIN=Domestica; Sus scrofa (Plg) NCBI_TaxID=9823; MYH7_PIG 1155 1258 1305 1693 1359 Ko Y g δ g δ q ò g ò q ò g δ q δý

Db 1024 KVKLEQHVDDLAGSLEQE	Qy 545 KALKYMEDYSLR : Db 1081 KKKDFELNALNARIEDEGAL	Qy 597 ITKDENKPDEKILEVSDIVK :::: :: Db 1139 LSRELEEISERLEEAGGATS	Qy 655 QENKQEPYYLIVLKKEIDKL	1191 ALRK	Qy 715TKPGQQAGSALEGD : Db 1245 LEKMCRTLEDQMNEHRSKAE		DD 1304 -GKLTYTQQLEDLKRQLEEE	Qy 821 DPLDLLFNIQNNIPVWXSMF	880 KKVSTSVKTLSSSS	1401	Qy 937 NIYQELIGQKSS Db 1460YEESQSELESSQKEARSL	Qy 982 NDESKRKK Db 1513 TEQLGSSGKTIHELEKVRKQ	Qy 1013 LKLER-LFDKKKTVGKYKM :: :: Db 1570 AEMERKLAEKDEEMEQAKRN	Qy 1071 IAETENTLENTKILLKHYKG : : : : : Db 1622 LNEWEIQLSHANRMAAEAQK	QY 1131 KLKDNLNLEKKKLSYLSSGL : : ::: : : Db 1667 -LKENIAIVERRNNLLQAEL	QY 1184 SYKKFLÞEGTDVATVVSESG 	Qy 1233 VDDEVDDVIIVPIFGESEED ::::::::::::::::::::::::::::::::::	1292 VYRSLKKQLENNVMTF	Db 1828AEQKRNAESVKGMRKSE: Oy 1351 KFLNKEKRDKFLSS	: 1879NRQAEEA	RESULT 55 SCP1_HUMAN ID SCP1_HUMAN STANDARD;
CC use by non-profit institutions as long as its content is in no way CC modified and this statement is not removed. Usage by and for commercial CC entities requires a license agreement (See http://www.isb-sib.ch/announce/CC or send an email to license@isb-sib.ch).	EMBL; U75316 HSSP; P08799 InterPro; IP		Pfam; PF0061 Pfam; PF0157 Pfam; PF0273	PRINTS; PRO ProDom; PD0	SMART; SM0001 SMART; SM0024 PROSITE; PS5(Myosin; Muse ATP-binding	DOMAIN 18	DOMAIN 839 1935 NP_BIND 178 185 DOMAIN 655 677	DOMAIN 757 771 ACTIN-BINDING. MOD_RES 129 129 METHYLATION (TRI-)	MOD_RES 695 695 ALKTLATION (SH-1)	Query Match 3.9%, Scor Best Local Similarity 18.7%, Pred Astches 286, Page Astche	QY 28 LVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGTAVTTSTPGSKGSVASGGSGSVASGGS 87	QY 88 VASGGSVASGGSVASGGSGNSRRINPSDNSSDSDAKSYADLKHRVRNYLLTIKELK 143	144 YPQLEDLTNHMLTLCDNIHGFKYLIDGYEBINELLYKLNFYFD	187 LLRAKLNDVCANDYCQIPEN	219 KLVFGYRKPLDNIKDNVGKMEDYIKKNKKTIENINEL :: :: :: :: :: :: ::	DD /98 KMEFKKLLERRUSLLIIQWNIRAFMSVKNMPWMKLYFKIKPLLESAETEKEMATMKEE 855 QY 256 IEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNE 313	EARRKELEEKMYSLLQEKNDLQLQ DK INEIKNPPPANSGNTPNTLLDKNKK	Db 913 IQLEAKVKEMTERLEDEEEMNAELTAKKRNVEDECSELKRDID 955	Qy 369 FTDPLELEYYLREKNKNIDISAKVE-TKESTEPNEYPNGVTYPLSYNDINNALNEEGG 427 :	QY 428 DLINPFDYTKEPSKNIYTDNERKKFINEIKEKIKIESDKKSYEDRSKSLNDITKE 487 ::

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GSLEQEKKVRMDLERAKRKLEGDLKLT-QESIMDLENDKQQLDERL 1080
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EKVRKQLEAEKLELQSALEESEASLEHEEGKILRAQLEF---NQIK 1569
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NNIDLINFEKMMGKRYSYKVE---KLTHHNTFASYENSKHNLEKLT 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSDIVKVQVQKVLLMNK - · IDELKKTQLILKNVELKHNIHVPNSYK 654
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976 AA.

PRT;

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Matches 236;
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CYTOGENET. CELI GENEL. 78:103-104(1997).

SYNAPTONEMAL COMPLEXES (SCS), FORMED BETWEEN HOMOLOGOUS
CHROMOSOMES DURING METOTIC PROPHASE.

CHROMOSOMES DURING METOTIC PROPHASE.

SYNAPTONEMAL COMPLEXES, BETWEEN LAIFERLE ELEMENTS IN THE NUCLEUS.
FOUND ONLY WHERE THE CHROMOSOME CORES ARE SYNAPSED. ITS N-TERMINUS
CHRONIOS THE CENTRE OF THE SYNAPTONEMAL COMPLEX WHILE THE CTERMINUS EXTRADONEMAL COMPLEX WILL INTO THE LATERAL DOMAIN OF THE SYNAPTONEMAL COMPLEX (BY SITILARITY).

CHOMAIN CONSISTS OF AN ALPHA-HELICAL STRETCH OF 700 AA RESIDUES, FLANKED BY N- AND C-TERMINAL GLOBULAR DOMAINS. THE CTERMINAL COMPLEX (BY SINAL GLOBULAR DOMAINS. THE CTERMINAL COMPLEX (BY SINAL GLOBULAR DOMAINS. THE CTERMINAL COMPLEX (BY SINAL GLOBULAR DOMAINS. THE CTERMINAL COMPLEX (BY SINAL GLOBULAR DOMAINS.)
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NUCLEAR LOCALIZAȚION SIGNAL (POTENTIAL).

NUCLEAR LOCALIZAȚION SIGNAL (POTENTIAL).

NUCLEAR LOCALIZAȚION SIGNAL (POTENTIAL).

ARG/LYS-RICH (BAȘIC).
                                                                                                                                                                                                                                                                                                                          Tanaka H., Uchida K.,
Matsumiya K., Namiki
                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                               Okuyama A., Nishimune Y.; "Assignment of synaptonemal complex protein 1:(SCP1) to human chromosome 1p13 by fluorescence in situ hybridization and its expression in the testis.";
                                                                                                                                                                                                                   "Human synaptonemal complex protein 1 (SCP1): isolation and characterization of the cDNA and chromosomal localization of
                                                                                                                                                                                      Meuwissen R.L.J., Meerts I., Hoovers J.M.N., Leschot N.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell division; Phosphorylation;
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F -> Y (IN REF. 2)
F -> T (IN REF. 2)
F -> T (IN REF. 2)
E -> D (IN REF. 2)
N -> S (IN REF. 2)
K -> N (IN REF. 2)
K -> N (IN REF. 2)
015431; 014963;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Synaptonemal complex protein 1 (SCP-1 protein)
                                                                                                                                                                                                                                                                                                                         Kondoh N., Nishina Y., Tsuchida J., Koga M.,
Inazawa J., Taketo M., Nozaki M., Nojima H.,
                                                                                                                                                                TISSUE=Testis;
MEDLINE-97224467; PubMed-9119375;
                                                                                                                                                                                                                                                                                                            MEDLINE-98037449; PubMed-9371398;
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                                                                                                                                                                                                                                                        Genomics 39:377-384(1997).
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DNA-binding; Coiled coil.
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MIM; 602162; -.
                                                                                 (Human).
                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                        NCBI_TaxID=9606;
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                                                                   SYCPI OR SCPI
                                                                                  Homo sapiens
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TVLPKRGQRPKLSSKRE (IN REF. 2).
LTSHCNKLSLENK -> YFTLQQASPPPN (IN REF.
2).
N -> I (IN REF. 2).
K -> T (IN REF. 2).
E -> D (IN REF. 2).
E -> D (IN REF. 2).
E -> D (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | :| |: |: || |: | 426 TINNKEVELEELKKVLGEKETLIYEN-----KQFEKIAEELKGTEQELIGLLQAREKEVH 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     781 FLNTSYICHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMF 840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           388 ISAKVETKES-----TEPNEYPNGVTYPLSYNDINNALNELNSFGDLINPFDYTKE 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   439 PSKNIYTDNERKKFINEIKEKIKIEKKKIESDKKSYED----RSKSLNDITKEYEKLLNE 494
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204; Mismatches
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STATN-ATCC 35092 / DSM 1617 / P2;

MEDLINE-21332296; PubMed-11427726;

MEDLINE-21332296; PubMed-11427726;

MA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

MA wayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

A wayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Thi-Ngoc H.P., Redder W.F., Duguet M., Gasterland T.,

Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

L. -FONGTION: Involved in DNA double-strand break repair (DSBR). The

rad50/mrell complex possesses single-strand endonuclease activity.

RAd50 provides an ATP-dependent control of mrell by unwinding
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the European Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
                                                          , 956 LKD&DTFYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKL 1015
                                                                                                                                                                          ERLFDKKKTVGKYKMQIKKLT-LLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAET 1074
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                                                                                                                  ------LGLYKSKEQEQSSL----RASLEIELSNLKAEL----LSVKKQLEI 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --GISKDKRDYLWTSAKNTLSTPLP----KAYTVKTPTKPKLQQRENLNIPIEESKKKR 882
----KLQKEIDKRCQH-----KIAEMVALMEKHKHQYDKIIEERDSE---- 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----FLPEGTDVATVVSESGSDTLEQ-SQPKKPASTHVGAES-----NTITT 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     883 KMAFEFDINSDSSETTDLLSAVSE--EETLKTLYRNNNPPASHLCVKTPKKAPSSLTT 938
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InterPro; IPR003439; ABC_transportr.
InterPro; IPR003405; SMC_C.
InterPro; IPR003405; SMC_N.
Pfam; PF02463; SMC_N: 1.
Pfam; PF02483; SMC_C; 1.
DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete proteome.
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SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA double-strand break repair rad50 ATPase.
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                                                                                                                                      Indels 357;
                                                                                          Length 864;
                     COILED COIL (POTENTIAL).
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                                                                                                                                      Conservative 200; Mismatches 321;
  ATP (BY SIMILARITY)
                                                                                        Score 331.5; DB
Pred. No. 0.00021
                                           864 AA; 101601 MW;
                                                                                          3.98;
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37
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                                                                       ----LIAELKEVIKNKN 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Adductor muscle;

MEDLINE-92011955; PubMed-1917970;

MEDLINE-92011955; PubMed-1917970;

Nyitray L., Goodwin E. B., Szent-Gyoergyi A.G.;

"Complete primary structure of a scallop striated muscle myosin heavy chain. Sequence compearison with other heavy chains reveals regions that might be critical for regulation.";

J Blol. Chem. 266:18469-18476(1991).
--- FUNCTION: MUSCLE CONTRACTION.
--- FUNCTION: MUSCLE CONTRACTION.
--- FUNCTION: MYSSIN IS A PROFEIN THAT BINDS TO F-ACTIN 6 HAS ATPASE
--- SUBDULTY THAT IS ACTIVATED BY F-ACTIN.
--- SUBDULT: MUSCLE MYSSIN IS A HEXAMERIC PROFEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBDULTS (MHC), 2 ALKALI LIGHT (HAIN SUBUNITS (MLC)
--- SUBCELLULAR LOCATION: THICK filaments of the myofibrils.
--- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
--- SIMILARITY: CONTAINS 1 1Q DOMAIN.
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MEDLINE-94173332; PubMed-8127365;
ALE X., Harrison D.H., Schlichting I., Sweet R.M., Kalabokis V.N.,
Szent-Gyorgyi A.G., Cohen C.;
"Structure of the regulatory domain of scallop myosin at 2.8-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myosin heavy chain, striated muscle.
Agguipecten irradians (Bay scallop).
Eukaryota; Metazoa: Mollusca; Bivalvia; Pteriomorphia; Pectinoida;
Pectinoidea; Pectinidae; Argopecten.
                                                                                                      |: |: :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| 
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MEDLINE-91088319; PubMed-2263488;
Nyltray L., Goodwin E.B., Szent-Gyorgyi A.G.;
"Nucleotide sequence of full length cDNA for a scallop striated muscle myosin heavy chain.";
Nucleic Acids Res. 18:7158-7158(1990).
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MEDLINE-96419133; Pubmed-8805510;
                                                                       NYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHH---
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01-WAR-1992 (Rel. 21, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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Structure of the regulatory domain of sc
resolution: implications for regulation.
Structure 4:21-32(1996).
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THE (BY SIMILARITY).
ALKYLATION (SH-1) (BY SIMILARITY).
ALKYLATION (SH-2) (BY SIMILARITY).
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RODLIKE TAIL (S2 AND LMM DOMAINS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myosin; Muscle protein; Coiled coil; Thick filament; Actin
ATP-binding; Alkylation; Calmodulin-binding; 3D-structure.
DOMAIN 1 777 MYOSIN HEAD-LIKE.
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llarity 18.6%; Pred. No. 0.00051;
Conservative 249; Mismatches 466;
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PDB; 1MDC; 11-JUL-96.
InterPro; 1PR000049; IQ_region.
InterPro; 1PR0002928; Myosin_tail.
InterPro; IPR002017; Spectrin.
InterPro; IPR002017; Spectrin.
InterPro; IPR001609; myosin_head;
Pfam; PF00063; myosin_head; 1.
Pfam; PF001612; 10; 2.
Pfam; PF01576; Myosin_tail; 1.
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PRODOM; PD000935; myosin_head; 1.
SMART; SM00015; IQ; I.
SMART; SM00242; MYSC; 1.
EMBL; X55714; CAA39247.1;
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A40997; A40997
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nes 261; Conserv
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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MEDLINE=92041770; PubMed=1939030;
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SEQUENCE OF 1145-1270.
MEDLINE-89228549; Pubmed=2713098;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY SEQUENCE OF 1-808.
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ERVKRELEENVRRKEAEISSLNSKLEDEQNLVSQLQRKIKELQARIEELEEELEAERNAR 1126
                                    1511 DQLSEGGRSTHELDKARRRLEMEKEELQAALEEAEGALEQEEAKVMRAQLEIATVRNEID 1570
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                                                                                                              NIKTEGQSDNSEPSTEGEITG-QATTKPGQQAGSALEGDSVQAQAQ-----EQKQAQPP
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MYSS_CHICK
DYSS_CHICK
AC P13538; 01328;
DT 01-JAN-1990 (Rel. 13, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DF Myosin heavy chain, skeletal muscle, adult.
OS Gallus gallus (Chicken).
OS Gallus gallus (Chicken).
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                                                                   HVPNSYK--QENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKK----
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Matsuda G.; STRAIN=White leghorn; TISSUE-Pectoralis muscle; Chao T.H., Bandman E., Moore L.; "Cloning, nucleotide sequence and characterization of a full-length cDNA encoding the myosin heavy chain from adult chicken pectoralis "The primary structure of skeletal muscle myosin heavy chain: III. Sequence of the 22 kDa fragment and the alignment of the 23 kDa, 50 kDa, and 22 kDa fragments.";
J. Biochem. 110:68-74(1991). Maita T., Yajima E., Nagata S., Miyanishi T., Nakayama S., Matsuda ("The primary structure of skeletal muscle myosin heavy chain: IV. Sequence of the rod, and the complete 1,938-residue sequence of the ij. chain: II. Matanabe B.; "Amino-acid sequence of the short subfragment-2 in adult chicken in adult chicken TISSUE=Pectoralis muscle;
MEDLINE-92041767; PubMed=1939027;
Hayashida M., Maita T., Matsuda G.;
"The primary structure of skeletal muscle myosin heavy chain:
Sequence of the amino-terminal 23 kDa fragment.";
J. Biochem. 110:54-59(1991). . ; G "Amino-acid sequence of the hinge region in chicken myosin subfragment-2."; Matsuda Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases TISSUE=Pectoralis muscle;
MEDLINE=92041768; PubMed=1939028;
Komine Y., Maita T., Matsuda G.;
"The primary structure of skeletal muscle myosin heavy sequence of the 50 kDa fragment of subfragment-1.";
J. Blochem. 110:60-67(1991). Matsuda TISSUE-Pectoralis muscle; MEDLINE-92041769; PubMed-1939029; Maita T., Miyanishi T., Matsuzono K., Tanioka Y., "Complete amino-acid sequence of subfragment-2 skeletal muscle myosin."; MEDLINE-87092420; PubMed-3467365; Maite T., Hayashida M., Tanioka Y., Komine Y., "The primary structure of the myosin head."; "The Orlal. Acad. Sci. U.S.A. 84:416-420(1987). Biol. Chem. Hoppe-Seyler 370:1027-1034(1989) Biol. Chem. Hoppe-Seyler 370:549-558(1989)

METHYLATION

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551
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697
707
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                                                                                                                                       Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
ATP-binding; Methylation; Alkylation; Phosphorylation; Acetylation;
Calmodulin-binding; Multigene family; 3D-structure.
                                                                                                      Holden H.M.; "Three-dimensional structure of myosin subfragment-1: a molecular
                                                                                                                                                                                                                                                                          SUBFRAGMENT (S2).
-1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                     'Genomic clones encoding chicken myosin heavy chain genes.";
                  Moriarity D.M., Barringer K.J., Dodgson J.B., Richter H.E., Young R.B.;
                                                                                 Rayment I., Rypniewski W.R., Schmidt-Base K., Smith R., Conchick D.R., Benning M.M., Winkelmann D.A., Wesenberg G.,
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ATP (POTENTIAL).
ACTIN-BINDING.
                                                                X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 1-843
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InterPro; IPR000048; IQ_region.
InterPro; IPR004009; Myosin_N.
InterPro; IPR0012028; Myosin_tail.
InterPro; IPR001609; Myosin_tead.
Pfam; PF00063; Myosin_head.
SEQUENCE OF 1857-1938 FROM N.A. MEDLINE=87217964; Pubmed=3034534;
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Pfam; PF01576; Myosin_tail; 1.
Pfam; PF02736; Myosin_N; 1.
ProDom; PD000355; myosin_head; 1.
                                                                           MEDLINE=93303624; PubMed=8316857;
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EMBL, M16575, AAA48970.1; --
PIR: PX0050; PX0051.
PIR: A26821; A26821.
PIR: S02082; S02082.
PIR: S04501; S04501.
PIR: S04515; S05515.
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SMART; SM00242; MYSc; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     524 LTHHNTFASYENSKHNLEKLTKALKY------MEDYSLRNIVVEKELKYYKNLISKIE 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 KMEDYIK--KNKKTIENINELIEESKKTIDKNKNATKEEEKKK--LYQAQYDLSIYNKQL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EEAHNLISVLEKRIDTLKKNE----NIKELLDKINEIKNPPPANSGNTPNTLLDKNKKI 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        894 QAEADSLADAEERCDQLIKTKIQLEAKIKEVTERAEDEEE---INA-----ELTAKKRKL 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EEHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKNKNIDISAKVE-TKESTEPNEYPNG 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative 233; Mismatches 434; Indels 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1938;
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METHYLATION (TRI-).
METHYLATION (MONO-).
ALKYLATION (SH-1).
ALKYLATION (SH-1).
C -> Q (IN REF. 7 AND 8
L -> F (IN REF. 1).
E -> D (IN REF. 5).
S -> A (IN REF. 5).
HV -> QL (IN REF. 5).
S -> A (IN REF. 5).
I -> V (IN REF. 10).
I -> V (IN REF. 10).
IHG -> FH (IN REF. 10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.9%; Score 331; DB 1; 19.1%; Pred. No. 0.00053;
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                                                                                                                                                                           KYKM-QIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENTLENTKILL 1085
                                                                                                                                 SESGSDTLEQS----QPKKPASTHVGAESNTITTSQ-----NVDDEVDDV---- 1240
                                                                                                                                                                                                                      -----IIVPIFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIENE 1280
                                                                                                                                                                                                                                                               : : | | : : | : | 1800 DEAEQLALKGGKKQLQKLEARVRELEGEVDSEQKRSAEAVKGVRKYERRVKELTYQCEED 1859
984 -ESKRKKLEEDINKLK--------KTLQLSFDLYNKYKLKLER-LFDKKKTVG 1026
                                                                                                                                                              LSSGLHHLIAELKEVIKNKNYTGNSPSENNTDV-----NNALESYKKFLPEGTDVATVV 1199
                                                                                                                                                                                                                                                                                           1281 YE-VLYLKPLAG----VYRSLKKQLENNVMTFNVNVK--------DILNSRF 1319
                                                                                                                                                                                                                                                                                                                1860 RKNILRLODLVDKLOMKVKSYKROAEEAEELSNVNLSKFRKIOHELEEAEERADIAESOV 1919
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                                                                                                                     1086 KHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1744 AA
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NCBI_TaxID=8355;
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NK 1921
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PIR; JH0720; JH0720.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRI-DT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      368 LFTDPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266 KLQRKAEALEQEKQDLRGQIAEVLEDRQQLMHLKMSLSLEVATYRSLLEA-----ES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COIL 2B.
W; 6502EAC9FE6C4E93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.9%; Score 330.5; DB 1;
18.0%; Pred. No. 0.00049;
ive 311; Mismatches 574;
                                                                                                                            coil; Neurone.
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Copyright (c) 1993 - 2003
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Listing first 180 summaries
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myosin heavy chain

A/Cross-references: EMBL:X15063; NID:99896; PIDN:CAA33163.1; PID:99897
R;Wyler, P.J.
Nucleic Acids Res. 17, 5401, 1989
A;Title: Nucleotide and deduced amino acid sequence of the gpl95 (MSA-1) gene from Pl
A;Title: Nucleotide and deduced amino acid sequence of the gpl95 (MSA-1) gene from Pl
A;Title: Nucleotide and deduced amino acid sequence of the gpl95 (MSA-1) gene from Pl
A;Title: Nucleotide and deduced amino acid sequence of the gpl95 (MSA-1) gene from Pl
A;Molecule type: mRNA
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A;Molecule type: mRNA
A;Cross-references: EMBL:X15063
C;Superfamily: major merozoite; surface antigen
F;1-19/Pomain: signal sequence #status predicted <MAT>
F;20-1639/Product: major merozoite surface antigen #status predicted <MAT> major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) N;Alternate names: gp195 surface antigen C;Species: Plasmodium falciparum ö purine NTPase [imp myosin heavy chain dystrophin, muscle tanabin - African hypothetical prote C.Species: Plasmodium falciparum
C.Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jun-2000
C.Accession: S05603; S04850
R.Myler, P.J. 241 YIKKNKTIENINELIEESKKTIDKNKNATKEEEKKKIYQAQYDLSIYNKQLEEAHNLIS 300 480 61 AVTTSTPGSKGSVASGGSVASGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDS 120 Gaps 9 9 1 MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGT 1 MXIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGT 241 YIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLIS VLEKRIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKT 361 IKFNIDSLFTDPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNAL NELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKEKIKIEKKKIESDKKSYEDRSKS LNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMED ; 0 Length 1639; Indels Score 8424; DB 2; Pred. No. 1.5e-253; ;; 0 Mismatches A;Reference number: S05603
A;Reference number: S05603
A;Accession: S05603
A;Accession: S05603
A;Accesion: S05603
A;Accesion: 105603
A;Residues: 1-1639 < MYL> ALIGNMENTS G82875 B90395 A40997 A27605 JH0720 ; 0 100.08; 100.0%; Best Local Similarity 100. Matches 1639; Conservative 1883 864 1938 3685 332 331.5 331.5 331 330.5 Query Match 121 361. 121 181 421 301 176 177 178 179 180 ò g δ g ò qq δ Op οy g Ω Db δ q да .

1 10:57:13 2003

Tue Apr

Db 1561 QE Qy 1621 NF Db 1621 NF	RESULT 2 A24594 probable maj C;Species: P C;Date: 29-A C;Accession: R;Holder, A.	Nature 317, A, Title: Pri A, Reference A, Accession: A, Molecule t A, Residues: C, Superfamil C, Keywords:	Query Matc Best Local Matches 16	Qy 1 MK 1 Db 1 MK	Oy 61 AV Db 61 AV	Oy 121 DA Db 121 DA	Oy 181 LN Db 181 LN	Oy 241 YI 11 Db 241 YI	Qy 301 VL Db 301 VL	Qy 361 IK Db 361 IK	Oy 421 NE 11 Db 421 NE	Oy 481 LN 11 Db 481 LN	Qy 541 EK Db 541 EK	Qy 601 EN Db 601 EN	Qy 661 PY
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481 LNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMAGKRYSYKVEKLTHHNTFASYENSKHNL 540	601 ENKEDEKILEVSDIVKVQVQKVLLANKIDELKKTQLILKNVELKHNIHVPNSYKQENKQE 660	721 AGSALEGDSVQAQAQEQKQAQPPVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYE 780	DSLNNSLSQLFMEIYEKEMVCNLYKLKDNDKIKNLLEBAKKVSTSVKTLSSSSMQPLSLT 90	901 POOKFEVSANDDISHSTNLNNSLKLFENILSLGKNKNIYQEIIGQKSSENFYEKILKDSD 960 	961 TFYNESFTWFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFD 1020 	1021 KKKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKBAEIAETENTLEN 1080 	1081 TKILLKHYKGLVKYYNGESSPLKTLSEESIOTEDNYASLENFKVLSKLEGKLKDNLNLEK 1140 	1141 KKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVS 1200 	1201 ESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGGVV 1260 	1261 TGEAVTPSVIDNILSKIENEYEVLYLKPLACVYRSIKKQLENNVMTFNVNVKDILNSRFN 1320 	1321 KRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFAN 1380 	1381 DVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLFVIHLE 1440 	1441 AKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLSTDYNHNNLLTKFLS 1500 1111111111111111111111111111111111	1501 TGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYK 1560 	1561 QEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSS 1620
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jor surface antigen (83K, 19K, 42K) precursor - malaria parasite (Plasmodi
Plasmodium falciparum
                                                                                                                                                                                                             ..A.; Lockyer, M.J.; Odink, K.G.; Sandhu, J.S.; Riveros-Moreno, V.; Nicholl 270-273, 1985
imary structure of the precursor to the three major surface antigens of Pl number: A24594; MUID:86014355; PMID:2995820
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Aug-1987 #sequence_revision 29-Aug-1987 #text_change 09-Jun-2000
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Pred. No. 2.3e-246;
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11 Similarity 97.9%;
605; Conservative
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YYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQ 720

C;Accession: A25120 R;Mackay, M.; Goman, M.; Bone, N.; Hyde, J.E.; Scaife, J.; Certa, U.; Stunnenberg, H. EMBO J. 4, 3823-3829, 1985 A;Title: Polymorphism of the precursor for the major surface antigens of Plasmodium f A;Reference number: A91030; MUID:86136024; PMID:3004972 A;Accession: A25120 A;Molecule type: DNA A;Residues: 1-1631 AMAC> C;Comment: The merozoite stages of different strains have strain-specific surface ant C;Comment: P. falciparum has three stages: sporozoite, merozoite, and gametocyte. The C;Comment: P. falciparum has three stages: sporozoite, merozoite rangementocyte. The C;Superfamily: major merozoite surface antigen C;Keywords: glycoprotein; merozoite surface antigen C;Keywords: glycoprotein; merozoite surface antigen #status predicted <mat> F;1-19/Domain: signal sequence #status predicted <mat> F;1-14/Domain: signal sequence #status predicted <mbn> F;1614-1631/Domain: membrane anchor #status predicted <mbn> F;1614-1631/Domain: membrane anchor #status predicted <mbn> F;97,259,755,759,835,911,955,1049,1156,1165,1436,1563/Binding site: carbohydrate (Asn</mbn></mbn></mbn></mat></mat>	Query Match 94.6%; Score 7965; DB 1; Length 1631; Best Local Similarity 95.3%; Pred. No. 2.4e-239; Matches 1563; Conservative 19; Mismatches 48; Indels 10; Gaps 3; QY 1 MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGT 60 Db 1 MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMYLNEEEITT 60 QY 61 AVTTSTPGSKGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSGNSRTNPSDNSSDS 120 CQY 61 KGASAQSGTSGT-SGTSGFSRSNTLPRSNTSSGASPPADASDS 111	Qy 121 DAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYK 180	1912 VLEKRIDTLEKKNENIKELLÖKINEIKNPPPANSGNTPHTLLÖKNKLIEBHEKEIKETAKT 1921 VLEKRIDTLEKKNENIKELLÖKINEIKNPPPANSGNTPNTLLÖKNKLIEBHEKEIKETAKT 1922 VLEKRIDTLEKKNENIKELLÖKINEIKNPPPANSGNTPNTLLÖKNKKIEBHEKEIKETAKT 1921 IKFNIDSLETDPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNAL 1921 IKFNIDSLETDPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNAL 1921 INELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKEKKIESDKKSYEDRSKS 1932 IKFNIDSLETDPLELEYYLREKNKNIDISAKVETKERKKIESDKKSYEDRSKS 1933 IKFNIDSLETDPLELEYYLREFKNINTDLINEIKERIKERIESDKKSYEDRSKS 1934 INDITKEYEKLINEIYDSKFNNINTDLINEIKERIKKEIKKKIESDKKSYEDRSKHNI 1935 INDITKEYEKLINEIYDSKFNNINTDLINEIKERIKKEIKKRIESDKKSYEDRSKHNI 1936 INDITKEYEKLINEIYDSKFNNINTDLINEIKRIENIETLYBNIKKDEEQLFEKKITKD 1936 INDITKEYEKLINEIYDSKFNNINTDLINEIKRIENIETLYBNIKKDEEQLFEKKITKD 1937 EKLTRALKYMEDYSLRINIVVEKELKYYKNLISKIENEIFTLVBNIKKDEEQLFEKKITKD 1938 EKLTRALKYMEDYSLRNIVVEKELKYYKNLISKIENEITLUBINIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI
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ilarity 60.1%; Pred. No. 7.8e-152;
Conservative 221; Mismatches 342;
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Matches 1052; Conserv
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major merozoite surface antigen precursor - malaria parasite (Plasmodium falcipa C; Species: Plasmodium falciparum C; Species: Plasmodium falciparum C; Species: Plasmodium falciparum C; Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jun-2000 C; Accession: A45948 R; Chang, S.P.; Kramer, K.J.; Yamaga, K.M.; Kato, A.; Case, S.E.; Siddiqui, W.A. Exp. Parasitiol. 67, 1-11, 1988 A; Title: Plasmodium falciparum: gene structure and hydropathy profile of the major A; Reference number: A45948 MUID:89005525; PMID:3049134 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-1726 CHA> A; Residues: 1-1726 CHA> A; Cross-references: GB:M37213 C; Superfamily: major merozoite surface antigen C; Keywords: surface antigen
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                                                             S.E.; Siddigui, W.A.
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major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) C.Species: Plasmodium falciparum forcipate antigen precursor - malaria parasite (Plasmodium falciparum) C.Species: Plasmodium falciparum forcipate antigens of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of th
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1 MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 60.1%; Score 5065; DB 2; Best Local Similarity 60.1%; Pred. No. 1.3e-149; Matches 1042; Conservative 227; Mismatches 338;
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            A.Accession: A26868
A.Molcoule type: DNA
A.Residues: 1-1701 <TAN
C.Superfamily: major merozoite surface antigen
C.Keywords: surface antigen
E.1-19-Domain: surface antigen
F): 1-10-Domain: signal sequence #status predicted <SIG>
F): 20-1701/Product: major merozoite surface antigen #status predicted
                                                                                                                       Length 1701;
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Reference number: A26868; MUID:88011243; PMID:3079521
                                                                                                                                                    338;
                                                                                                                       60.0%; Score 5053; DB 2; 60.1%; Pred. No. 2.9e-149;
                                                                                                                                                    225; Mismatches
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R;Tanabe, K.; Mackay, M.; Goman, M.; Scaife, J.G.
J. Mol. Biol. 195, 273-287, 1987
A;Title: Allelic dimorphism in a surface antigen gene of the malaria parasite Plasmodium
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                                                      KEENHIKKLLEEOKOITGTSSTSSPGNTTVNTAQSATHSNSQNQQSNASSTNTQNGVAVS
                                                                                                                                                    AND---DTSHS----TNLNNSLKLFENILSLGKNKNIYQEL-IGQKSSENFYEKILKDSD
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                                                                                               ----MQPLSLTPQDKPEVS
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C;Species: Plasmòdium falciparum
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988
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EBAKKYSTSVRTLSSSS	C:Superfamily: major merozoite surface antigen C:Keywords: surface antigen	Ouery Match 36.7%; Score 3093.5; DB 2; Length 1751; Best Local Similarity 38.2%; Pred. No. 1.2e-88; Matches 704; Conservative 316; Mismatches 517; Indels 307; Gaps 4	1 MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKWYLNEGTSGT 60	61 AVTTSTPGSKGSVASGGSGAVASGGSVASGGSVASGGSGGSGNSRRTNPSDNSSDS 120	121 DAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYK 180 : :: : : :	181 LNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMED 240 : :: : :	241 YIKKNKKTIENINBL-IEESKK	262	292 LEEAHNLISVLEKRIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIE 348 :	349 EHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKNKNI-DISAKVETKESTEPNE 402	403YPNGVTYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNI-YTDNERKKFINE 455	456 IKEKIKIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGK 515	516 RYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIE 575 1 1 1 1 1 1 1 1 1	576 NEIETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKVOVQKVLLMNKIDELKKTQ 635 : : : : :	636 LILKNVELKHNIHVPNSYRQENRQEPYLLIVLKKEIDKLKVFMPKVESLINEEKK 690 :111 ::1 :::1	691NIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSA-LE 726	727	772 LDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLFNI 829 : : : : :: :: :: ::	Qy 830 QNNIPVMYSWFDSLNNSLSQLFMEIYEKEMVCNLYKLKDND-KIKNLLEEAKKVS 883
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                                                                                                                                                               2; Length 1086;
                                                                                                                        tandem repeat
A; Residues: 1-1086 < CoLA>
A; Cross_references: EMBL:X61930
A; Experimental source: isolate RO-71
C; Genetics:
A; Gene: MSA1
C; Superfamily: major merozoite surface antigen
C; Keywords: glycoprotein; merozoite; surface antigen;
                                                                                                                                                          Query Match 35.6%; Score 2999.5; DB Best Local Similarity 57.3%; Pred. No. 5.9e-86; Matches 637; Conservative 147; Mismatches 238
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                                                                                                                                                                                                                             1069 VSLDHYGKYKLKLERLLKKKNKISNSKDQIKKLTSLKNKLERRQNLLNNPTSVLKNYTAF 1128
                                                                                                                                                                                                                                                                                                                                                                           KVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNAL 1182
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                                                                                                                                                                                                                                                                                                              ONNLPAMYSIYDSMSNELONLYIELYOKEMVYNIYKNKDTDKKIKAFLETLKSKAAAPAO
                                                                                                                                                                                                                                                                                         FNKKKEAEIAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENF
                                        884 TSVKTLSSSSMQPLSLT-PQDKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYGEL
                                                                      953 SAAKPSGQAGTTPVTTTAPVTTTTVTPSPQTSVVTSTPPTPQAEEN-RRVGGNSEEKPE-
                                                                                                                                                                                                         LSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVLQNFSVF
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us-09-269-874a-3.rpr

467 IESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTH 1	649 700 709 755 766 795 820 853	833 EIYERBWYCHYKKDHÖKIKNELEEAKKVSTGVYKTESSSAMOPESTIPPODKEEVSAN [1:1:1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1017 RLEDKKKTVGKYKMQIKRLTLLKEQLESKLNSLNNPKHVLQNFSVFINKKREAEIAETEN 1076	1192 GTDVATVV
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	ах геvea	;		
	RESULT 10 A39401 merozoite surface antigen 1 precursor - Plasmodium vivax C;Species: Plasmodium vivax C;Species: Plasmodium vivax C;Species: Plasmodium vivax C;Species: Plasmodium vivax C;Species: Pasmodium vivax C;Species: Pasmodium vivax C;Species: David, P.H. C;Species: Primary H.A.; Longacre, S.; Khouri, E.; David, P.H. R;del Portillo, H.A.; Longacre, S.; Khouri, E.; David, P.H. A;Title: Primary structure of the merozoite surface antigen 1 of Plasmodium vivax A;Reference number: A39401; MUID:91219506; PMID:2023952 A;Accession: A39401 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1726			

<u>ک</u> ۾	, 1 1	MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGT 60 :	
λ	61	AVTTSTPGSKGSVASGGSVASGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDS 120	
ą	55	1 1 1 1 1 1 1 1 1 1	
۲ <u>۲</u>	121	DAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYK ### PARKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYK ##################################	
2 2	181		
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× 4	241	YIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQ 291	
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Δ	345	KKIEEHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKNKNIDISAKVETKESTE 399	
ą	363		
<u> </u>	400	PNEYDNGVTYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKF 45	
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<u>ჯ</u> ფ	453	INBIKEKKKIEKKKIESOKKSYEDRSKSLANDITKETEKLLNEIYDSKFNNNIDLTNFEKM 512	
Δž	513	MGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLIS 57	
ą	540		
λ	573	KIENEIETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLIMNKIDELK 632	
ą	598		
λ	633	KTOLILKNVELKHNIHVPNSYKOENKOEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNI 692	
ą	647		
λį	693		
ð	707	EQGPAITGESEEVPSGP	
λ	728	DSVQAQAQEQKQAQPPVPVPPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYI 787	
ą	767		
<u>~</u>	788	CHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNN 845	
q	821		
λ	846	SLSQLFMEIYEKEMVCNLYKLKD-NDKIKNLLEEA	
ą	881	GLQNIYTELYEKEMMYHIYKLKDENPSIKSLLVKAGVIEPEPVAAPTPVTPAATEQQQQQ 940	
Ϋ́	880		
q	941	ATPDVQSDAPAPSDVSQQPETPVTSTTPEVTTSTEASSSAPGEGTPSGEAGASGTEGATA 1000	

AG546
major merozoite surface antigen precursor - Plasmodium chabaudi chabaudi
C;Specias: Plasmodium chabaudi chabaudi
C;Specias: Plasmodium chabaudi chabaudi
C;Specias: Plasmodium chabaudi chabaudi
C;Specias: Plasmodium chabaudi chabaudi
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Aug-1999
C;Accession: A45546
Mol. Biochem Parasitol. 43, 231-244, 1990
A;Title: Molecular cloning and sequence analysis of the gene encoding the major meroz
A;Reference number: A45546; MUID:91218805; PMID:2090945
A;Accession: A45546
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C;Keywords: surface antigen

35; 540 LNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMED 240 334 363 EPVQVPAVQVLTEEEKAKKIAELYAQIKEIAKTIKFNLDGIFVDPVELEYYKKEKKNESC 422 437 617 647 677 707 757 827 121 DAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYK 180 EPSKNIYTDNERKKFINEIKEKIKIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIYD 497 KLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKD-NDKIKN 874 Gaps 9 68 9 SKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRN :| |::|: | |::| | |::| | |::| | |::| | |::| | |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| 61 AVTTSTPGSKGSVASGGSGGSVASGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDS YIKKNKKTIENINELIEESKKTI------DKNKNATKEEEKKKLYQAQYDLSIYNKQ LEEAHNLISVLEKRIDTLKKNENIKELLDKINEIKNPPPANSG-------303 SSNTKTTTTDKAVTTQTATKATGTETNTGTETNTGTETNTATGTTTATGTTTATGTPTVT ------KNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLELEYYLRE-KNKNI DISA---KVETKESTEP--NEYPNGVTYPLS----YNDINNALNELNSFGDLINPFDYTK ITEDLTTNEQARKNLIKAIKKKIEAEEQKLVELKDDYDTKLAAFNGQKTPFKEAAKKFYE 558 IVVEKELKYYKNLISKIENEIETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKV **QVQKVLLMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVF** GTESTEETPAASKPAEGAASTGATTPTEQEAAPTEQEAQPAAPETPAAFATTPAAPAT PPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEES--1 MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGT 61 PVDPF----TNP----TNP----TNP-----MPKVESLINEEKKNIKTEG-QSDNSEPSTEGEITGQATTKPGQQA-------------PVPVPVPEAKAQVPT 605; Indels 366; Length 1785; 19.8%; Score 2509; DB 2; Similarity 31.6%; Pred. No. 1.5e-70; 98; Conservative 324; Mismatches 605; --NTPNTLLD-----298; Query Match Local Best Loca Matches 335 849 123 241 243 168 181 292 343 387 438 481 541 722 758 69 498 g 엄 ò õ a Óγ g οy qq ŏ ò g ò g δý a ŏ qq Ω g à g ô g ò g ογ g ò g ò g ò g

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RESULT 14 S47282 merozoite surface antigen 1 g

- malaria parasite (Plasmodium falciparum) (strain RO-71)

E C;Species: Plasmodium falciparum
A;Variety: Strain RO-71
C;Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jun-2000
C;Accession: S47282
R;Tolle, R.; Bujard, H.; Cooper, J.A.
Submitted to the RMBL Data Library, July 1994
A;Description: Plasmodium falciparum: recombination within the C-terminal region of A;Reference number: S47282 ö

Gaps

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1479

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300

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1419

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glycoprotein 185 - malaria parasite (Plasmodium falciparum) (isolate Honduras C.Species: Plasmodium falciparum
C.Species: Plasmodium falciparum
C.Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jun-2000
C.Accession: A25814
R.Howard, R.F.; Ardeshir, F.; Reese, R.T.
R.Howard, R.F.; 205, 1986
A;Title: Conservation and antigenicity of N-terminal sequences of GP185 from dA;Reference number: A25814; MUID:87106855; PMID:3542719
                                                                                                                                                                                                                                                                                                                                                                                      VGIADLSTDYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQ 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKI 1599
                                                                                                        1240 VIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQ 1299
                                                                                                                                                                                             DAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFRYLIDGYEEINELLYK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                   LENNVMTFNVNVKDILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRD
                                                                                                                                                                                                                                               KFLSSYNYIKDSIDTDINFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLN
                                                                                                                                                                                                                                                                                                                  NIETLYKTVNDKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNF
                                                                                                                                                                                                                                                                                                                                    241 VGIADLSTDYNHNNLITKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQ
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   tandem repeat
                                    Length 400;
                                                                       Indels
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 :Keywords: glycoprotein; merozoite; surface antigen;
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                                  Score 2101; DB 2;
Pred. No. 1.2e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1187; DB 2;
Pred. No. 1.2e-30;
                                                                     Mismatches
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A; Molecule type: mRNA
A; Residues: 1-196, 'T', 198-233 <HOW>
C; Superfamily: major merozoite surface
C; Keywords: 91ycoprotein
                                  Similarity 100.0%; Pour Conservative 0;
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95.18;
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                                                                     Matches 400;
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Best Local Si
Matches 232,
                                    Query Match
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R:Blackman, M.J.; Ling, I.T.; Nicholls, S.C.; Holder, A.A.
MALL Biochem. Parasitol. 49, 29-33, 1991

A:Title: Proteolytic processing of the Plasmodium falciparum merozoite surface protein-1 A:Accession: A45545

A:Accession: A45545

A:Accession: A45545

A:Residues preliminary

A:Molecule type: DNA

A:Residues: 1-400 CBLA

A:Note: sequence extracted from NCBI backbone (NCBIN:77612, NCBIP:77621)

C;Superfamily: major merozoite surface antigen
                                                                                                                                                                         5;
                                                                                                                                                                                                            FDKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENTL 1078
                                                                                                                                                                                                                                                                              1079 ENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNL 1138
                                                                                                                                                                                                                                                                                                                                                 1139 EKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATV 1198
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                                                                                                                                                                                                                                                                                                                                                                                                                      VSE-----SGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVP 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1245 IFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNV 1304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       478
                                                    PID:9535258
                                                                                                                                                                                                                                                                                                61 ENTKILLKHYKGLVKYYNGESSPLKTLSEVSIQTEDNYANLEKFRALSKIDGKLNDNLHL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                            597
                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36;
                                                                                                                                        651;
              A, Molecule type; DNA
A; Residues: 1-651 <TOL>
A; Cross-references: EMBL:235329; NID:9535257; PIDN:CAA84558.1;
A; Experimental source: strain RO-71
C; Superfamily: major merozoite surface antigen
C; Keywords: 91ycoprotein; merozoite; surface antigen
                                                                                                                                                                         Indels
                                                                                                                                        Length
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                                                                                                                                                                       82; Mismatches 114;
                                                                                                                                       25.5%; Score 2146; DB 2; 64.5%; Pred. No. 8.3e-60;
                                                                                                                                     Query Match 25.5's
Best Local Similarity 64.5'
Matches 422; Conservative
A; Accession: S47282
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C;Species: Plasmodium falciparum
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
C;Datession: B54498
R;Peterson, M.G.; Coppel, R.L.; McIntyre, P.; Langford, C.J.; Woodrow, G.; Brown, G.V Mol. Biochem: Parasitol. 27, 291-302, 1988
A;Title: Variation in the precursor to the major merozoite surface antigens of Plasmo A;Reference number: A54498; MUID:88142999; PMID:2449612
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          morozoite surface antigen - Plasmodium vivax (fragment)
C;Species: Plasmodium vivax
C;Species: Dlasmodium vivax
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 11-Jan-2000
C;Accession: A45949
R;del Portillo, H.A.; Gysin, J.; Mattei, D.M.; Khouri, E.; Udagama, P.V.; Mendis, K.N
Exp. Parasitol. 67, 346-353, 1988
A;Title: Plasmodium vivax: cloning and expression of a major blood-stage surface anti
A;Reference number: A45949; MUID:89052826; PMID:3056739
A;Status: preliminary
                                                                                     major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciกลาแก
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AVTTSTPGSKGSVASGGSGSVASGGSVASGGSVASGGSVASGGSGN--SRRTN----- 112
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                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-281 <PET>
A; Residues: 1-281 <PET>
A; Cross-references: GB:M19144; NID:g160414; PIDN:AAA29654.1; PID:g552205
C; Superfamily: major merozoite surface antigen
C; Keywords: surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 TSSGASPPADASDSDAKSYADLKHRVRNYLFTIKQLKYPESLDLPNHMLTLCDNIHGFKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 LIDGYEBINELLYKLNPYFSLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 -----PSDNSSDSDAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 PLDNIKDNVGKMEDYIKKNKTTIANINELIEGSKKTIDQNKNADNEEGKKKI 281
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C;Superfamily: major merozoite surface antigen
C;Keywords: surface antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1096.5; DB
Pred. No. 9.3e-28;
8; Mismatches 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 13.0%;
Best Local Similarity 77.7%;
Matches 227; Conservative
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nes 245; Conserv
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A; Residues: 1-636 <DEL>
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                                                                                                                                                                                                                                                                                                                     merozoite surface antigen
                                                                                                                                                                     C;Species: Plasmodium yoelii
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1027 KYKMOIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENTLENTKILLK 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1087 HYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYL 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1207 LEQSQPKKPASTHVGAESNTI------TTSQNVDDEVDDVIIVPIFGESE 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDYDDLGQVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVN 1310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1311 VKDILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKD 1370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1371 SIDTDINFANDVLGYYKILSEKYKSDLDSIKKYI--------ND-KQGENEKYLPFLNNIE 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1423 TLYKTVNDKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADF----KKNNN 1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             967 FTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVG 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1147 SSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSESGSDT 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1479 FVGIADLSTDYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGM--LNIS-QHQCV-K 1534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1535 KQCPQNSGCFRHLDEREECKCLLNYKQ-EGDKCVENPNPTCNENNGGCDADAKCTEEDSG 1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 YYKARTKYFTSEAVPLKTLSKASLDRESNYLKIEKFRAYSRLELRLKKNINLGKERISYV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         348 MTNGLNNKSQKRNDFLEVLSHELDLFKDLSTNKYVIRNPYQLLDNDKKDKQIVNLKYATK 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            468 GLYETVIGQAEEYSEELQNRLDNYKNEKAEFEILLFKNLEKYIQIDEKLDEFVEHAENNKH 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAADAPATPEGAVPGAVPGAVPGAVPGAVPGSGTDTRVAGSSVDD-----N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       528 IASIA------LINILINKSGLVGEGESKKILAKML--NMDGMDLLGVDPKHVCVDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RDIPKNAGCFRDDNGTEEWRCLLGYKKGEGNTCVENNNPTCDINNGGCDPTASCQNAEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 680;
                                                                                                                                             major merozoite surface antigen - Plasmodium yoelii (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A)Cross-references: GB:J03612; NID:g160678; PID:g160679
A)Experimental source: strain 17XL
A)Note: the authors translated the codon GTA for residue 429 of C;Superfamily: major merozoite surface antigen
C;Superfamily: surface antigen
                                                                                                                                                                                                                       C,Accession: A28121
R;Burns Jr., J.M.; Daly, T.M.; Valdya, A.B.; Long, C.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 602-606, 1988
A;Title: The 3' portion of the gene for a Plasmodium yoelli
A;Reference number: A28121; MUID:88124889; PMID:2448778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNGKKITCECTKPDSYPLFDGIFCSSSNFLGISFLLILMLILYS 1637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    635 ENSKKIICTCKEPTPNAYYEGVFCSSSSFMGLSILLIITLIVFN 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 13.5%; Score 1135; DB 2; Local Similarity 36.2%; Pred. No. 1.6e-28; les 255; Conservative 142; Mismatches 247;
                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-680 <BUR>
                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A28121
229 YIKK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
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                                                                                  RESULT 17
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Db 61 IGKLETFITKNKETISNINKLISDENAKRGGQSTNTTNGPGAQNNAAQGSTGNTETGTRS 120	Db 61 AVTTSTPGSGGSVTSGGSGGSVASVASGGSGGSVASGGSGNSRRTNPSDNSSDS 114
Qy 272	Qy 121 DAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFRYLIDGYEEI 174
QY 300 SVLEKRIDTLKKNENIKELLDKIN-EIKNPPPANSGNTPNTLLDKNKKIEEHEKE 353	RESULT 21 \$03390 glycoprotein, 190K - malaria parasite (Plasmodium falciparum) (isolate Bandia-Senegal C;Species: Plasmodium falciparum
239 IVANAKTVNFDLDGLFTDAEELEYYLREKAKMAGTLIIPESTKSAGTPGKTVPTLKETYP 405 NGVTYPLSYNDINNALNELNSFGDLINPFDYTKFPSKNI-YTDNERKKFINEIKEKI 519 HISTSYLAENSTYELFERSPETFGDIONP-DDGKOEKGTIINFFRKELIETMANT 299 HISTSYLAENSTYELFERSPETFGDIONP-DDGKOEKGTIINFFRKELIETMANT	A; Variety: isolate Bandia-Senegal C;Date: 21.Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jun-2000 C;Accession: S03290 R;Scherf, A.; Barbot, P.; Langsley, G. Nucleic Acids Res. 17, 1774, 1989 A:#itle: Genuence and langth nolementhism of a maint malaria vaccine candidate analys
461 KIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYK : : :	2646601
QY 521 VEKLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEIET 580	A;Residues: 1-146 <sch> A;Cross-references: EMBL:X13782 C;Superfamily: major merozoite surface antigen C;Keywords: glycoprotein</sch>
QY 581 LVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLILKN 640 : : : :	Query Match 8.4%; Score 710.5; DB 2; Length 146; Best Local Similarity 97.9%; Pred. No. 3.9e-16; Matches 143; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 641 VELKHNIHVPNSYKQENKQEPYZLIVLKKEIDKLKVFMPKVESLINEEKKNIKTE 695. 1 ::	Qy 28 LVKKLEALEDAVLTGYSLFQKEKMYLNEGTSGTAVTTSTPGSKGSVASGGSGGSVAS 84
QY 696 GQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQAQPPV 744	Qy 85 GGSVASGGSVASGGSGNSRRTNPSDNSSDSDAKSYADLKHRVRNYLLTIKELKY 144
RESULT 20 A25522 major merozoite surface protein - malaria parasite (Plasmodium falciparum) (fragments)	Qy 145 PQLFDLTNHMLTLCDNIHGFKYLIDG 170
C;Species: Plasmodium falciparum C;Date: 06.Jan-1988 #sequence_revision 06-Jan-1988 #text_change 09-Jun-2000 C;Accession: A25522; A22828	RESULT 22 PQ0125
R;Cheung, A.; Leban, J.; Shaw, A.R.; Merkli, B.; Stocker, J.; Chizzolini, C.; Sander, C. Proc. Natl. Acad. Sci. US.A. 83, 8328-8332, 1986 A;Title: Immunization with synthetic peptides of a Plasmodium falciparum surface antiger A;Reference number: A25522; MUID:87041450; PMID:3534885	major merozoite surface antigen - malaria parasite (Plasmodium falciparum) (isolate B N'Alternate names: gp195, PMMSA, PSA C; Species: Plasmodium falciparum C; Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jun-2000
A; Accession: A2552, A; Status: preliminary A; Molecule type: DNA	C; Accession: PQ0125 R; Kimura, E.; Mattei, D.; di Santi, S.M.; Scherf, A. Gene 91, 57-62, 1990
A; Residues: 1-168 <che. R;Cheung, A.; Shaw, A.R.; Leban, J.; Perrin, L.H. EMBO J. 4, 1007-1011, 1985</che. 	A;Title: Genetic diversity in the major merozoite surface antigen of Plasmodium falci A;Reference number: PQ0120; MUID:90382698; PMID:2205540 A;Accession: PQ0125
A;Title: Cloning and expression in Escherichia coli of a surface antigen of Plasmodium f. A;Reference number: A22828; MUID:85257491; PMID:3894010 A;Accession: A22828	A;Molecule type: DNA A;Residues: 1.138 <rins A:Cross-references: GB:M32116: NID:q160502: PIDN:AAA29707.1; PID:q552216</rins
NA CCH37 CEBYOAAA CB.WIAKAAA CB.WASAQAA NID.,GOGKS. DIDN.CAAASESEA 1.	1
A;Closs references: GB:A02400; GB:M10940; GB:M20260; NID:99002; FIDN:CAA20234.1; FID:994 C;Superfamily: major merozoite surface antigen Ouery Match 9.7%: Score 815: DR 2: Ienath 168:	Ouery Match 7.8%; Score 659.5; DB 2; Length 138; Best Local Similarity 93.6%; Pred. No. 1.4e-14; Matches 132: Conservative 2: Mismatches 4: Indels 3: Gabs 1:
Similarity 93.7%; Pred. No. 2.7e-19; 3; Conservative 2; Mismatches 3;	KKLEALEDAVLTGYSLFQKEKMVLNEGTSGTAVTTSTPGSKGSVASGGSVASGGSVA 89
1 MKIIFFLCSFLFFIINTOCVTHESYOELVKKLEALEDAVLTGYSLFOKEKMVLNEGTSGT	1 KKLEALEDAVLTGYSLFQKEKMYLNEGTSGTAVTTSTPGSSGSVASGGSVASVASGG 57
Db 1 MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMYLNEGTSGT 60 Qy 61 AVTTSTPGSKGSVASGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDS 120 [OY 90 SGGSVASGGSVASGGSGNSRTNPSDNSSDSDAKSYADLKHRVRNYLLTIKELKYPOLED 149

729 SVQAQAQEQKQAQPPVPVPEAKAQVPTPPAPVNNKTENV : :	0	:			
<u> </u>	e de de de de de de de de de de de de de				
	#text_change 15-Oct-1999 repetitive region with a predicted 47969 su repetitive region with a predicted	6.5; DB 2; Length 1939; -1.2e-11; -1.2e-11; -1.2e-11; -1.2e-11; -1.2e-11; -2.2e-12; -2.2e-12; -2.2e-12; -3.2e-12; -3	SKTEDAKEGHKNELNELNNQ 472 -NIKELLDKINEIKNPPPAN 332 -NIKELLDKINEIKNPPPAN 332 -NIKELLDKINEIKNPPPAN 332 -NIKELNDLINNKN 527 NIDSLFTDPLELEYLREKNK 384FMLEEKLKEKEN 580FMLEEKLKEKEN 580		GEKHKEVVAGLEAKHNLEEG 959
150 LFNHMLTLCDNIHGFKYLIDG 170 	lar protein chain chair amodium chair amodium chair amodium chair amodium chair also chair amodium chair amodium chair also chair amodium chair also chair amodium chair also chair amodium chair amodium chair amodium chair and amodium chair and amodium chair also chair amodium chair and amodium chair and amodium chair and amodium chair and amodium chair amodium cha	Ouery Match 7.2%; Score 606.5; DB 2; Length 1939; Best Local Similarity 22.6%; Pred. No. 1.2e-11; Matches 394; Conservative 280; Mismatches 588; Indels 481; GS MISSDARSYADEKHRVRNILLTIKELKYPQLFDLTNHMLTLCDNIHGFKY; 117 SSDSDARSYADEKHRVRNILLTIKELKYPQLFDLTNHMLTLCDNIHGFKY; 1	LTKEIKLLE LKKNE LNKDKQTLG LKKDKQTLG LIKTIKFN LI LI LIKTIKKNE	\$81 YDLNDEISTLRNSTYVREKEFIEMKEFFFFFKKIEBKKIEBDKKSTED \$81 YDLNDEISTLRNSTYVREKEFIEMKEFFFFKKIEBDKKSYED \$82 TKEPSKNIYTDDERKKFINE	REVVAGLEEKHKEVVAELEEKHKEEIAKLEEGHKEVMAELGEKHKEVVAGLEAKHNLEEG

Qy 680 KVESLINEEKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALEG 727 B 11 1 1 1 1 1 1 1 1 1	Qy 845 NS-LSQLFWEIYEKEWVCNLYKLKDNDKIKNLLEEAKKVST 884		1195 QADKSEKKMNEIKNEQIRIED-EVAKNNKSNKAILDIQLSVEPFKIKFLKIKDLRTKSDD 1098ESSPLKT-LSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHL	DD 1312 NSKIKNIESNNNQHKKNYELGIVEKINEIARANKDQIESTQKLIIPTIKNLISFFKRADL 13/1 QY 1167TGNSPSENNTDVNNALESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTH 1219 DD 1372 EGIDTNKNLGKYNTEMNNIYEFIKSYLITHYLETVSKEPITYEQIKNR 1422 QY 1220 VGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDD 1255 DD 1423 ITAONELLYNIKNYKAKSYLDDIENALFKNKLNDVNDKFTNEYSKVNKGFDN 1482	1256 LGQVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDIL :	1352FLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYYKIL 1597 ILKRSQELQKKEQQALNLIFENRLLHDK-VQATNELKDTLSDLKNKKEQILNKVKLLHK 1390	:	QY 1477 NNFVGIADLSTDYNHNNLLTKFLSTGMVF-ENLAKTVLSNLLD 1518 1
rESULT 24 rhoptry protein - Plasmodium yoelli (fragment) c;Species: Plasmodium yoelli c;Species: Plasmodium yoelli c;Species: Plasmodium yoelli c;Species: Plasmodium yoelli c;Species: Plasmodium yoelli c;Accession: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000 c;Accession: 128676, A45521 R;Sinha, K.A.; Keen, J.K.; Ogun, S.A.; Holder, A.A. Mol. Blochem. Parasitol. 76, 329-332, 1996 A;Title: Comparison of two members of a multigene family coding for high-molecular mass A;Reference number: 220507; MUID:97077455; PMID:8920022	A; Modecule type: DNA A; Residues: 1-2401 <sin> A; Residues: 1-2401 <sin> A; Residues: 1-2401 <sin> A; Residues: 1-2401 <sin> A; Residues: 1-2401 <sin> A; Residues: 1-2401 <sin> A; Residues: 1-2401 <sin> A; Réperences: EMBL: U36927; NID: g1041784; PID: g1041785; PIDN: AAB41263.1 B; Rémen, J.; Holder, A.; Playfair, J.; Lockyer, M.; Lewis, A. Biochem. Parasitol. 42, 241-246, 1990 A; Richen. Parasitol. 42, 241-246, 1990 A; Reference number: A45521; MUID: 91101660; PMID: 2270106 A; Reference number: A45521 A; Reterence number: A45521, MUID: 91101660; PMID: 2270106 A; Reference number: A45521, MUID: 91101660; PMID: 2270106 A; Reference number: A45521, MUID: 91101660; PMID: 2270106 A; Reference number: A45521, MUID: 91101660; PMID: 2270106</sin></sin></sin></sin></sin></sin></sin>	A;Residues: 2260-2401 <kee> A;Residues: 2260-2401 <kee> A;Cross-references: GB:M34281 Query Match Best Local Similarity 21.5%; Pred. No. 1.7e-11; Matches 390; Conservative 291; Mismatches 607; Indels 524; Gaps 87; Oy 123 KSYADLKHRVRNYLLTIKELKYPOLFDLTNHMLTLCDNIHGFRXLIDGYEEINELLYKLN 182</kee></kee>	250 KAVDLKKEIEKDNYIDELAKEPPYQIT	348 ETVKSHILINIETINKLISETILDIIKYIYGEITNELNKILEDFKNKENGLSNKIDEYAKEN 407 278 LYQAQYDLSIYNKOLEEAHNLISVLEKRIDTLKKNENIKELLOKINEIKNPPPA 331 1	PNEMKYQRPSIEIKIMKDEFLSKVNKYNDFDKVYKEKVESEHNKFTELIN 503 KVETKESTEP-NEYPUGVTYPLSYNDINNALNELNSFGDLINPFDY 435 :: : : : : KITTEVSDEEIKKYENKFNDSKSLINETKKSIEEEYQNINTLKKVDDYIKVCLN 557 TKEPSKNIYTDNERKKFINEIKEKIKIEKKIESDKKSYEDRSKS 480	QTTLKDKLNQNIKTIKETNSIDKIYTDKFENILTDKKT-ELETKFTGLS LNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHH	NTFASY	IVLKKEIDKLKVFMP : :: ENIVEKIDKKKNIYK

	760 APVNN-KTENVSKLDYLEKLYEF-LNTSYICHKYILVSHSTMNEKILKQYKI	OY 1019 FDKKKTVGKYKMOIKKLTLLKEOLESKLNSLNNPHHULOMFSVFFNKKKEREIAE 1073 Db 1029 VYKKOSNAQCVDHKKKSWILLKDKSKEKIKDKENOLINPKHULOMFKEEDELKKKDDEI Db 1029 VYKKOSNAQCVDHKKKSWILLKDKSKEKIKDKENOLINVEKNEEKDLKKKDDEI OY 1074 TENTLENTKILLKHYKGLWYYNGESPLKTLSESIQTEDNYASLENFKVLSKLE 1129 Db 1082	1238 DDVILVPIFGESEEDVDDLGQVVTGEAVTPSVIDNILSKIEN-EYEVLYLKPLAGY 1245 ENNLAWKLDENEDN
1586	RESULT 26 Cyff622 Cyff72 Cyff622 Cyff622 Cyff72 Cyff622 Cyff72 Cyff622 Cyff72 Cyff622 Cyff72 Cyff622 Cyff72 Cyff72 Cyff72 Cyff72 Cyff72 Cyff72 Cyff72	Query Match 6.64; Score 559.5; DB 2; Length 1979; Best Local Similarity 22.34; Pred. No. 3.4e-10; Matches 370; Conservative 314; Mismatches 609; Indels 373; Gaps 82; Qy 110 RTNDSDNSSDSDAKSYADLKHRVRNYLLTIKELKYPQLEDLTNHMLTLCDNIHGFKYLID 169	Db 213 KINEKEKNIIKKEETPHNIEKEYLENIKER ETISIEIIDIKHLEKLKIEIKEKKEET- 268 Qy 279 YQAQYDLSIYUKQLEETHNIISVLEKINER ETISIEIIDIKHLEKLKIEIKEKKEET- 268 Db 269

238 MEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEA	782 296 841 319 901 357 955 391 1015	1074 NKKNNDGDNKSQEDDYGNKKKNNDDDDDDSYKIELIVDELNKCKNYTDEELYELMKGS 1133 481 LNDITKEY	1248 EKIILDEQINEKEKKINIINEKYLILEKEYEEYQNKNIFINAQIENLEKEKKQLQEEI 597 ITKDENKPDEKILEVSDIVKV-QVQKVLLMNKIDELKKTQLILKNVELK		787IC	1656 LINKSNEDKLKYINSLCDEKDKYDIVVKDIRNNRNEIDKLNNDINEKS 859 MYCNLYKLKDNDKIKNLEERAKKVSTSVKTLSSSSMOPLSLTPQDKPEVSANDDTSHS 1706 YEIKLLKHENNNLINEMNILKNKETENMNIKQKEEDYIKLIKKDKTNIQ	917 TNLNNSKLFENILSLGKNKNIYQELIGOKSEBNFYEKTLKDSDFFYNEFF 967 11 1 1 1 1 1 1 1 1 1
Db 1560 YSRYYGLREDLCKEEIVPSKIGNISNKNENNNKKNNTCDGXDEKYT 1605	RESULT 27 B25120 major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (st oy major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (st ox pecies: Plasmodium falciparum) (st ox pecies: 20-Aug-1987 #sequence_revision 20-Aug-1987 #text_change 09-Jun-2000 (st ox pecies) (st ox ox ox ox ox ox ox ox ox ox ox ox ox	Query Match 6.3%; Score 529; DB 2; Length 115; Db Best Local Similarity 91.7%; Pred. No. 1.2e-10; Matches 111; Quart 11; Quart 11; <td>(21 D 121 15 D 115</td> <td>alciparum) nge 09-Jun-2000</td> <td></td> <td>Oy 108 SRRTNPSDNSSDSDAKSYADLKHRVRNYLLTIKELKYPQLEDLTNHMLTL 157 Cy 10 </td> <td>Qy 196CANDYCQIPPHLKIRANELDVLKKLVFGYRKPLDNIKDNVGK 237 Qy 196CANDYCQIPPHLKIRANELDVLKKLVFGY</td>	(21 D 121 15 D 115	alciparum) nge 09-Jun-2000		Oy 108 SRRTNPSDNSSDSDAKSYADLKHRVRNYLLTIKELKYPQLEDLTNHMLTL 157 Cy 10	Qy 196CANDYCQIPPHLKIRANELDVLKKLVFGYRKPLDNIKDNVGK 237 Qy 196CANDYCQIPPHLKIRANELDVLKKLVFGY

Best Local Similarity 20.8%; Pred. No. 1.6e-08; Matches 355; Conservative 306; Mismatches 552; Indels 494; Gaps 86	QY 132 VRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYKLN 182 : :	Qy 183 FYFDLLRAKLNDVCANDYCQIPFNLKIRAN 212	QY 213ELDVLKKLVFGYRKPLDNIKDNVGK-MEDYIKNKKTIENINEL 255 :	OY 256 IEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEE 294 :	QY 295 AHNLISVLEKRIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLL 341 : : : : : : : : : Db 244 SFNFYENKYKLIENSIELIMESVKNKINEKEDFILNRLNEELQNKFKDILVYV 296	QY 342 -DKNKKIEEHEKEİKEIAKTIKFN	QY 371 DPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGYTYPLSYNDINNALNELNSFGDLI 430 1 1 1 1 1 1 1 1 1	QY 431 NPFDYTKEPSKNIYTDNERKKFINEIKE-KIKIEKKKIESDKKSYED 476	OY 477 RSKSLNDITKEYEKLLNGIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENS 536	QY 537KHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEIETLVENIK 586 : : : ::: - : : Db 516 MESKYKSFTDKLTAGMDEFSLMYGEKFETLSQEATNNYQEFQDLNKKLENEIESFYNMFE 575	QY 587 KDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLANKIDELKKTQ 635	QY 636 LILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKK 690	OY 691 NIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSV 730	QY 731 QAQAQEQKQAQPPVPVPPARAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTS 785 1	Qy 786 YICHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLFNI 829 ::	QY 830 ONNIPVMYSMFDSLANNSLSQLFMEIYEKEMVCNLYKLKDNDKIKNLLEEAK 880 : : :	QY 881KVSTSVKTLSSSSMQPLSLTPQDK	QY 913 TSHSTNLNNSLKLFENILSLGKNKNIYQELIGQKSSENFYEKILKDSDT 961
DD 1813 QINYUDNNLLKNRLDQLFNINQDLQKHLDTNQKHLEQLKYDYIEIKERLKIEKTK 1867	OY 1020 DKKKTVGKYKMOIKK-LTLLKEQLESKLNSLNNPKHVLONFSVFFN 1064 1868 INKQEKYIIQLQKDNNLILNDFNSTTTTNNNNNNNNNNNNNNNNNTYQQFIH 1925	Qy 1065 KKKEAEIAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKV 1124 Db 1926 SLKANLENSRLELKELSNL	Qy 1125 LSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSE 1173 ::	QY 1174 NNTDVNNALESYKKELPEGTDVATVVSESGSDTLEQ 1209 L : : : : : Db 2004 ENFMLLENKEEVEKQIEQLNHDHKLFISTKNNDIQIIENEKLQEQVDQYITTINEKDKII 2063	QY 1210SQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVT 1261	QY 1262 GEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFN 1308 1224 NQHINQGTNQHI-NQGTNQHQTDTCDGPNYNYVKQNATNREDNKNKERNLSQEIYKYINEN 2182	QY 1309 VNVKDIINSRFNKRENFKNVL-ESDLIPYKDLTSSNYVVKDPYKFL 1353 ::: :: :	Qy 1354NKEKRDKFLSSYNYIKDSIDTDINFANDVLGYYKILS 1390 Db 2243 NNIQEKDEIIENLKNKYNNKLDDLINNYSVVDKSIVSCFEDSNIMSPSCNDILAVFNNLS 2302	QY 1391 EKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLEV 1436 ::	OY 1437 IHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLSTDVNHN 1492 DD 2363 VNNLQLNKDNDNIIIIKFNILKLFRLGSCYLXIINRNLKEI 2403	OY 1493 -NLLTKFLSTGMVFENLAKTVLSNLLDCNLQGMLNISOHQCVKKQCPQNSGCFRHLDERE 1551	OY 1552 ECKCLLNYKOEGDKCVENPNPTCNEN 1577 DD 2444 EILKLKNNLQDNESCIQNLNNYLKKN 2469	RESULT 29 G70163		<pre>RifiaSer, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, S Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997</pre>	A; Witchors: Smith, H.O.; Venter, J.C. A; Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi. A; Reference number: A70100; MUID: 98065943; PMID: 9403685 A; Accession: G70163	A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-2166 < KLE> A; Coss-references: 6B: AE001153; GB: AE000783; NID: 92688419; PIDN: AAC66876.1; PID: 9268842 A; Experimental source: strain 81	Query Match 6.0%; Score 507; DB 2; Length 2166;

LQDKRTDIASFQANIDITLDSLNVKFNDINKEING 1016	FYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLS 1004 : : : : : : : :	FDLYNKYKLKLERLFDKKKTVGKYKMQIKK 1034	-LTLLKEQLESKLNSLNN-PKHVLQNFSVFFNKKKEAEIAËTENTLENTKILLKHYKGLV 1092 : : : : : : : : TNELKNNIESKSEFLNDLYKERFKLIESNFEERYSTFLIESEGAISKIRDEIYKTL- 1193	KYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSG 1149 :: :: : : : : : : : :	LHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKPLPEGTDVATVVSESGSDTL 1207 :: - - - - - - - - -	TTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVT 1261 	GEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKD 1313 	ILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLÄREKRDKFLSSYNYIKDSID 1373 . :: :: :	TDINFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIE-TLYKTVNDKI 1432 	DLFVIHLEAKVLNYTYEKSNVEVĶIKELNYLKTIQDKLADFKK 1475 : : : : : : : ELIQSFRLDIEQKMKDDKENFYLDFTKEFSSKKKDMQSEIĄLMETNITGKV-DEFVDFVN 1536	NHNNLLT 1496 22 NH 1563	al coiled-coil protein - fission yeast (Schizosaccharomyces pombe) -Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 n: 738077 R: Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. R: Churcher, 21767 n: T3807 n: T3807 n:
2 KKFAAVLNNSEEFVKEVDSLLQDKRTDIASFQANIDITLDSLNVK						EQSQPKKPASTHVGAESNTIT 					S NNNFVGIADLSTDYNHNNLLT : NKQSIIDSWFLNIKDDVKDWQEKSYST	RESULT 30 T38077 Hypothetical coiled-coil protein - fissing protei
962	962	1005	1035	1093	1150	1208	1262	1314	1374	1433	1476	RESULT 30 T38077 T38077 C.Species: Sc. Species: Species: Sc. Species: Specie
qq	Oy Dp	Qy	Qy Db	Qy Db	Q	Qy Db	Oy Db	Qy Db	Oy Dp	Qy Db	Oy Dp	RESULT TJ38077 hypothe C; Speci C; Date: C; Acces R; Connc R; Conn

KRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGK----YKMQIKKLTLLKEQ 1041 1042 LESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENTLENTKILLKHYKGLVKYYNGESSP 1101 1102 LKTLSEESIQTEDNYASL-ENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEV 1160 353 RNTIGSLKDSRTSNSQLEEEMVELKESNRTIHSQLTDAESKLSSFEQENKSLKGSIDEYQ 412 439 642 819 926 880 NDQILTQLAELSKNYDSLEQESAQLNSGLKSLEAEKQLLHTENEELHIRLDKLTGKLKIE 939 440 SKNIYTDNERKKFINEIKEKIKIEKKK ------IESDKKSYEDRSKSLNDITKEY - 488 489 -EKLLNEIYDSKFNN----NIDLTNFEKMMGKRYSYKVEK---LTHHNTFASYENSKHN 539 540 L----EKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEIETLVENIKKDEEQL-- 592 641 642 LQLERANFEQKESTLSDENNDLRTKLLKLEESNKSLIKK---QEDVDSLEKNIQTLKE-D 697 643 LKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSD--N 700 SEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQAQPPVPVPVPVPEAKAQVPTPPA 760 820 CDPL----DLLFNIQN-----NIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKD 868 LSIYNKQLEEAHNLISVLEKRI------DTLK-KNENIKELLDKINEIKNPPPANS 333 334 GNTPNTLLD---KNKKIEEHEKEIKEIAKTI------KFNIDSLFTDPLELEYYLREKN 383 165 KYLIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGY 224 221 E---KDYEKIKEDV------SSIKASLABEQASN------KSLRGEQERLEKLLVSS RKPLDNIKDNVGKMEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYD 582 LCNAFQEKLAKSVMQLKENEQNFSSLDTSFKKLNESHQELENNHQTITKQLKDTSSKLQQ 593 -----FEKK---ITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVE 761 PVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEESKL-SS NDKIKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTSH--STNLNNSLKLF ENILS-LGKNKNIYQELIGQKSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDES 384 KNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSFGDL----INPFDYTKEP VANYSDAIVHKDKLIEDLSTRISEFDNLKSERDTLSIKNEKLEKLL-------746 TNAILSSELT------KSSEDVKRLTANVETLTQDSKAM-----701 869 225 263 285 307 467 927 qq QQ qq qq Dp οy δλ q δ δ QQ οy Ω Ωÿ qq qq δ Ω ò qq δy qq qq QQ δλ g Ω q οy δ Ω ò

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1161 IKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSESGSDTLEQSOPKKPASTHV	Db 241 KKIAELVAQIKEIAKTIKFNLDGIFVDPVELEEF 274
DD 1163SNSNNEALVEERSDLANRLSDMKKSLSDSDNVISVIRSDLV 1203 Ov 1221 Gargingtherning	RESULT 32
1204RVNDELDTLKKDKDSLSTQYSEVCQDRDDLLDSLKGCEESFNKYAVSLR	20/79.7 transport protein USO1 - yeast (Saccharomyces cerevisiae) N/Alternate names: protein D2552; protein YDL058Ψ
OY 1263 EAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFN-VNVKDI-LNSRFN 1320 	C:Species: Saccharomyces cerevisiae C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 21-Jul-2000 C;Accession: S67593; A38455; S30782 R:Blooker. H : Brandt. D
1321 KRE-NFKNVLESDLIPYKDLTSSNYVVKDPYK-FLNKE	submitted to the Price; Sequence Database, July 1996 A; Reference number: S67587
Db 1313 TTDAEFTKVVADLEKLQHEHDDWLIQRGDLEKALKDSEKNFLRKEAEWTENIHSLEE 1369	A; Molecule type: DNA A; Residues: 1-1790 < BLO> A; Residues: 1-1790 < BLO> A; Residues: 1-1790 < BLO>
1370 GKEETKKEIAELSSRLEDNQLATNKLKNOLDHLNQEIRLKEDVLKEKESLIISLEESLSN	A:CLOSS-Terterinces: Embi://Arthor. N.D.:gr451030; F.D.:e233003; F.D.:gr451039; RIPS:IDD030 A:Experimental source: strain S280c R:Nakajima, H.; Hirata, A.; Ogawa, Y.; Yonehara, T.; Yoda, K.; Yamasaki, M.
QY 1390 -SEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDL 1434 1	J. Cell Biol. 113, 245-260, 1991 A.Title: A cytoskeleton-related gene, USO1, is required for intracellular protein tra A.Reference number: A38455; WUID:91185402; PMID:2010462 A;Accession: A38455
Qy 1435 FVIHLEAKVLNYTYEKSNV-EVKIKELNYLKTIQDKLADFKKNNNFVGIADL 1485 : :	A;Molecule type: DNA A;Residues: 1-389, TA', 392-724,'S',726-1790 <nak> A;Cross-references: GB:X54378; NID:94777; PIDN:CAA38253.1; PID:94778 A:Note: the authors translated the codon ACT for residue 768 as 11e</nak>
Qy 1486 STDYNH-NNLLTKFLST 1501 Dh 1547 CENTRON MAY ARENCE AND CONTROL OF 1550	R; Hostetter, M.K.; Herman, D.J.; Bendel, C.M.; McClellan, M.; Tao, N.; Kendrick, K.E submitted to the EMBL Data Library, February 1993 A; Description: An integrin analogue in Saccharomyces cerevisiae.
RESULT 31	A;Keterence number: 530/82 A;Accession: S30782 A;Molecule type: DNA A;Kesidues: 71-846,'E',848-923,'K',925-1252,'I',1254-1318,'V',1320-1460,'S',1462-1580
A45518 merozoite surface antigen 3103 - Plasmodium chabaudi adami C;Species: Plasmodium chabaudi adami C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 11-Jan-2000	A.Cross-references: EMBL:L03188 C;Genetics: A;Gene: SGD:USO1; INT1 A;Gross-references: SGD:S0002216; MIPS:YDL058w
C; Accession: A45518 R; Lew, A.M.; Beck, D.J.; Thomas, L.M. Mol. Biochem. Parasitol. 41, 289-291, 1990 A; Title: A second region recognized by the protective monoclonal antibody 5C10/66 in the A; Reference number: A45518; MUID:90377298; PMID:2398918	A:Map position: 4L C:Keywords: coiled coil; transmembrane protein F:326-342/Domain: transmembrane #status predicted <tm1> F:394-410/Domain: transmembrane #status predicted <tm2> F:517-633/Domain: transmembrane #status predicted <tm3></tm3></tm2></tm1>
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Query Match 5.9%; Score 495.5; DB 2; Length 284; Best Local Similarity 39.4%; Pred. No. 3.7e-09; Matches 108; Conservative 36; Mismatches 57; Indels 73; Gaps 3;	158 CDNIHGFKYLIDGYEEINELLYKLNFYFDLLRAKLNDV
Qy 178 LYKLNFYFDLLAAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRRPLDNIKDNVGK 237 ::: :	196
238 MEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIY : : :	OY 230 NIKDNYGKMEDYIKKNKKTIENINELIEESKKTIDKNKNA-TKEEEKKK 277 OY 230 NIKDNYGKMEDYIKKNKKTIENINELIEESKKTIDKNKNA-TKEEEKKK 277 : :
289 NKOLEBAHNISVLEKRIDTIKKNENIKELLDKINEIKNPPPANSGNTPN 111 1 1 1 1 1 1 1 1 1	QY 278 LYQAQYDLSIYNKQLEBAHNLISVLEKRIDTLKKNENIKELLDKINEIKNPPPANSGNTP 337 : : : : : :
339	QY 338 NTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKNKNIDISAKV 392 Db 729FEEVEKLQRQCTK-LKGEITSLQTETESTHENLTEKLIALTNEHKELDEKY 778
Oy 345 KKIEEHEKEIKEIAKTIKFNIDSLFTDPLELEYY 378 :	393 ETKESTEPNEYPNGVTYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKF

g &	: : : :: ::	do oy		KEQA IHLEAKY
g		qq	1749 т	DLDEKI
Oy Dp	503 NIDLINFEKMMCKRYSYKVEKLTHHNFPASYENSKHNLEKLTKALKYMEDYSLRNIVVEK 562 :: : : : : : 894 NVNHQKETKSLKEDIAAKITEIKAINENLEEMKIQCNNLSKEKEHISK 941	RESULT T28317 ORF MS	RESULT 33 T28317 ORF MSV156 hypoth	hypotl
\$ G	563 ELKYYKNLISKIENBIETLVENIKKDEGQLFEKKITKDENKPDEKILEVSDIV 615	C; Sp C; Da C; Ac C; Ac	C; Species: Metano C; Date: 21-Jan-2(C; Accession: T28: R; Afonso, C:L:;	Jan-2() T28.
ç, qa	616 KVQVQKVLLMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLK 675 	J. V A;Ti A;Re A;Re	irol. 7 tle: Th ference	3, 53. e genc numbe : T28
දි පි	676 VFWPKVESLINEEKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQ 735 1029KTISDLEQTKEEIISKSDSSKDEYESQISLLKEKLETATTANDENVNKISE 1079	A;St A;Mo A;Re A;Cr	A;Status: prelim: A;Molecule type: A;Residues: 1-11; A;Cross-reference	relim type: 1-113 erence
ò	736 BOKQAOPPVPVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVS 795	C;Ge A;No	C;Genetics: A;Note: MSV156	156
oy Oy	1080 LTKTREELEAELAAYKNLKNELETKLETSEKALKEVKE 1117 796 HSTMNEKILKQYKITKEEESKLSSCDPLDLLFNIQN	On Be Ma	Query Match Best Local Matches 28	ch 1 S1m: 287;
qq	1118NEBHLKEEKIQLEKEATETKQQLNSLRANLESLEKEHEDLAAQLKKYEEQIANKER 1173	Qy	132 V	VRNYLL
δy		qa	54 I	IKNYNK
QQ	QYNEEISQLNDEITSTQQENESIK-KKNDELEGEVKAMKSTSEEQSNLKKSEIDALNL	Qy		KLNDVC!
Oy Dp	902 QDKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNI 938 : :: : :: :: ::	qa Vo	100 - 247 K	KTIENI
ογ	939 -YQELIGQKSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDESKRK 988	qa	150 N	: I
QQ	KYLEL QKESEKIKEEL DAKTTELKIQLEKITNLSKÄKEKSESELSKLKKTSSEERK	Qy		EKRIDTI
ે દ	989 KLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNS 1048 11 1 1 1 1 1 1 1 1 1	qa a	199 1	FKNIDN
3 8	LINDYKHVLQNFSVFFNKKKEAEIAETENTKILLKHYKGLVKYYNGESSPLK-	5 A		KKQEEL:
QO	:	Qy	418 N	NALNEL
ΟÝ	1104TLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKE 1159	q	295 N	NLQNEII
Dp	1446 KITRNDEKLLSIERDNKRDLESLKEQLRAAQESKAKVEBĞLKKLEBESSKEKABLEKSKE 1505	Qy	478 5	SKSLND
οy	VIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTH 121	qq	321 D	DKNINN
q	MMKKLESTIESNETELKSSMETIRKSDEKLEQSKKSAEED 154	δλ		HNLEKL:
δ	VGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIEN :	do .		ININEL
g .	IKNLQHEKSDLISRINESEKDIEELKSKLRIEAKSGSELETVKQELNN	ο _γ		KKITKDI : :
දු පු	1280 BYEVLYL	g V	400 E	EKLDTE QENKQEI
٥y	1310 ESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGY 1385	qa	426 K	: :: KIDEQTI
QQ	1645	Oy	715 T	TKPGQQ/
ολ	1386 YKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLFV 1436	QQ	446 -	1

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65;
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127 <AFO>
ces: EMBL:AF063866; NID:g4049647; PIDN:AAC97677.1; PID:g4049717
                                                                                                                                                                                                    thetical protein - Melanoplus sanguinipes entomopoxvirus noplus sanguinipes entomopoxvirus 2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
2AWKRDEDTVKKTTDSQRQEIEKLAKELDNLKAENSKLKEANEDRSEIDDLMLLV 1748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTIKELKY-PQLFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYKLNFYFDLLRA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CANDYCOIPENLKIRANELDVL----KKLVFGYRKPLDNIKDNVGKMEDYIKKNK 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INELIEESKKT----IDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVL 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LF -- TDPLELEXYLREKNKNID-ISAKVETKESTEPNEYPNGV--TYPLSYNDIN 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKEKIKIEKKKIESDKKSYEDR 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.7%; Score 483; DB 2; Length 1127;
milarity 19.7%; Pred. No. 4.2e-08;
Conservative 247; Mismatches 430; Indels 490; Gaps
                                                                                                                                                                                                                                                                                  Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L. 33-552, 1999
nome of Melanoplus sanguinipes entomopoxvirus.
ber: Z20484; MUID:99102612; PMID:9847359
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                                        KVLNYTYEKSNVEVKI 1457
| :::|:|
KNAKYRSKLKDLGVEI 1769
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reticulocyte-binding protein 1 - Plasmodium vivax
C;Species: Plasmodium vivax
C;Species: Plasmodium vivax
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 28-Apr-1995
C;Accession: A42771
R;Galinski, M.R.; Medina, C.C.; Ingravallo, P.; Barnwell, J.W.
Cell 69, 1213-1226, 1992
A;Title: A reticulocyte-binding protein complex of Plasmodium vivax merozoites.
A;Reference number: A42771; MUID:92315338; PMID:1617731
A;Accession: A42771
A;Accession: A42771
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2829 <GAL>
A;Rote: sequence extracted from NCBI backbone (NCBIN:108114, NCBIP:108115)
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DOLEY MAICH 85712 CONSERVALIVE 20.9% SOCIE 477: DB 2: LeAGGH 2829; MAICHES 3721 CONSERVALIVE 300; MISMBECHES 317; INGLE 4400; GAPS 97 QY 115 DRESSINGASYADLIKHVRETLITIEKEKFOLT-DIKNIKITLCONTINGEKKLIDOYEE 173 DB 90 DORENSTÄAALAKRIVSDELORITETEKKKSAVETYSTIGSLEKANDSLIKE 954 QY 114 INEELL-YKLINGYEFEDLIASETTEKKEKFOLT-DIKNIKTELONTINGEKKINDSLEN 954 QY 261 LETRAMELDVILK LIPETYBELLOTE 11 ::::::::::::::::::::::::::::::::::																		
MACCH MOST S. 5.7%. SCOTE 4.77, DB 2; Length 2829; \$\$ 372; CONSETVALIVE 20.9%, Pred. As. 1,8007; \$\$ DISSOSAKSYADLKHVENVLITIKELYPOLIFOLIPHHITLCUNHGEKYLLOSEE 173; \$\$ DISSOSAKSYADLKHVENVLITIKELYPOLIFOLIPHHITLCUNHGEKYLLOSEE 173; \$\$ DISSOSAKSYADLKHVENVLITIKELYPOLIFOLIPHHITLCUNHGEKYLLOSEE 173; \$\$ DISSOSAKSYADLKHVENVLITIKELYPOLIFOLIPHHITLCUNHGEKYLLOSEE 173; \$\$ DISSOSAKSYADLKHVENVLITIKELYPOLIPHHITLCUNHGEKYLLOSEE 173; \$\$ DISSOSAKSYADLKHVENVLITIKELYPOLIPHHITLCUNHGEKYLLOSEE 173; \$\$ DISSOSAKSYADLKHVENVLITIKELYPOLIPHHITLCUNHGEKYLLOSEE 173; \$\$ DISSOSAKSYADLKHVENVLITIKELYPOLIPHHITLCUNHGEKYLLOSEEN 174; \$\$ DISSOSAKSYADLKHVENVLITIKELYPOLIPHHITLCUNHGEKYLLOSEEN 174; \$\$ DISSOSAKSYADLKHVENVLITIKELYPOLIPHHITLCUNHGEKYEN 1014 \$\$ LIKEL	⊢				<u></u>	6 14	14	т (л т	L L						ш			Query Best Match
	SLKLFENILSLGKNKNI-YQELIGQ-KSSENFYEKILKDSDTFYNESFTNFVKSKADDIN	KLKDNDKIKNILEBAKKVSTSVKTLSSSSMQPLSLTPQDKDEVSANDDTSHSTNLNN : : : : : : : : : : : : : : : : : :	KOYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLY	PVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKIL::::::::::::::::::::::::::::::::::::	EKKNIKTEGOSDNŠEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQAQPPV		E-LKKTQLILKNV-ELKHNI66 : : : : : :	IETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKID ::: : : : : : : : : :	HHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLIS-KIENE 5 :: : : : : : :	IESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYK-VEKLT	VTYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKEKIKIEKKK 466	AKTIKENIDSLETDPLELEXYLREKNKNIDISAKVETKESTEPNEYPNG 	NENIKELLDKINEIKNPPPANSGNTPNTLLDKNKK-IEEHEKEIKEI- 357 :: : : :: :: :: :: ::	ELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKK 311 	LKIRANELDYLKK-LVFGYRKPLDNIKDNVGKMEDYIKKNKKTIENIN-	4 INELLYKLNFYFDLLRAKLPFN	DNSSDSDAKSYADLKHRVRNYLLTIKELKYPQLF-DLTNHMLTLCDNIHGFKYLIDGYEE	atch .5.7%; Score 477; DB 2; Length 2829; cal Similarity 20.9%; Pred. No. 1.8e-07; 372; Conservative 300; Mismatches 617; Indels 490; Gaps

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RESULT 35
T18427
T18427
T18427
T18427
Typothetical protein C0335c - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Accession: T18427
R;Lawson, D; Bowman, S; Barrell, B.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z18935
A;Accession: T18427
                                         A; Intro
A; Note:
                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3724 <LAW>
A;Cross-references: EMBL:298547; NID:e1325376; PID:
C;Genetics:
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Note: C0335c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKTIV---DELKT-LNDISECSSVLNNVVSIVKKVKESKHADYRRDANSMYESMVT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SL---NDESKRKKLEEDI---NKLKK--TLQLSFDLYNKYKLKLERLFDKKKTVGKYKMQ 1031
                                                                                                                                                                                                                                                                                                        IGEHLDEIKRNVTETLSSY-EIDQKMEMMSKNLLEKKSK
                                                                                                                                                                                                                                                                                                                                                             LVQAKTEYEQILENIKQNDDMLQNIFLKKVSIIEYFENVKKKKESILNDLYE--QERLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGGVQNMLALYDKLNEE-KREMDELYRNISETKLKQMEHSTDVFKPMIELHKGMNETNNK 2302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---ANDVLGYYKILSEKYKSDLDSIKKYIND-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSKL----TFSSASEIVQNADTYS-VNFAKHEK--ESLNAIRDIKKELYLFHQNSDISIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESDLIPYKDLTSSNYVVK--DPYKFLNKEKRDKFLSSYNYIKD-----SIDTDINF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYSNSITQLEGIVVSAGESKEDIEKLERSNEEMRNISEKISTIDSKVIEMNSTIDELYKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSNDVIQKERESEQLAKDA------TDIYNVIKLKNEFNEKLEEAKNKEEVVSEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- LANYFLSDEAKISSGMEFNAEMKSNFKTDLELEIFSVIS-----NSNELLKKIEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELAEKEEEHLRRREEEAIFLLNDIKKVESLKLLKEMMKKVSAEYEGMKRDHTSVSQLVQD
                                                                                                                                                                                                                                                                                                                                  ISQH-QCVKKQCPQNSGCFRHLDEREE--CKCLLNYKQE 1562
                                                                                                                                                                                                                                                                                                                                                                                                                   DNYQIVEEHKKQFSILIDRTNALMDDIEIFKKENNY-NLMEVNTETIHRVNDYIEKITNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLLEKEKKLKSVNDHMHSMEAEMIKNGLKYTPESVQNINNIYSVIEAEVKTLEEIDRDYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLNNIETLYKTVNDKIDLFVIHLEAKVLNYTYEK-----SNVEVKIKEL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKF----LPEGTDVATVVSES
                                                    307/1;
  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --LKPLAGVYRSLK-----KQLENNVMTFNVNVKDILNSRFNKRENFKNVL 1329
20.
                                                                                                                                                                                                                                                                                                                                                                                                                                               --LKTIQDKLADFKKNNNFVGIADLSTDYNH------
  . 78;
                                                                                                                                                                                                                                                                                                                                                                                       --NNLLTKFLSTGMVFENLAK---TVLSNLLDGNLQGMLN 1526
                                                                               NID:e1325376; PID:e1325379;
  Score
Pred.
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 477;
No. 2.
  DB 2;
.5e-07;
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               Length
               3724;
                                                                                 PIDN:CAB11104.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KNIYTDNERKKFINEIKEKIKI-----EKKKIESDKKSYEDRSKSLNDITKEYEKLLNE 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SILTINQNDKKYKKKKKKYSELQDSNISSN-----NTLTS-----KRYTYTCGMDKETK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEHPDEQNQS-----LNKNKCLTGTNKKEK------YMIPKGTEYQDKEKES 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVFGYRKPLDNIK----DNVGKMEDYI--KKNKKTIENINELIEES------KKTIDKN 266
                                                                                                                                                                                                                                                                                                                                                                          QNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKDNDKIKNL----LEEAKKVSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEKIL----EVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IYDSKENNNIDLTNEEKMMGKRYSYKVEKLTHHNTEASYENSKHNLEKLTKALKYMEDYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E---TDEQNKRRNTEVASICNVCNVETNEKQRKKTNKK----KSVQKDDLVEENALLDNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSFGDLINPFDYT----KEPS 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYK--LNF-----YFDLLRAKLNDVCANDYCQIPFNL-----KIRANELDVLKK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VQNIWMNILNKKMDDKFSKVEYFKIMLRIC-----KVLIPQFDIKEIIKIVNDEWINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRNYLLTIKELKYPQLFDLTNH---MLTLCDNIHGFKYLIDGY------
                                    KLERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVLQNF---SVFFNKKKE-- 1068
                                                                                                                       ESKRKKLEEDINKL-
                                                                                                                                                              DNNINNIYDESINNIYDESINNIYDESI----NNIYDESINNIYDENINNIYDENINNIYD
                                                                                                                                                                                        ----NIYQELIG----QKSSENFYEKILKDSDTFYNESFTNFVKSKA-----DDINSLND
                                                                                                                                                                                                                                                   SRTNDTFNIKDISL - - -
                                                                                                                                                                                                                                                                                        VKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFENILSLGKNK.....
                                                                                                                                                                                                                                                                                                                                   KNNIFKKDEKYNSLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDSTFEL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DKTIYNNNEEQTDDLNRNINKIESINNNND------NNNNINN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRNIVVEKELKYY - - - - - - KNLISKI - - - ENEIETLVENIKKDEEQLFEKKITKDENKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         II-----IDGINFDDVT-----KECKIIDDN---NNENIDNNI----YVENNK 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FSENYKLENSFLYDMDDDGDNSLIPKNLFE--NLLN-NKQHNDYLQRNIILMDVND-INP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNATKEEEKKKLYQA--QYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLDKINE 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMINFKRTAENKKLSLYNDINIIEKHVIKEKNKNILKNLQSFKRSSMQIQNLKKKHFIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGKKYLNESSEENAFFELSDIWTPTINAYDYAHFLKSLEYRITYIEIKTKDGRIIKKKPM
                                                                           ENTINITYDEGINKICDDNÍLENKNIKTTNDIVQVEENNESIEKNELMISLNKDINNTYNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----YLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLFNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            344;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKEFNKI----RTEHILNKESISKHIK-----GSPSRDKEIKKLYTTNKN
FKENVDIFINKIKRESLLKIDKNIKDNN-NDDEYIMDNFYENDFIINHKMEIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              290;
                                                                                                                                                                                                                                                 NDDLEKEKRKKKSQHFIDNLVKADKNEISENINKIC
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                                                                                                                       -KKTLQLSF--DLYNKYKL 1013
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A; Residues: 1-1875 < BAL>
A; Cross-references: EMBL: Z28320; NID: g486586; PID: g486587; MIPS: YKR095w
A; Experimental source: strain S288C
R; Bou, G.; Esteban, P.F.; Baladron, V.; Gonzalez, G.A.; Cantalejo, J.G.,
Yeast 9, 1349-1354, 1933
A; Title: The complete sequence of a 15 820 bp segment of Saccharomyces of R; Reference number: S40644; MUID: 94205265; PMID: 8154186
A; Accession: S40647
A:Experimental source: strain S288C
R:Koelling, R.; Nguyen, T.; Chen, E.Y.; Botstein, D.
Mol. Gen. Genet. 237, 359-369, 1993
A:Title: A new yeast gene with a myosin-like heptad repeat structure.
A:Reference number: S31207; MUID:93247549; PMID:8483450
A:Accession: S31207
A:Molecule type: DNA
A:Residues: 1-300,'A',302-1875 <KOE>
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                                                                                                                                                                                                                                                                                                                                                                                                                       V.; Gonzalez, G.A.; Cantalejo, J.G.; Remacha,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211
     IQIYTAADKEVNNSTNGPGLNNIL-----ITLRRERDILDTKVTVAERDAKMLRQKISL
                                                          DKPEVSANDDTSHSTN---LNNSLKLFENILSLGKNKNIY--QELIGQKSSENFYEKI--
                                                                                                                 HTYKGQVKTLNL-SRDQLENALKENEKSWSSQKESLLEQLDLSNSRIEDLSSQNKLLYDQ
                                                                                                                                                                                                                             QNNNKEVEAVKSEYESKLSKIQNDLDQQTIYANTAQNNYEQELQKHADVSKTISELREQL
                                                                                                                                                                                                                                                                                                                                                                                                VPEAKAQVPTPPAPVNNKTENVSKLDYL-EKLYEFLNTSYICHKYILVSHSTMNEKIL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                       YKDLYETTSQS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQAQPPVPVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QKKIDELEDALSELKKETSQKDHHIKQLEEDNNSNIEWYQNKIEALKKDYESVITSVDSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENKPDEKILEVSDIVKVQVQK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELLNLKEEQKLR-VHLEKNLKQELNKLSPEKDSLRIMVTQLQTLQKEREDLLEETRKSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TKALKYMEDYSLRNIVVEKELKYYKNLISKIENEIETLV---ENIKKDEEQLFEKKITKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNEIYDSKFNNNIDLTNFEK-MMGKRYSY-----KVEKLTHHNTFASYENSKHNLEKL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFDYTKEPSKNIYTDNERKKFINEIKEKIKIEKKKIESDKKSYEDRSKSLNDITKEYEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSFGDLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENIKELLDKI-NEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLFTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLK-------KN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANELDVLKKLVFGYRKPLDNI - - - - - - KDNVGKMEDYIKKNKKTIENINELIEESKKTI
                                                                                                                                                                   YEKEMVCNLYKLKDNDKIKNLLEEAKKVSTSVK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QTDIEKLQYKVKSLEKEIEEDKIRLHTYNVMDETINDDSLRKELEKSKINLTDAYSQIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKSKQSLQKIESETVNEAKEAIITLKSEKMDLESRIEELQKELEEL-KTSVPNEDASYS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -NDLQTLTKQRLDLCRQIQYLLITNSVSNDSKGPL-----RKEEIQFIQNIMQEDDSTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----TESDSQK------VVTERLVEFKNIIQLQEKNAELLKVVRNLADKLESKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRESTENMSLLNKEIQDLYDSKSDISIKLGKEKSSRILAEERFKLL------
                                                                                                                                                                                                                                                                   KQYKITKEE-ESKLS----SCDPLDLLEN-IQNNIPVMYSMFDSLNNSLSQLFMEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----SNTLDLTKAENDQLRKRFDYLQNTILKQDSKT-HETLNEYVSCKSKLSIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NVTIKQLTETKRDLES
                                                                                                                                                                                                                                                                                                                                            -TDEKTSLEDKISLLKEQMFNLNNELDLQKKGMEKEKADFKKRISIL 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----LQQTNSKLD-ESFKDFTNQIKNL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -VLLMNKIDELKK-----TQLILK
                                                                                                                                                                      -TLSSSSMQPLS----LTPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -QVQDLQTRISQI---
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1123

902 1064 854 747

687

865

925

639 805 600 696 491

746 543 431

650

371

564 312 520

1177 955

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A;Cross-references: EMBL:L01992; NID:g171958; PIDN:AAA34783.1; PID:g171959 C;Genetics:
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	155	EDI TANI	יים עעחסו	V	111 GUDODNOODO-DAVOVADIUDVDNVIIB-IVEI VODOI EDI ENUNT 155		י באניניים ו	a violonia di	1
78;	Gaps	489;	Indels	545;	datches 346; Conservative 289; Mismatches 545; Indels 489; Gaps 78;	289;	servative	346; Cor	fatches
		1875;	Length	DB 2;	5.6%; Score 474.5; DB 2; Length 1875;	 	5.6	tch	uery Match
					ross-references: SGD:S0001803; MIPS:YKR095w position: 11R	303; м	SGD:S00018	ross-references:	ross-re

419	156	368	111	ry Ma t Loc ches	•
419 PIINSFKERTDMLENELNNAALLLEHTSNEKNAKVKELNAKNQKLVECE 467	156 TLCDNIHGFKYLIDGYE-EINELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIR 210	368 TDEADEDNENLSAKSSSDFIFLKKQLIKERRTKEHLQNQIETFIVELEHKV 418	:	ry Match 5.6%; Score 474.5; DB 2; Length 1875; t Local Similarity 20.7%; Pred. No. 1.4e-07; ches 346; Conservative 289; Mismatches 545; Indels 489; Gaps	•
四…	QIPFNL	,	LFDLTN	1875;	
467	LKIR 210	-HKV 418	NHML 155	; Gaps	
•	_	-	-	7:	

epitope of a protective umber: A44997; MUID:9104 B44997 liminary; nucleic acid spe: DNA -476 <lew -476="" <le<="" <lew="" th=""><th>Qy 1524 MLNISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENPNP 1572 : : : : : : : : : : : : </th><th>Qy 1344 YVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYYKILSEKYKSDLDSIKKY 1403 </th><th>1173 ENNTDVNNALESYKKFLPEGTDVATTVSESGSDTLEQSQPKKPASTHVGAESNTITT 122 </th><th>Qy 1039 KEQLESKLNS-LNNPKHVLQNFSVFFNK-KKEAEIAE 1073 </th><th>QY 956LKDSDTFYNESFTNEVKSKADDINSLNDESKR 987 : : : : : : : : : :</th></lew>	Qy 1524 MLNISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENPNP 1572 : : : : : : : : : : : :	Qy 1344 YVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYYKILSEKYKSDLDSIKKY 1403	1173 ENNTDVNNALESYKKFLPEGTDVATTVSESGSDTLEQSQPKKPASTHVGAESNTITT 122	Qy 1039 KEQLESKLNS-LNNPKHVLQNFSVFFNK-KKEAEIAE 1073	QY 956LKDSDTFYNESFTNEVKSKADDINSLNDESKR 987 : : : : : : : : : :
Qy 672 DKLKVFMPKVESLINEEKKNIKTEGQSDNSEPSTEG	not compared with conce fth 482;	RESULT 38 RESULT 38 Merozoite surface antigen 1 Plasmodium chabaudi adami (strain DK) C; Species: Plasmodium chabaudi adami C; Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 11-Jan-2000 C; Accession: A44997 R; Lew, A.M.; Beck, D.J. MOl. Biochem. Parasitol. 42, 153-154, 1990 A; Title: The epitope of a protective monoclonal antibody occurs in a region of microh	301 TETTTPAESASTEPTPKAPTATPTSETVTQEGTTPAAPKAQEGASSSAPAQPAPAKPAPA 910 NDDTSHSTNLNNSLKLFENILSLGKNKNIYQELIGQKSSENFYEKILKDSDTFYNESFTN	Db 121 PAAPATPAAPAAPAKPVMTKLYYLEKLKKELAFSYSCHKYVLLQNSTINKDALSKYALTP 180 Qy 812 EEESKLSSCDPLDLLF	Db 1 ERLAKFIPKIDNMIEKEKQKMEQEHVATGESEQASSASGTGSSTETTSQTAPAVPAAPAP 60 Qy 722

DP PP	Qy Db	ОУ	B 68	DP QA	P 64	8 양		> C > > > >	2 2 2 2 C 2	CCC T B B	Qу	Оy	Qy Db	Qy Db	g 49
							Que:	Res Cro Exp Gen	11 Tit Ref	RESULT B42771 reticu C;Spec C;Date C;Acce					
616 250	556 217	496 186	441 138	385 85	332 42	272 1	Query Mat Best Loca Matches	ecul idue idue ss-r erim erim etic	le: le: eren essi	T 39 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1024 471	964 412	904 361	886 301	,828 241
KVQVQKVLLMNKIDELKKTQLILKNVELKHNIHVDNSYKOENKQEDYYLIVLKKEIDKLK 675 :: : : : : : : : : : : :	RNIVVEKELKYYKNLISKIENEJETLVENIKKDEBQLFEKKITKDENKPDEKILEVSDIV 615	YDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYMEDYSL 555 :	KNIYTDNERKKFINEIKEKIKIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEI 495 :: : :	NIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSFGDLINPFDYTKEPS 440 	NSGNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKNK 384	EEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLDKINEIKNPPPA 331	Match 5.4%; Score 457.5; DB 2; Length 1252; Local Similarity 21.1%; Pred. No. 2.9e-07; es 306; Conservative 228; Mismatches 458; Indels 455; Gaps 71;	A; Molecule type: DNA A; Rolecules: 1-1252 <gal> A; Cross-references: GB: M88098; NID: g160627; PID: g160628 A; Experimental source: strain Belem, merozoites C; Genetics: A; Gene: RBP2</gal>	; ingravallo, P.; Barnwell, J.W. 19 protein complex of Plasmodium vivax merozo 11D:92315338; PMID:1617731	2 - Plasmodium vivax (fragment _revision 12-Mar-1993 #text_ch	TVGKYKMQIKKL 1035 : : : QIEAANQKVKEI 482	NESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKK 1023 : :	KPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQELIGQKSSENFYEKILKDSDTFY 963	VKTLSSSSMQPLSLTPQD 903	-NIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKD-NDKIKNLLEEAKKVSTS 885 : :::: :: : :: :: SAIQNNMPTMYSLYENVVDGLQNIYTELYEKEMMYHIYNLKDKNPAVKALLAPAQEATTE 300

Оy	ОУ	Qу Дъ	Qу Db	Оу	DЬ	Qу	Qу	Оу	Оу	dq Qy	Оy	Qу рь	Оу	Оу Дъ	Ф	Оγ	Ωу
1531 1169	1485 1115	1429 1060	1381 1000	1329 953	1273 898	1219 . 846	1182 786	1123 745	107 4 700	1034 641	988 581	951 521	903	844 412	785 380	725 352	676 295
QCVKK 1535 : : TLESIKK 1175	LSTDYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQH- 15::::::::::::::::::::::::::::::::::::	NDKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIAD 1484 	DVLGYYKILSEKYKSDLDSIKKYINDKOGENEKYLPFLNNIETLYKTV 142 	LESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFAN 138 DTDSLNTALDELLKKGRTCEVSRYKLIKDTVTKEISDDTELINTIEK 999	ILSKIENEYEVLYLKPLAGYYRSLKKOLENNVMTFNVNVKDILNSRFNKRENFKNV 132	HVGAESUTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDN 127;	LESYKKFLPEGTDVATVVSESGSDTLEQSOPKKPA-ST 121	KVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVN-NA 11 :	TENTLEN-TKILLKHYKGLVKYYNGESSPLKTLSBESIQTEDNYASLENF 112	KLTLLKEQLESKLNSLNNPKHVLQNESVFFNKKKEABIAE 107	KKLEEDINKLKKTLQLSFDLYNKYK-LKLERLFDKKKTVGKYKMQIK 103 : : : : : : : : : : : : :	FYEKILKDSDTFYNESFTNFVKSKADDINSIND-ESKR 987	DKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQELIGQKSSEN 950 :	NNSLSQLFMEIYEKEMVCNLYKLKDN-DKIKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQ 902	SYICHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMY-SMFDSL 843	LEGDSVQAQAQEQKQAQPPVPVPVPPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNT 784	VFMPKVESLINEEKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSA 724
	1530 1168	1,484 1114	28 59	1380 999	28	72 7	1218 845	1181 785	22	9	1033 640	0	20	ω δ	μ ω	9 4	1 4

Qy 662 YYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQA 721 :::	QY 604 PDEKTLEVSDIVKVQVQKVLLMNKIDELKKTOLILKNVELKHNIHVPNSYKQENKQEP 661	QY 560VEKELKYYKNLISKIENEIETLVENIKKDEEQLFEKKITKDENK 603	QY 505 DLINFEKMAGKRYSYKVEKLTHHNTFAS-YENSKHNLEKLTKALKYMEDYSLRNIV 559	QY 476 DRSKSLS04 1::	QY 418 NALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINE-IKEKIKIEKKKIESDKKSYE- 475	Qy 384KNIDISAKVETKESTEPNEYPNGVTYPLSYNDIN 417	QY 325 IKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKN- 383	QY 265 KNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLDKINE 324	QY 214 LDVLKKLVFGYRKPLDNIKDNVGKMEDYIKKNKKTIENIBLIEESKKTID 264	QY 162 HGFKYLIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANE 213	QY 102 SGGSGNSRRTNPSDNSSDSDAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNI 161 : : :::::	Query Match 5.4%; Score 453.5; DB 1; Length 2485; Best Local Similarity 20.7%; Pred. No. 8.5e-07; Matches 361; Conservative 257; Mismatches 579; Indels 543; Gaps 84;	A;Gene: PFB0150c C;Superfamily: malaria parasite serine/threonine-specific protein kinase PFB0150c; prote C;Keywords: phosphotransferase F;2087-2352/Domain: protein kinase homology <kin></kin>	Residues Cross-ref Experimer Genetics	Reference number: A71600; MUID:99021743; PMID:9804551 Accession: H71621 Status: preliminary; nucleic acid sequence not shown; translation not Molecule type: DNA	er, M.J.; Tettelin, H.; Carucci, D.Jer, M.J.; Tettelin, H.; Carucci, D.Jea, M.; Salzberg, S.; Zhou, L.; Sutt 282, 1126-1132, 1998	H71021 H71021 Serine/Threonine-specific protein kinase (EC 2.7.1) PFB0150c - malaria parasite (Plasm C; Species: Plasmodium falciparum (Plasm C; Species: Plasmodium falciparum (Plasm C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 (Plasm C; Date: 10-Sep-1999 #text_change 10-Sep-1999 (Plasm C; Date: 10-Sep-1999 #text_change 10-Sep-1999 (Plasm C; Date: 10-Sep-1999 #text_change 10-Sep-1999 (Plasm C; Date: 10-Sep-1999 #text_change 10-Sep-1999 (Plasm C; Date: 10-Sep-1999 (P	RESULT 40
RESULT 41 T18444		1557 INVKORGDKOVENDADTONENNGGODADAKOTEEDIGGSNGKKTTOCTOTKEDIGSVELTENG	1868	1378 FANDVLGYYKILSEKYKSDLÖSIKKYINDKQGENEKYLPFLNNIETLYKTYNDKIDLFVI	1319 1773	1259 1732	2 1	QY 1164KNYGNSBESHNIDYNNALESYKKFLPEGIDVATVYSESGSDILEQSQPKKPASTHY 1220	1124 · 1568	1077 TLENTKILLKHYKGLVKYYNGESSPLKTLSBESIQTEDNYASLENFK : : : : : : : : : : : : : : : : : : :	4 SKLNSLNIP	1390	943 IGQKSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDIN	QY 883 STSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNTYQEL 942 : : :	Qy 836 MYSMFDSLNNSLSQLF-MEIYEKEMVCNL-YKLKDNDKIKNLLEEAKKV 882 :: :: :: :	Oy 782 LNTSYICHKYILVSHSTMİEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPV 835	QY 722 GSALEGDSVQAQAQEQKQAQPPVPVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEF 781 Db 1173	Db 1134 NEIYVDNDKELEIVNEEKKLIYPENYESDVHKNMNMSIN 1172

840	781 EKKKYVHDHRKDNIIKRNKEFINIYKGKRNYANVEIGSEVCNNKVNVKGDDNKMMVENKQ	Ф
759	701 SEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQ-EQKQAQPPVPVPVPVPEAKAQVPTPP	ОУ
700	653YKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDN ::	Оу
721	62 IDALLDHIEEKKKTGHKEINLYKEIKNEYQKMLNDENSIMLEHEKKYNTHQVNNNLCDTK	Вb
652	QLILKNVELKHNIHVPNS	Qy
661	613 KKKKIEIEEEKKKKIEMEEEKNKIDDEKKNTYANDKIISHIDNVNCNIK	ΔЬ
620	KKITKDENKPDEKILEVSDIVKVQVQ	Qy
563 612	504 IDLINFEKMMGKRYSYKVEKLTHHNIFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKE ::	В <i>с</i> ў
576	28 DYEGYDPEKKKKKLDDHIYTQQKEYKNNINDILKDHHLNDKETKEKKNE	dd
503	LLNEIYDSKFNNN	Qy
527		Db
446	0	Qy
468	419 YVHFKNNDDSSIKKKNNSSECLDEQKKKTYKYTIIEQKRYNFNDRDNNNA	рь
388	EIKEIAKTIKFNIDSLFTDPLELEYYLREKNKNIDI	Qy
418	362 VELRNKDNLVVNDNIINKSFEK-NNILYIKTSDSLNENYNERKIYKEINKEEYSNKNE	₽ 5
361	FVNKENEWNITTOLITEN HALL TOUT EVALUATION OF THE ACTION OF THE FUNK ENEMNENK NKKSVKED GLHNVL	g B
282	NKKTIEN:INELIEESKKTIDKNKNATKEEEKKKKYQAQ	Qy
304	YKRKIDK-DDNLSKKKKRPNYLFNKDGEH	рь
244	KLVFGYRKPLDNIKDNVGKMEDYIKK	Qy
255	228 TNNHIIHHISNKTSLIENNKKKEENIFP	οь
192	LTLCDNIHGFKYLIDGYEEINELLYKLNFYFDLLRAKL	Qy
227	181 NGNNIMNGNNIMNGNNNINRNNIMNGNNNINRNNIMNRNNI	DЬ
132	GNSRRTNPSDNSSDSDAKSYADLKHRV	Qy
ps 76;	Match 5.3%; Score 448; DB 2; Length 1650; Cocal Similarity 20.3%; Pred. No. 7.9e-07; es 327; Conservative 263; Mismatches 581; Indels 442; Ga	Query Best Match
	Map position: 3;Introns: 1597/3; 1625/3;Note: C0385c	A; Map A; Int A; Not
112.2	;Residues: 1-1650	A; Res
	ACCESSION: T18444 Status: preliminary; translated from GB/EMBL/DDBJ Molecule type: DNA	A; Acc
	R;Lawson, D.; Bowman, S.; Barrell, B. submitted to the EMBL Data Library, August 1997 A;Reference number: Z18935	R; Law submi A; Ref
2000	process color marging parasite (riasmoutum ratciparum) asmodium falciparum t-1999	C; Spe
	protein CO385c - malaria parasite	hypot

Qy 760 APWIN KTEN	1509 PDNILIHYSNEHLNNKIYKYGV-IKLADFGFSCQLKNKRQKRSTFCGTID 1557	Db
760 841 806 896 863 934 999 992 967 1050 1017 1110 11170 11167 11167 1123 1123 11324 11359 11372	IDLFVIHLEAKVLNYTYEKSNYEVKIKELNYLKTIQDKLADFKKNNNFVGIAD	Qy
760 841 806 896 8963 934 9909 992 967 1050 1017 1110 11170 11109 1123 1123 11259 13324 1332	:	Db
760 841 806 896 863 934 999 992 967 1050 1017 1110 1170 11109 1123 1123 11259 1381 1312		Qy
760 841 806 896 8963 934 9909 992 9967 1050 1110 11170 11109 1123 11269 11321	KEIIIQASLKHINILELIAYFE	ДЬ
760 841 806 896 896 934 992 992 967 1050 1017 1110 1170 1170 11051 1170 1123 1123 11324		Qy
760 841 806 896 863 934 999 992 967 1050 1017 1110 1170 11109 1123 1123 1125	IVDKYPIGNGRTGLVFKAIIKKEENKKVA	Ф
760 841 806 896 896 934 909 992 967 1050 1110 1170 11170 11109 1123 11269 1211	- V	Qy
760 841 806 896 863 934 992 992 9105 1050 1107 1110 1170 11109 1123 11167		Db
760 841 806 896 8963 934 9999 992 967 1050 1017 1110 1170 11101 1170 1167		Qy
760 841 806 896 896 934 909 992 967 1050 1110 1170 1170 1109	1269 RKQSNSCDNNTTSLKNKMIINSNSEKANSSNSQNNEKKEMSYFEWLANEKKKKEI	Db
760 841 806 896 863 934 992 992 9105 1050 1107 1110 1170 1109	1	Qy
760 841 806 896 863 934 909 992 1050 1110 1170	NIKNNDNINS	Db
760 841 806 896 863 934 909 992 992 1050 1110 1170		Qy
760 841 806 896 8963 934 909 992 997 1050 1051	NDKYLIEKDGFKDIINE	Db
760 841 806 896 863 934 909 992 992 1050 1110		Qy
760 841 806 896 863 934 909 992 992 1050		Db
760 841 806 896 863 934 909 909 967		Qy
760 841 806 896 863 934 909 992	YTCIRNKMNVDSIKLNDKADLYKDKKKTSFNDI	Db
760 841 806 896 863 934 909		Qy
760 841 806 896 863 934		Db
760 841 806 896 863 934		Qy
760 841 806 896 863		Db
760 841 806 896	LYKLKDNDKIKNLLEEAKKVSTSV	Qy
760 841 806	YPHLYSNKNEDKDKKSIFLKNINENIKKNYK	Db
760 8 4 1	0	Qy
760		Db
		Qy

RESULT 42
\$288.51
\$288.51
\$Centromere protein E - human
N:Alternate names: centromere 312K protein; kinesin-related protein CENP-E
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 19-Jan-2001
C;Accession: S28261
R;Yen, T.J.; Li, G.; Schaar, B.T.; Szilak, I.; Cleveland, D.W.
Nature 359, 536-539, 1992
A;Title: CENP-E is a putative kinetochore motor that accumulates just before mitosis.
A;Reference number: S28261; MUID:93024922; PMID:1406971
A;Accession: S28261
A;Accession: S28261
A;Accession: S28263 <YENA;Cross-references: EMBL:215005; NID:929864; PIDN:CAA78727.1; PID:929865
C;Genetics:

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A;Gene: GDB:CENPE
A;Cross-references: GDB:361164; OMIM:117143
A;Map position: 4q24-4q25
C;Superfamily: centromere protein E; kinesin motor domain homology
C;Keywords: ATP; coiled coil; microtubule binding; mitosis; nucleotide binding;
F;7-335/Domain: kinesin motor domain homology <KMOT>
F;86-9J/Region: nucleotide-binding motif A (P-loop)
F;486-2183/Domain: coiled coil #status predicted <COI>
F;92/Binding site: ATP (Lys) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 LIDGYEEI-----NELLYKLNEYFDL--LRAKLNDVCANDYCQI-----PFNLKIR-ANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 5.3%;
Local Similarity 18.4%;
                                                                                                                                                                ILKN----VELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEK---
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                                  EQKQAQPPVPVPVEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVS 795
                                                                                                                                             LSRTCDRLAEVEEKLKEKSQQLQEKQQQ----LLNVQEEMSEMQKKINEIENLKNELKNKE 1171
                                                                                                                                                                                                                                                         VENIKKDEEQLFEKKITKDEN-----KPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQL
                                                                                                                                                                                                                                                                                             TGETKDEFQQKMVGIDKKQDLEAKNTQTLTADVKDNEIIEQQRKIF-SLIQE-KNELQQM
                                                                                                                                                                                                                                                                                                                                 ---SKHNLEKLTKALKYMEDYSLRNI------VVEKELKYYKNLISKIENEIETL
                                                                                                                                                                                                                                                                                                                                                                     KSDIHDT-VNMNIDTQ-----EQLRNALESLKQHQETINTLKSKISEEVSRNLHMEEN 1000
                                                                                                                                                                                                                                                                                                                                                                                                           LNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHH----NTFAS-----YEN
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                                                                     LTLEHMETERLELAQKLNENYEEVKSITKERKVLKELQKSFETERDHLRGYIREIEATGL 1231
                                                                                                        ---KNIKTE----GOSDNSEPSTEGEITGOATTKPGQQAGSALEGD-----SVQAQAQ
                                                                                                                                                                                                                     LESVIAEKEQL---KTDLKENIEMTIENQEELRLLGDELKKQ-QEIVAQEKNHAIKKEGE 1114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 443.5;
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1232

QTKEELKIAHIHLKEHQETIDELRRSVSEKTAQIINTQDLEK------

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RESULT 'B71612	В	Qy	Db	Qγ	뭥	Qy	DЬ	Qy	В	Qy	DЪ	Qy	뮹	Qy	Db	Qy	₽.	Qy	Ъ	Qy	В	Qy	Ф	Qy	뮹	Qγ	ф	Qy	ф	Qy	Ъ	Ϋ́	Db	Qy
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al protein PFB0555c - malaria parasite (Plasmodium falciparum)	KIKEEQHECI 2153	KQEGDKCV 1567	MESLREKCSRIKELLKRYSEMDDHYECLNRLSLDLEKEIEFHRIMKKLKYVLSYVT 2143	QCPQNSGC	EEIRIVAKERDELRRIKESLKMERDQFIATLREMIARDRQNHQVKPEKRLLSDGQQHL 2087	-	QELQKKELQLLRVKEDVNMSHKKINEMEQLKKQFEPNYLCKCEMDNFQLTKKLHESL 2029	LAE	EIQQE-LKTARMLSKEHKETYDKLREKISEKTIQISDIQKDLDKSKDELQKKI 1972	NEKYLPFL	SVMKERDNLRRVEETLOETKARDL 1920	DLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNY	KANEHOLITLKKDVNETOKKVSEMEQLKKOIKDOSLTLSKLEIENLNLAQELHENLEEMK 1885	NEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILN 1316	KAQDLKIQEELRIAHMHLKEQQETIDKLRGIVSEKTDKLSNMQKDLENSNAKLQEKIQEL 1825	IIVPIFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIE 1278	KENLRETITRDLEKQEELKIVHMHLKEHQETIDKLRGIVSEKTNEISNMQKDLEHSNDAL 1765	ATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDDV- 1240	IETENIRLTQILHENLEEMRSVTKERDDLRSVEETLKVERDQL 1705	TGNSPSENNTDVNNALE	LKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCEIEHLKEQFETQKLNLEN 1662	TLENTKILLKHYKGLVKYYNGESSPLKTLSEESI-QTEDNYASLENFKVLSKLEGKLKDN 1135	ELKQFKEHRKAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEEMKRVQEALQIERDQ 1608	KLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETEN 1076	QEETINELRVNLSEKETEISTIQKQLEAINDKLQNKIQEIYEKEEQLNIKQISEVQENVN 1548	LEEDINKLKKTLQLSFDLYN-KYKLKLERLFDKKKTVGKYKMQIK 1033	QESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIVAKHLETEEELKVAHCCLKE 1488	GOKSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDESKRKK 989	SKQEQSLMMKEK	SMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQELI 943	LRINEKFQESQEEIKSLTKERDNIKTIKEALEVKHDQIKEHIRETLAKIQESQ 1383	LSQLFMEIYEKEMVCNLYKLKDNDKIKNLLEEAKKVSTSVKTLSSS 892	: : :	HSTMNEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNS 846

Qy 617 VQVQK-VLLMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYL 664 : : :	QY 596 KITKDENKPDEK	QY 545 KALKYMEDYSLRNIVVEKELKYYKNLISKIENEIETLVENIKKDEEQLFEK 595	Qy 501 NNNI	Qy 477F 500 : : :	QY 421 NELNSFGDLINPFDYTKEPSKNIYTDNERKKF-INEIKEKIKIEKKKIESDKKSYED- 476 ::	QY 378YLREKNKNIDI-SAKVETKESTEPNEYPNGYTYPLSYNDINNAL 420	QY 354IKEIAKTIKFNIDSLFTDPLELEY 377	QY 316 KELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKE 353 :	QY 265KNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENI 315	Qy 214 LDVLKKLVFGYRKPLDNIKDNVGKMEDYIKKNKKTIENINELIEESKKTID 264	Qy 166 YLIDGYEEINELLYKLNEYFDLLRAKLNDVCANDYCQIPENLKIRANE 213	OY 118 SDSDAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFK 165	Query Match 5.3%; Score 442.5; DB 2; Length 3973; Best Local Similarity 20.6%; Pred. No. 3.1e-06; Matches 394; Conservative 262; Mismatches 571; Indels 689; Gaps 94;	C;Accéssion: B71612 R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O. Science 282, 1126-1132, 1998 A;Title: Chromosome 2 sequence of the human malaria parasite plasmodium falciparum. A;Reference number: A71600; MUID:99021743; PMID:9804551 A;Accession: B71612 A;Status: preliminary: nucleic acid sequence not shown; translation not shown A;Residues: 1-3973 <gar> A;Cross-references: GB:AE001402; GB:AE001362; NID:g3845213; PIDN:AAC71900.1; PID:g384521 A;Experimental source: clone 3D7 C;Genetics: A;Gene: PFB0555c C;Superfamily: Plasmodium falciparum hypothetical protein PFB0555c</gar>
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1856	809 FLFINYKKKEYIEEKKNGNQNVINIKDEDKHITNIK-DGDKHITNIKDG	- سر	
1573	DGNLQGMLNISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPT	0у 1:	
1808	760NEEQKNNELISYPYNNMLQNNIIFVKFFLYTQNLLQIIFQNNYIFFLSD	Db 1	
1515	67 QDKLADFKKNNNFVGIADLSTDYNHNNLLTKFLSTGMVFENLAKTVLSN	Оу 14	
1759	712FNNIKNEEENILLQNNSMSSSIYIDKKLMKDTKEMEDLFNKTKDMKNY	Db 1'	
1466	TLYKTVNDKIDLFVIHLEAKVLNYTYEKSNVEVKIKEL-NYLKTI	Qy 1,	
1711	659 VFNKPFDNNNNNNNNNNNNNNNNNNNTPNYIPENNNNNYRMDIKKRYPPESYDNNYYM	Db 1	
1415	360 KELSSYNYIKDSIDTDINFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYL	0у 1:	
1658	624 LMNNHYTMNY-LTDVMLLQKDYIYNIDNNMNEHKQN	Db 1	
1359	LNSRFNKRENFKNYLESDLIPYKDLTSSNYVVKDPYKFLNKEKRD	Qy 1:	
1623	580 DVFNEIMRNIIINHNSLIKDHNDMCTKKKRINIFQISSPATSEQ	Db 1:	
1299	GEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQ	Qy 1:	
1579	546 SYRGEEKDTLDVINTESVHQNRNEDDIDGSINSL	Db 1:	
1243	184 SYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIV	Qy 1:	
1545	97 -YINLERVKQVFYEHNIMMDVHMKSHLHHDIDVYYGHDNSYNNI-YQKIIK	Db 14	
1183	IAELKEVIKNKNYTGNSPSENNTDVNNALE	0у 1:	
1496	437 NEDNEFESIESKYINKIEVEIYSSSSSSTSSNSSEVENVSKEYMMKMCISIINNMIGVVK	Db 1	
1133	083ILLKHY-KGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLK	0у 1	
1436	391 NREKNINIKKLVKLFFISFYKYLKNYFLQIYYHFFYNNQIYNRKNY	Db 1:	
1082	030MQIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENTLENTK	0у 1	
1390	331 ICTSLLLKIFKRIIKKKSNSYFLFNIYKAFENDIKLILDSINILIKKWVVWTFKNCDNIF	Db 1:	
1029	KKKTVGKYK	ν.	
1330	271 HLPNFEKSYNINYVVEDISFDDIFLISIMDLWETNNNNNLLNLINDLLKIYEEEKKKKIY	Db 1:	
991		Qy	
1270	213 NNSSNNSSNNSSNNSSNRSSGRNNSSDEVVVDPYDYNNYYECKDSNKFGVVVNYFYA	Db 1:	
965	YNE	Qy	
1212	161 DNNKYNDGNTFLSSQDEEKSKSFDSSDSCSVDEKESSKGLYGNDFVNSSDHN	Db 1:	
913	LSLTPQDKPEVSANDDT	Qy	
1160	103 DIKENFRIDISFLKIFFLLNDVRQINLNESNGRKDKLESKAKRRIQKLDVHRYTYNEN	Db 1:	
867	DSLNNSLSQLYKLK	Qy	
1102	054VSNLYRDIENEYDENHLERRKDRNVFSSNMNDDKKYNNLSDFKYTKEN	Db 1	
823	773 DYLEKLYEFLNTSYICHKYILVSHSTMNEKILKOYKITKEEESKLSSCDPL	Qy	
1053	028VHRKSSKYHRNNQEEYSHNNKTNDNS	Db 1	
772	713 ATTKPGQQAGSALEGDSVQAQAQEQKQAQPPVPVPVPEAKAQVPTPPAPVNNKTENVSKL	Qy	
1027	983 RFQIMIVRCLSFLLKKKNINKLNAYIFQLFSYLENDQININEKGM	Db	
717	660IVLAKETUKEKVEMENVESELNEEKKNIKTEGQSUNSERSTEGELTGQ	VΥ	

Qy 506 LTNFEKMMGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELK 565	Oy 273 EEKKKLYOAQYDLSYINKOLEEAHNLISVLEKRIDTIKKNE-NIKELLDKINEIKNPPPA 331 Oy 274 EEKKKLYOAQYDLSYINKOLEEAHNLISVLEKRIDTIKKNE-NIKELLDKINEIKNPPPA 331 Db 352LQQENELFAKHLEHQQNEFEQKQSDSLLKKLEŢEYKALQHKINEFKN 397 OY 332 NSGNTPNTLLDKKIEEHEKEIKEIAKTIKFNIDSLFTDPLEIKYYLREKKNIDISAK 391	Query Match 5.2%; Score 440; DB 1; Length 1805; Best Local Similarity 19.7%; Pred. No. 1.5e-06; Matches 334; Conservative 301; Mismatches 566; Indels 492; Ga 133 RNYLLTI	Science 270, 397-403, 1995 A;Title: The minimal gene complement of Mycoplasma genitalium. A;Reference number: A64200; MUID:96026346; PMID:7569993 A;Accession: A64224 A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-1805 <tigr> A;Cross-references: GB:U39699; GB:L43967; NID:g1045903; PID:g1045905; TIGR:MG218 A;Enentics: A;Genetics: A;Genetics: GG3 C;Superfamily: Mycoplasma genitalium hypothetical protein MG218</tigr>	Oy 1574 CNENNGGCDADAKCTBEDSGSNGKKITCECTKPDSYPLFDGIFCSSSNFL 1623
OY 1363 SSYNYKOSIDTDINFANDVLGYKILSEKYKSDLDSIKK 1402	1318 HELSNETERKRAVLEDQISYFEKQRKQATD-AILASHKEVKKKEGELQK 1225 NTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDN 1225 NTITTSQNVDDEVDDVIIVPIFGESEEDYD		832 921 892 963 935 1023	Db 694 KEIEATEKOLLNDVNNAEVIQADLAQLNQSLNQERSELQNÁKORIADFHNDSLKKL 749 Qy 705 TEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQAQPPVPVPPEA 751

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interaptin - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C;Accession: T14867
R;Rivero, F.J.; Kuspa, A.; Brokamp, R.; Matzner, M.; Noegel, A.A.
J. Cell Biol. 142, 735-750, 1998
A;Title: Interaptin, an actin-binding protein of the alpha-actinin superfamily in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: Z18248; MUID:98365468; PMID:9700162
A;Accession: T14867
A;Accession: T14867
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1738 <RIV>
A;Cross-references: EMBL:AF057019; NID:g3549260; PID:g3549261; PIDN:AAC34582.1
C;Genetics:
A;Gene: abpD
A;Introns: 173/2; 1680/1
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Best Local Simi
Matches 302;
1011 IQQLQSQLNEQRQ-----QQSNQLSEKDQQLNQLIEKNQFDQKEQQLKQQSIENDLFEK 1064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFDYTKEPSKNIYTDNERKKFINEIKEK----IKIEKKK----IESDKKSYEDR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKNKNIDISAKVETKESTEPNEYPNGVTYPLSYND----INNALNE---LNS-FGDLIN 431
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                                               MPKVESLINEEKKNIKTEGQSDNSEPSTEGEIT-----GQATTKPGQQAGSALEGD----
                                                                                                                                                                                                                                                                              KDHQDQLELLEKQLKQLQQEYDQLNETNQSIENQLNQQNLINKENLNEKEQELLKLQNQL
                                                                                                                                                                                                                                                                                                                                                                   QLSSNSNIDQQLQSTIIELSELKEQKELNDSKLIEKEKQL-QQLQQEFDQLNEKN----Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKDKEIE----KLSNQQEQQQDEKINNLLLEIKEKDCLIERINQQLLENIDLNSKYQQLLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QATNSELMEKIGGLMNDLTDIPTQDIKEKD--EIIANLKIESEKNLKCFQDDFNALQSRY
                                                                                          ENQLKSIQNELN-----QLIEKN-ESDHK------EQQLKQQSIENDLIEKENQ-----
                                                                                                                                       QVQKVLLMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVF
                                                                                                                                                                                    NQQIEKIQFDQQEFSKQNSINIELVNEKNEKLIQLQQDYDQLKQQNRSNDEKDENDLIEK
                                                                                                                                                                                                                                 ETLVENIKKDEEQLFEKKITKDE--NKPDEKILEV-----
                                                                                                                                                                                                                                                                                                                           ENSKHNLEKLTKALKYME-----DYSLRNIVVEKELKYYKNL-----ISKIENEI 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFENFK-----LNSSKEKENQLNELQSKQDERFNQLNDEKLEKEKQLQSIEDEFNQYKQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.2%; Score 438; DB 2; I illarity 21.0%; Pred. No: 1.7e-06; Conservative 254; Mismatches 528;
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PQ0120 RESULT 46

C;Accession: PQ0120
R;Kimura, E; Mattel, D.; di Santi, S.M.; Scherf, A.
Gene 91, 57-62, 1990
A;Title: Genetic diversity in the major merozoite surface
A;Reference number: PQ0120; MUID:90382698; PMID:2205540
A;Accession: PQ0120. major merozoite surface antigen - malaria parasite (Plasmodium falciparum) N;Alternate names: gp195, PMMSA, PSA C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jun-2000 - malaria parasite (Plasmodium falciparum) (isolate $\ensuremath{\mathsf{PSA}}$ antigen of Plasmodium

falcı

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C;Superfamily: major meroz
C;Keywords: glycoprotein; A;Molecule type: DNA A;Residues: 1-144 <KIM> A;Cross-references: GB:M32111; NID:9160490; PIDN:AAA29701.1; C;Superfamily: major merozoite surface antigen PID:g552211

Query Match 5.2%; surface antigen Score 435.5; Pred. No. 1.2 5; DB 2; 1.2e-07; hes 24;

30 KKLEALEDAVLTGYSLFQKEKMVLNEGTSGTAVTTSTPGSKGSVASGGSGGS-VASGGSV 88

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Matches

Local

Similarity

Conservative

8;

Mismatches

Indels Length 144;

21;

Gaps

5,

Db 151	SDSDAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEINE :	Surface-located membrane protein lmp3 precursor - Mycoplasma hominis C;Species: Mycoplasma hominis C;Species: Mycoplasma hominis C;Species: Mycoplasma hominis C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000 C;Accession: JC6009 R;Ladefoged, S.A.; Jensen, L.T.; Brock, B.; Birkelund, S.; Christiansen, G. J. Bacteriol. 178, 2775-2784, 1996 A;Title: Analysis of 0.5-kilobase-pair repeats in the Mycoplasma hominis lmp gene system A;Reference number: JC6009; MUID:96213016; PMID:8631664 A;Accession: JC6	Db 1 KKLEALEDAVLTGYGLFHKEKMILNEEEITTKGASAQGSSGFSGTSG 51 Qy 89 ASGGSVASGGSVASGGSGNSRRINPSDNSSDSDAKSYADLKHRVRNYLL 137
Qy 1310 NVKDILN	1080	528 N 766 T 766 T 826 L 637 - 674 L 945 Q 997 L 1035 - 837 K	Qy 550 MEDYSLRNIVVEKELKYYKNLISKIENEIETLVENIKKDEEQLFEKKI 597

23	O1 ENKPDERILEVSDIVKVQVQKVLLMNKIDELKTQLLILKNVELKHNIHVPNS 652	Oy 60:
4	05 LDKYQKLENYGQVLGLILKDNSDAIATKVQAIFKDVVNEANFQDVLKVLLVSQTKKFMGF 1164	Db 1105
	8 IVVEKELKYYKNLISKIENEIETLVENIKK	Оу 55
4	11 KMMGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRN 557 	оу 511 рь 1050
φ ⁻	EKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFE 	
	84 KNIDISAKVETKESTEPNEYPNGVTYPLSYNDI 416 	Qy 384 Db 879
	53EIKEIAKTIKFNIDSLFTDPLELEYYLREKN 383 	Qy 353 Db 819
œ Ñ	102 INEIKNPPPANSGNTPNTLLDKNKK	Qy 322 Db 769
\	63 IDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLI-SVLEKRIDTLKKNENIKELLDK 321 : : : : : : : :	Qy 263 Db 714
	26 - KPLDNIKDN VGKMED YIKKNKKTIEN INELIEESKK 262 	Qy 220 Db 65
	72 EEINELLYKLNEYFDLLRAKLNDVCANDYCQIPFNLKIRANEL-DVLKKLVFGYR 22 	Qy 17:
	19 DSDAKSYADLKHRVRNYLLTIKELKYPQLEDLTNHMLTLCDNIHGFKYLIDGY 171	Qy 119 Db 544
88	Match 5.2%; Score 434.5; DB 2; Length 2819; Local Similarity 19.7%; Pred. No. 3.8e-06; ess 371; Conservative 299; Mismatches 614; Indels 599; Gaps	Query Ma Best Loo Matches
N00153	9M.D:11353084 727; PIDN:CAC13486.1; GSPDB:G	A; Reference A; Accession A; Status: p A; Molecule A; Molecule A; Residues: A; Cross-ref A; Experimen C; Genetics: A; Gene: MYP A; Genetic C
F.; Moszer, I.; Mycoplasma pulm	on: A90551 d, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; G cids Res. 29, 2145-2153, 2001 The complete genome sequence of the murine respiratory	C; Access R; Chambau Nucleic 1 A; Title:
(strain UAB CT	48 ved hypothetical protein MYPU_3130 [imported] - Mycoplasma pulmonis les: Mycoplasma pulmonis : 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-200	RESULT 48 A90551 conserved C; Species C; Date: 1

1460L																																			
460L	DP 65	рь	Qy	Db	Qу	Db	Qγ	DЬ	Qy	Db	Qу	Db	Qy	Db	Qy	DЪ	Ωу	DЬ	Qy	Db	VΩ	Db	VΩ	Db	Qγ	Db -	Qγ	В	Qy	Db	γQ	Db	ν	망	Qy
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STDYNHNNLLTKFLS-TGMVFENLAKTVLSNL	NEKYLPFLNNIETLYKTVN -DKI -DLFVIHLEAKVLNYTYEKSUNVEVKIKE 1 : :	-EKLLKNTSVQNFVKDKFIENISKSIPIEQNN	TDINFANDVLGYYKILSEKYKSDLDSIKKYINDKQGE	NPQSKTNDLFASIQEILKSKFDFSQNGLFEVLSIILKSNILDSKSINNKEYIQKVKT 2	IPYKDLTSSNYVVKDPY		NEYEVLYLKPLAGVYRS	LKTEVN				TKVEIFNFSSLLKPIMDQKDNYFSLVKTLATINWKLMESQNTDALKNAL 1	KLSYLSSGL	-LKKSKITLQNDEIDSIVNFVNESLVVLEKTDLIDKLYDLVVSSFNAKVSDK 1		VVSQKE-EYSKLNSYQEILYKFLSSNKNETLNFFKKQIGEIKNSKLINPLAKSFIESE 1	z	SISSILRVFLRKEKALELMLKKQFRNFELHDIKVDDAINLIKFIFRDNQVIDFIETIINR 1	INSLNDESKRKKLEEDINK		NKNIYQELIGQKSSENFYEK	: LNQLLKDFFALLEKNK		KFSAQIIDTIFANKNKYLAYENLNDFLIDALVDNKENIINLSSNTLGKIKTDDE 1		AKNDYLLTKFISPIVDKTIDFDSATKSSIVKLIKNVLSDEQNL		ISNLYDLVLSALSINQESSSVLTKVENITHKALDQQNSYFAVIKTLLSVKEGDV		NKETVVNYLKELSFEIKSSNIIQRLLGQTINALVTPNGEKIFSDTELQSLSTLINESLDL 1		: LSKEKLASAYTPVYEFVKFYLKNEKTTNFSDLLIDSLFKDFSQYQQANSFEELIYLVLRN 1		SQNSESIKNLLKTFTKSALSRDEFYEKTIKVF	
516	1459 2223	2169	1410	2136	1350	2079	1295	2026	1249	1966	1196	1906	1150	1857	1098	1806	1047	1749	996	1689	954	1637	911	1577	871	1523	816	1463	769	1403	740	1343	689	1283	677

Qy 561 EKELKYYKNLISKIEMETETLVENIKKOEEQLEKKITKDENRDEKILEVSDIVKVQVQ 620 1	34 KKKIEEHEKEIAKTI-KENIDISAKVETKENIDISAKVETKENIDISAKVETKENIDISAKVETKENIDISAKVET	Query Match 5.1%; Score 433.5; DB 2; Length 1365; Best Local Similarity 21.1%; Pred. No. 1.8e-06; Matches 318; Conservative 251; Mismatches 530; Indels 411; Gaps 74; Qy 129 KHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEIN 175 : : : : : : : : : :	Db 2224 QLLAYLKSIINKLNVKVYSELH-DFSVNVLLSQLKSKMNIEFNNKEKE 2269 Qy 1517 LDGNLQGMLNISOHQCVKKQCPQ 1539
RESULT 50 E71606 E71606 Aypothetical protein PFB0765w - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000 C;Accession: E71606 R;Gardner, M.J; Tettelin, H.; Carucci, D.J.: Cummings, L.M.; Aravind, L.; Koonin, E. ; Pertea, M.J; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H. Science 282, 1126-1132, 1998 A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.	2 4 2 4 1 3 1	Qy 1065 KKREABIASTENTLENTKILLKHYKGLYKYNGESSPLKFLSEESIQTE 1113 Db 849 KLETTKNKLABELTKADAIKNNPSSSKOALKDSSQOVOKLGNELLKTITEEFGKVETK 906 Qy 1114 DNYASLENFKV	QADNLAKSIKEQL

Qy 8	Db 6	Оу в	0y , 7	Qy 6 Db 6	_		5 04	Qy 5 Db 4		0у 4	Db 3		Qy 4 Db 2		Qy	О У	Qy 2 Db 1	Db Cy	Qy 1	Query M Best Lo Matches	A; Reference A; Accession A; Accession A; Accession A; Molecule A; Residues: A; Cross ref A; Experimen C; Genetlcs: A; Gene: PFB C; Superfami	
62 NLYKLKONDKIKNLLBEAKKVSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTN 918	:: 87 KKKEEINKLV	804 LKQYKITKEEESKLSSCDPLDLLFNIQNNIPYMYSMFDSLNNSLSQLFMEIYEKEMVC 861	746 VPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTWNEKI 803 :	:86 NEEKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQAQPPVP 745 : :		29 DELKKTQLILKNVELKH	89 EEQLFEKKITKDENKPDEKILEVSDIVKVOVQKVLLMNKI	338 HNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEIETLVENIKKD 588 : : :	97 KKKCIENLKDELINIKKKMEDKMHMTNEMDLLSNKVEELNRINKTYEKNIVELN 4	188 YEKLLNETYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSK 537	ωu	7.0	108 TYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIK 457 10		352 KEIKEIAKTIKFNIDSLFTDPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGV 407	307	279 YQAQYDLSIYNKQLEBAHNLISVLEKRI 306 : : : : :	232 KDNVGKMEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKL 278	176 ELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNI 231 :	, Match 5.1%; Score 431; DB 2; Length 980; Local Similarity 23.1%; Pred. No. 1.5e-06; Pre	A;Reference number: A71600; MUID:99021743; PMID:9804551 A;Accession: E71006 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-980 <gar> A;Cross-references: GB:AE001417; GB:AE001362; NID:g3845271; PIDN:AAC71942.1; PID:g384527 C;Genetics: A;Experimental source: clone 3D7 C;Genetics: A;Gene: PFB0765w C;Superfamily: hypothetical protein MJ1322</gar>	

QY 1081 TKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGK 1131
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                                                                                                                 -KQGENEKYLPFLNNIETLYKTVNDKID-----LFVIHLEAKVLNYTYEKSNVEVK 1456
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YIL149c

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yeast (Saccharomyces

cerevisiae)

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A;Cross-references: GB:Z47047;
C;Genetics:
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A;Cross-references: SGD:S0001411
A;Map position: 9L
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A; Residues: 1-1679 <
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                                                    RIKIKSLEYEISKLKKETASFIPTKESLTRDFEQC------CKEKKELQ----M
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19 7%; Pred. No. 4.8e-06;
ative 296; Mismatches 583;
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RESULT 53
$41649
DNA polymerase - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:Date: 20-May-1994 #sequence_revision 26-May-1995 #text_change 0
C:Accession: $41649
R:White, J.H.; Kilbey, B.J.; de Vries, E.; Goman, M.; Alano, P.;
Nucleic Acids Res. 21, 3643-3646, 1993
A;Title: The gene encoding DNA polymerase alpha from Plasmodium fa;Reference number: $41649; MUID:93376482; PMID:8367280
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                                                                                                                                             KKQCPQNSGCFRHLDEREECKCLLN---YKQEGDKCVENPNPTCNENNGGCDADAKCTEE
                                                                                                                                                                                              PLISKKYIYLILEYFLF - - LLKDNL - KKIPSNLVEKNKSEQLNETQDTNNENDITSNQKE 1686
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myosin heavy chain - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YHR023w; type II myosin
C;Species: Saccharomyces cerevisiae
C;Date: 07-Oct-1994 #sequence_revision 11-Aug-1995 #text_change
C;Accession: S46773; S05806; S12323
R;pu, Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-45, 'T', 47-58, 'S', 60-329, 331-342, 'S', 344-528, 'ARGHDR', 536-540,
A; Cross-references: EMBL: X06,187; NID: g4015; PIDN: CAA29550.1; PID: g4016
R; Sweeney, F.P.; Watts, F.Z.; Pocklington, M.J.; Orr, E.
Nucleic Acids Res. 18, 7147, 1990
A; Title: The MY01 gene from Saccharomyces cerevisiae: its complete nucleotic A; Reference number: S12323; MUID: 91088308; PMID: 2263482
A; Accession: S12323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Keywords: actin binding; ATP; coiled coil; nucleotide F;78-779/Domain: myosin motor domain homology <MMOT> F;180-187/Region: nucleotide-binding motif A (P-loop) F;459-528/Domain: actin binding #status predicted <ACB> F;186/Binding site: ATP (Lys) #status predicted
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C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Superfamily: myosin heavy chain; myosin motor domain homology
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EMBO J. 6, 3499-3505, 1987
A;Title: The yeast MYO1 gene encoding a myosin-like protein
A;Reference number: S05806; MUID:88111539; PMID:3322809
A;Accession: S05806
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A;Residues: 1-1928 <DUZ>
A;Cross-references: EMBL:U10399; NID:g500689;
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A; Accession: S46773
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                                                                                         DPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSF----
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  GDLINPFDYTKEPSKNIYTDNERKKFINEIKEK---
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Pred. No. 6.2e-06;
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                                                                                                                                         -LIKESKLKLENEIKRLKDVINSKEEEIKS-FN
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; PMID:2263482
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                                                                                                                                                                                                 RENKRENEKNVLESDLIPYKDLTSSNYVVKDPYKELNKEKRDKFLSSYNYIKDSIDTD-I 1376
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                       IHLEAKVL-NYTYEKSNVEVKI 1457
                                                                 ELANKNRSEFEEATLKYEAQISDLEKYISQQELEMKKSIRDNSSYRDKVQEMAQEIEFWK
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                                                                                                           NFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLFV 1436
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A;Molecule type: DNA
A;Residues: 1-4550 <LAW>
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submitted to the EMBL Data Library,
A:Reference number: Z18935
A:Accession: T18440
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                                                                                                                                       EIAKTIKFNIDSLFTDPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KNENIKEL------DKINEIKNPPPANSGNTPNTLL-----DKNKKIEEHEKEIK
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                                                              EQLFEKKITKDENKPDEKILEVSDI~VKVQVQKVLLM~----
                                                                                                                                                                                                   ETKCIMKNNVCDGIYYLIRQENGLNICQKVNNNI----IKNKMKQEKFYKKKKQNKNN--
                                                                                                                                                                                                                                           EDRSKSLNDITKEYEKLLNEIYD----SKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTF
                                                                                                                                                                                                                                                                                       NDDDNNNNNN-----NDDDNNKDPT----LDGETRSYIDEINQKEINIFSKYIDKIIENV
                                                                                                                                                                                                                                                                                                                                    INNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKEK · IKIEKKKIESDKKSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KETHKNEIDHKEQKDTNCDNGIEEKKDQVSKSNNIISKVFHFFERKNNNIKKDEHKKEYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKLVFGYRKPLDNIKDNVGKMEDYIKKNKKTIENIN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389;
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19.1%;
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Pred. No. 1.8e-05;
38; Mismatches 679;
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pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria A; Reference number: A71600; MUID:99021743; PMID:9804
A;Accession: B71616
A;Status: preliminary; nucleic acid sequence not sho A;Molecule type: DNA
A;Residues: 1-2010 <GAR>
                                                                                                                                                                                                                                                              phosphatase (acid phosphatase family) PFB0380c - malaria parasite (Plasmodium C;Species: Plasmodium falciparum C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000 C;Accession: B7166 R;Gardner, M.J.; Tettelin, H; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Kooi
                                                                                                                                                                                                                                                                                                                                                                                 RESULT 57
B71616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-89 < HUI>
A; Residues: 1-80 < HUI>
A; Residues: 1-80 < HUI>
A; Residues: 1-80 < HUI>
A; Residues: 1-80 < HUI>
A; Note: sequence inconsistent with the nucleotide translation
A; Note: sequence extracted from NCBI backbone (NCBIN:89242, NCBIP:89243)
C; Superfamily: major merozoite surface antigen
                A; Experimental source: clone C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Roles of conserved and allelic regions of the major merozoite surface protei A;Reference number: A43854; MUID:92192814; PMID:1548068 A;Accession: A43854 A;Status: preliminary
                                        A; Cross-references: GB:AE001391;
A; Experimental source: clone 3D7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASGGSVASGGSVASGGSGNSRRT 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGTAVTTSTPGSKGSVASGGSGGSV 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASGGSVASGGSGASGGSVASTGSGNSRRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                             Tettelin, H; Carucci, D.J.; Cummings, L.M.; alzberg, S.; Zhou, L.; Sutton, G.G.; Clayton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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97.8%;
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                                                               GB:AE001362; NID:g3845168; PIDN:AAC71865.1; PID:g384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 417; DB 2; pred. No. 2.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89
                                                                                                                                                                       n malaria parasite
PMID:9804551
                                                                                                                                 shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 89
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                                                                                                                                 translation not shown
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                                                                                                                                                                                                   Plasmodium falciparum
                                                                                                                                                                                                                                             Aravind, L.; Koonin,
R.; White, O.; Smith
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	NNSLKLFENILSLGKNKNIYQELIGQKSSENFYEKIL 956	EVSANDDTSHSTNL	906	ρ
	VCNLYKLKONDKIKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQDKP 905	YEKEM : : RKKDMKIPPFASFI	1401	₽ &
	KEBESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLS-QLFMEI 854	S HSTMNEKILKQYKITKEEESKLS : : :: :: : : : S NFIINVRLYEKYNKENKTT	796 1356	g Qy
	VSKLDYLEKLYEFLNTSYICHKYILVS 795	QVPTPPAPVNNKTENVSKL :: : TNDQTNDQTN-	754 1305	B 6
	:	TNEQ	12	B 2
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	KDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLI 63 CHNKTNSSNTLQGNDREANILDADERDRLKRNKNI 12	EEQEEQ - - EEQNNFIIKRPNIN	117	B 8
	YMEDYSLRNIVVEKELKYYKNLISKIENEIETLVE-NIKKD 588 	EKLTKALK : : : KIIKKFIS	541 1115	ρ γ
	NNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSKHNL 540	KLLNEIYDSKFN-	1060	B 8
	NERKKFINEIKEKIKIEKKKIESDKKSYEDRSKSLNDITKEYE 489 	m D	1000	. D 0y
	KESTEPNEYPNGVTYPLSYN-DINNALNELNSFGD-LINPFDYTKEPSKNIYT 445;	ы н	394 948	DP QA
	NTPHTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKNKNIDIS-AKVE 393 ::		335	P Q
	QLEEAHNLISVLEKRIDTLKKNENIKELLDKINEIK-NPPPANSG 334 : : :	KKIH	276 855	B 6
	DYIKKNKKTIENINELIEESKKTIDKNKNATKEEEK 275 :: : : : :	DNIKDNVGKME : LNEFSKFFKLF	796	д 9
	INELLYKLNEYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPL 228	z d	173 739	용 왕
	ADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYE 172	SDAKSY : : NDYKSH	690	요 양
	SVASGGSGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSD 119	TAVTTSTPGSKG	668	B 6
	SFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSG 59 :	KITEC	625	β δ
87;	20.0%; Pred. No. 1.1e-05; ive 283; Mismatches 588; Indels 516; Gaps	ocal Similarity ; 347; Conservat	Best Lo Matçhes	

ps 72;	Query Match 4.9%; Score 412; DB 1; Length 3259; Best Local Similarity 19.8%; Pred. No. 2.2e-05; Matches 314; Conservative 301; Mismatches 592; Indels 376; Ga	
	Gene: Gene: Cross Map p Super Keywc	ECCAPA(
715	5714; PIDN:CAA53052.1; PID:g405	
membrane protei	376-kilodalton Golgi complex 3; PMID:7511208	>
Renz, M.	;Accession: Asossy; ss/sso ;Seelig, H.P.; Schranz, P.; Schroeter, H.; Wiemann, C.; Griffiths, G.; Cell Biol 14 2564-2576, 1994	₹ ₹J (;
1999	N;Alternate names: macrogolgin C;Species: Homo sapiens (man) C;Date: 19-Oct-1995 #sequence_revision 26-Jan-1996 #text_change 10-Dec-	000×4
	ESULT 58	A5
	1967 DKKIKKR	Db
	1518 DGNLOGMLNISQHQCVKKQCPQNSGCFRHLDEREEC	Qγ
1966	b 1936VVSENSCSDVITSLK	рb
1517	1458 KELNYLKTIQDKLADFKKNNNFYGIADLSTDYNHNNLLTKFLSTGMYFENLAKTVLSN	γо
1935	1902 QKYINDHNNINSYDNNINNGLINE	Db -
1457	1402 - KYINDKQGENEKYLPFLNNIETLYKTVNDKIDLF	ΟУ
1901	1851 I	Db
1401	1342 SNYVVKDPYKFLNKEKRDKFLSSYNYIK	VΩ
1341 1850	y 1288 PLAGVYRSLKKQLENNVMTFNVNVKD-ILNSRFNKRENFKNVLESDLIPYKDLTS	Db Db
1802	b 1757 KSNIHNNSSKYIFNTVRFFKMKDIAKINTNKKCDENSISCINNMRE	DЬ
1287	1238 DDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIENEYEVLYLK	Qy
1756	1710 NNICLKNNKNNIMHEDINANKRESLKKKKKKKKKNCIQKNNNICERK	뫄
1237	1178 VNNALESYKKFLPEGT	γо
1709	1660 -	Db
1177	1118 SLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSDSENNTD	γο
1659		망
1117	1066	Qγ
1612	 1566 NKKY	Db .
1065	1010KYKLKLERLFDKKKT	Qy
1565	: 1512 KNK	рь
1009	957	Qy
1511	1459 HASSRSVHVNQTDRTDVLSFIYHNNTANIFCCKDDCVWKVRETENEKKFEKCR	DЬ

1661	KHKELQKEYEILLQSYENVSNEAERIQHVVEAVRQEK	Db
1122	KGLVKYYNGESSPLKTLSEESIQTEDNYASL	Qy
1601	1562 NOSLSSSCESLKLALEGLTEDKEKLVKEIESL	Db
1074	1015 LERLFDKKKTYGKYKMQIKKLTLLKEQLESKLNSLNNPKHYLQNFSVFFNKKKEAEIAET	Qy
1561		Db
1014	963 YNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLK	Qy
1508	1468 PE-EIGEESRAKQQIQRKLQAALISRKEALKENKSLQEELSL	В
962	905 PEVSANDDTSHSTNINNSLKLFENILSLGKNKNIYQELIGQKSSENFYEKILKDSDTF	Qy
1467		
904	852 METYEKEMVCNLYKLKDNDKTKNLLE-EAKKVSTSVKTLSSSSMQPLSLTPQDK	, V
1412	1359 -VSHEAEVHAESLQQKLESSQLQIAG-LEHLRELQPKLDELQKLISKKEEDVSYLS	
851	-STMNEKILKQYKI	Qy
1358	1310 QLKEIEAEKVELELKVSSTTSELTKKSEEVFQLQEQINKQGLEIESLKT	Вb
792	Ş	Оу
1309	1250 STDQQESCSSTPGLEEPLFKATEQHHTQPVLESNLCPDWPSHSEDASALQGGTSVAQIKA	
736	704 STEGEITGQATTKPGQQAGSALEGDSVQAQAQE	Qy
1249	: :: : : : : : : : :	Db 1
703	655 QENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEP	9
1206	SPPCTGSSEHWKPELEEKILALEKEKEQLQKKLQEALTSRKAILKKAQEKER-HLREELK	-
654	614IVKVQVQKVLLMNKIDE-LKKTQLILKNVELKHNIHVPNSYK	Qy
1147	88 EQFQALVKQMNQTLQDKTNQIDLLQAEISENQAIIQKLITSNTDASDGDSVALVKETV	
613	닺	Qy
1087	037 VEEDKENKEYSEKCYTSKCQEIEIY-LKQTISEKEVELQHIRKDLEEKLAAE	Db 1
575	KLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYY	Qy
1036	SRLEEELANLKDESKKEIPLSETERGE	В
520	467 IESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYK	Qy
976	LNEEKFSLGVEIKTLKEQLNLLSRAEEAKKEQVEEDNEVSSGLKQNYDEMSPAGQISKEE	Db 5
י ע י ע	13 VNDTNNATN-ETNGEGOT INDEDVYKKENGENSKKETNETKEKKK	
916	ISSKVEELSQALSQKELEITKMDQLLLEKKRDVETLQQTIEEKDQQVTEISFSMTEKMVQ	₽,
412	AKTIKFNIDSLFTDPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTYPL-S	Qγ
Ci	97 QIHSLSIEAKSKDVKIEVLQNELDDVQLQFSEQSTLIRSLQSQLQNKESEVLEGAERVRH	망
356		Ωy
796	37 SAFTALSEERDQLLSQVKELSMVTELRAQVKQLEMNLAEAERQRRLDYESQTAHDNLLTE	Db ·
300	68 NATKEEEKKKLYQAQYDLSIYNKQLEK	VQ.
736		Db ?
267		Qy

Qy 230 NIKDNVGKMEDYIKKNKKTIENINELIEESK	OY 194 DVCANDYCQI-PF	QY 141 ELKYP-QLFDLTNHMLTLCDNIHGFKYL-IDGYEEINELLYKLNFYFDLLRAKLN	Query Match 4.9%; Score 411.5; DB 2; Length 1516; Best Local Similarity 21.3%; Pred. No. 9.6e-06; Matches 363; Conservative 262; Mismatches 559; Indels 523; Go	Oy 1531 OCVKOCPO-NSGCFRHLDERE 1552	Db 1888 QEEVTKMILLNOQIQEELSRVTKLKETABEEKDDLEERLMNOLAELNGSIGQy 1376 INFANDVLGYYKILSEKYKSDLDSIKKYINDKOGENEKYL	1231 QNVDDEVDDVIIVPIFGESEEDYDDLG	Qy 1123 KVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSE
K SLIQIYDDI	.VFGYRKPLD 229 :	FYFDLLRAKLN 193 LYFFFLR 89			LAELNGSIG 1938PFLNNIET 1423		GNSPSE 1173 ::

1213	56 ELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSESGSDTLEOSQPK	11:	ρ
1139	ū	110	р
1155	NYASLENFKVLSKLEG	109	Qy
1102		105	DЬ
1095		1037	Q
1050	KKG	9	Db
1036	INKLKKT	99	Qy
996	6	94	Db
886	QKS	9.	Qy
945	93 DKIKEKEKNNDTSSDDFENCSVQEKIYVNEKIEEYNNKNDDKSSSSSSIILEE-	89	рь
928	0 DKIKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQDKPEV-SANDDTSHSTNLNNSLKLE	87	9
892	5NNENKSLYEDGENFITRNEPITNEYEEKNNIIYISDEQKYNEEDII	84	В
869	2 NIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKDN	83	οy
844	KDLLLDDSQIFGDSLLADIKEYNYTAD	814	D
831	72 LDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLFNIQN	77	Qy
813	74 KYEIYNLELEQEEINEKKNYNKNNND	77	망
771	pvpvpvpeakaqvptppapv	71	Qy
773	34 EDIKNQIDEVTQECYRNNDIIRDTHDKSDIFKNIKIDNN	7:	망
716	AITAA	6.	Qy
733	4 LINKDLSKNTDNINIKDYNVLQKKKSKKKKKFLNDILNTYNFTTESKYQDL	67	Db
658	09 LEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELKHNIHVPNSYKQENK	60	Qy
673	6 KEEWYTDNRIKAIKSKDDMD	61	Db
809	62 KELKYYKNLISKIENEIETLVENIKKDEEQLFEK-KITKDENKPDEKI	56	Qy
615	64 LDTSNIFLEGKDEYKVYYVNKEEIRIPLFKEINKEIFEKLPLKLQYQILQDI	5	Db
561		5(Qy
563	ECSSEKINDNGISNKNINILELF	50	рь
503	5	47	Qy
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443		32	Db
447	KNDINNALNEL	4.	Qy
383	24 KNKENINNIYLDDDDEKEDIQNKNGVYNNDDIDEQIIRKKHMARKKYYESIPKTFKGFLC	ω	Ъ
409	60 TIKFNIDSLETDPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTY	36	Qy
323	69 ENINKLDNRNKDENNLSYSINYNKVQDVNNNNDDDKDKDKENINEVRRDQKNYVY	26	Db
359	04KRIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKK-IEEHEKEIKEIAK	3	Ş
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Db 1489 NPAGIIKSKRMSSALDHIKRRKSSK 1513
QY 1528 SQHQCVKKQCPQNSGCFRHLDEREECK 1554
Db 1444 FFPLLEKKRKTVDDLIDHIRANNKQKRQKNKTVHLDSKISPLIDI
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Db 1400 DIKSITKFLHKTTNISEEKVLNVLNPILQKYNVNVRTYQSKIED 1443
QY 1417 FLNNI-ETLYKTVNDKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLAD 1472
Db 1352 EIQQFLNTHKNYKLNWIFPNNFPDREVYKCFKYPKVCTDIKKFEWHVP
QY 1357 KRDKFLSSYNYIKDSIDTDINFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLP 1416
Db 1301 CGCDYTIGVHGIGIVNA-LEIIKAFPNFEDLKILKDIVSNPFRKIDKNMYNE
Qy 1306TFNVNVKDILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKE 1356
Db 1250 ISDDSDVLVFSGKTVIKNFFNKKKTVEVYEKKAIEEKLGLYQEELINISLL 1300
Qy 1251 EDYDDLGQVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVM-
Db 1198 KKLKKNNTEINDEMNDDIKLLLNFFGIPYIQSPCEAEAQCSYLNNKNYCDAI 1249
QY 1214 KPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESE 1250
Db 1140 DKKQVMDNFQMNTEQNNDKLKEDKLDEGAYFEYLEDNKIIDSYIKETNKENEELIKEY 1197

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pt-DOS/MS-DOS
APPLICATION NUMBER: US/O8/195,7
FILING DATE: 14-FEB-194
CLASSIFICATION UMBER: 32140
REFINITE JACOBS, Seth H
REGISTRATION NUMBER: 3180
REFERENCE/DOCKET NUMBER: 1180
REFERENCE/DOCKET NUMBER: 1180
TELEPHONE: 212-586-1461
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 377 amino acids
STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
ORGANISM: Plasmodium falcip:
STRAIN: WEL
US-08-195-705-5
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US-08-195-705-5
; Sequence 5, Application
; Patent No. 6420523
; Patent INFORMATION:
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                                                                                              Query Match
Best Local Similarity
Matches 353; Conser
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APPLICANT: Hui, George
APPLICANT: Barr, Philip
APPLICANT: Gibson, Helen
TITLE OF INVENTION: BACULOVIRUS PRODUCED PLASMODIUM
TITLE OF INVENTION: FALCIPARUM VACCINE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                1324
                                                                           1264
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CITY: New Y
STATE: N.Y.
COUNTRY: US
ZIP: 10111
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                                                    NFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVL 1383
             New York
N.Y.
Y: USA
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nilarity 93.6%;
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11880A3
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US-08-463-483A-23

US-08-471-046A-23

US-08-470-566B-23

US-08-469-334-23

US-09-300-529-23

US-08-477-831C-11
                                                                                              Score 1824.5; DB 4
Pred. No. 8.8e-90;
6; Mismatches 17;
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US-08-195-705-3
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  Best Local Similarity Matches 345; Conserv
                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212-586-1461 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL
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APPLICANT: Hui, George
APPLICANT: Barr, Philip
APPLICANT: Gibson, Helen
TITLE OF INVENTION: BACULOVIRUS PRODUCED PLASMODIUM
TITLE OF INVENTION: FALCIPARUM VACCINE
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,705
FILING DATE: 14-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-757-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 14-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                     MOLECULE TYPE:
HYPOTHETICAL:
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TOPOLOGY: li
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                  STRAIN:
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Score 1763.5; DB 4;
Pred. No. 1.5e-86;
7; Mismatches 22;
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                                                       Length 375;
Gaps
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Sequence 2, Application US/08195705 Patent No. 6420523
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APPLICANT: Huin, George
APPLICANT: Hui, George
APPLICANT: Barr, Philip
APPLICANT: Gibson, Helen
TITLE OF INVENTION: BACCIDOVIRUS PRODUCED PLASMODIUM
TITLE OF INVENTION: FALCIPARUM VACCINE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,705
                                                                                                                                    TELEFAX: 212-586-1461 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                       NAME: Jacobs, Seth H
REGISTRATION NUMBER: 32140
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-57-2200
                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1324 NFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVL 1383
TOPOLOGY: 1
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 45 ROCK
                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                    FILING DATE: 14-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSSNF 1622
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                                                                                                                                                                                                                                                                                                            APPLICANT: Chang, Sandra
APPLICANT: Hui, George
APPLICANT: Barr, Philip
APPLICANT: Gibson, Helen
TITLE OF INVENTION: BACULO
TITLE OF INVENTION: FALCIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
ORGANISM: plasmodium falci
STRAIN: falciparum uganda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1430
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            CLASSIFICATION: 435
ATTGRNEY/AGENT INFORMATION:
NAME: Jacobs, Seth H
REGISTRATION NUMBER: 321
                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1550
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                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                      APPLICATION NUMBER: FILING DATE: 14-FEF
                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                ADDRESSEE:
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REECKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSY
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                                                                      14-FEB-1994
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                                                                                    US/08/195,705
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Pred. No. 2.5
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TELEFAX: 212-586-1461
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
OPERATING SYSTEM: PC-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                 1608
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ORIGINAL SOURCE:
                                                                                                                                            NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                        APPLICANT: Kuepper, Hans
TITLE OF INVENTION: Prot
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                                                                                  STREET: 1300 I Street Washington
                                                                       STATE:
                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                    SYPLFDGIFCSSSNFLGISFLLILMLILYSFI 1639
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                                                                                                                                                                                                                                                                                                                                                                                      SYPLFDGIFCSSSNFLGISFLLILMLILYSFI 394
                                                                                                                                                                                                                                                                                                                                                                                                                                             DEREECKCLLNYKQEGDKCEENPNPTCNENNGGCDADATCTEEDSGSSRKKITCECTKPD
                                                      E: D.C.
20005-3315
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Enders, Burkhard
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 COMPATIBLE
PC-DOS/MS-DOS
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Protective Plasmodium Falciparum
Hybrid Proteins which Contain Part-Sequences of the Malaria
Hybrid Proteins which English Preparation and Use Thereof
                                                                                                                                 Henderson, Farabow,
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                                                                                                      Suite 700
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US-09-134-001C-3159
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PATENT NO. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: EDIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14 NUMBER OF SEQ ID NOS: 5674 SEQ ID NO 3159
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Best Local Similarity
Matches 115; Conserv
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                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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LENGTH: 115 amino acids
                                                                                                                                          7957
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REGISTRATION NUMBER: 32,220
REFERENCE,DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/806,471
FILING DATE: 13-DEC-1991
CLASSIFICATION: 424
                                                          8014 TMSHDEIENAINNIKHAINALDGEHKLQQAKENAN----LLINSLND------
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                      208
                                                                                                   161
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                                                                                                                                                                                                                                          Local
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                  KIRANELDVLKKLY--FGYRKPLDNIKDNVGKMEDYIKKNKKTIENINELIEESKKTIDK 265
                                                                                                                                    NKAKALNNDMKKLKDIVAQQDNVRQSNNY---INEDSTPQNMYNDTINHAQSIIDQVANP
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Pred. No. 6.9e-15;
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DEKQIQGLKQVIEDTKDALNGIQRLSKAKAKAIQYV----QSLSYINDAQRHI-----
                                     SEESIQ-----TEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEV 1160
                                                                            DELNNQAFPVQASSNYINSDEDLK-QQFDHALSNARKVLAKE-----
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                                                                                                                                                                                              FDLYNKYKLKLERLFDKKKTVGKYKM-----
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                                                                                                               NSLNNPKHYLONESVFENKKKEAEIAETENTLENT-KILLKHYKGLVKYYNGESSPLKTL 1105
                                                                                                                                                           IERLTAAKSKAEKLIDSLKFINKAQFTHANDEIMNTNSIAQLSRIVNQAFDLNDAMKSLR 8974
                                                                                                                                                                                                                                      INYI-----NADNLRKDNFTQAINNARDALNKTQGQNLDFNAIDTFKDDIFKTKDALN-G
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US-09-134-001C-5080 Sequence 5080, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION: APPLICANT: Lynn Doucette-Stamm et al APPLICANT: Lynn Doucette-Stamm et al APPLICANT: Lynn Doucette-Stamm et al APPLICANTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS FILE REFERENCE: GTC-007 CURRENT APPLICATION NUMBER: US 60/064,964 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14 NUMBER OF SEQ ID NOS: 5674 SEQ ID NO 5080 LENGTH: 3696 TYPE: PRT ORGANISM: Staphylococcus epidermidis US-09-134-001C-5080 Query Match Best Local Similarity 20.9%; Pred. No. 3.4e-12; Matches 314; Conservative 231; Mismatches 592; Indels 368; Gaps 67; DUSTANDAM NUMBER OF SEQ ID NOS: 567; OY 114 SDNSSDSDAKSADLEHRVUNLLT	Qy 1161 IKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHV 1220 Db 9070AENNIHNSDLSSLANTLSKASDLDNAKDL-RDTLESNSTSV 9111 Qy 1221 GAESNTITTSQNVDDEVDDVI
Db 2916 DNEYDNAKTSCLNNTTEYRPEYNKKNAILKLYDVDDTOPAIING-2960 Oy 709 ITGOATTKDGQQAGSALEGDSVQAQAQEQKQAQPPVPVPVPEAKAQVPTPPAAVNIK 765	Db 2464 AVQNINAVQVEVIKKQNVKN

	Query Match 4.2%; Score 356.5; DB 1; Length 3248; Best Local Similarity 18.9%; Pred. No. 1.2e-10; Matches 350; Conservative 304; Mismatches 631; Indels 569; Gaps 79;	; ORIGINAL SUBKLE: ; ORGANISM: HUMAN US-08-353-700-1 .		TOPOLOGY: linea MOLECULE TYPE: pr	TYPE: am STRANDEDN		TELECOMMUNICATION INFORMATION TELEPHONE: (215) 563-4100 TELEFAX: (215) 563-4044	CLASSIFICATION: 435 ; ATTORNEY/AGENT INFORMATION: ; NAME: REED, JANET E. REGISTPATION NINNERE: 36 252	OPERATING SYST	ZIP: 19103-2307 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible	601 MARKET STREET, SUITE 720 LADELPHIA USA	INVENTION: AND METHODS OF USE * SEQUENCES: 4 **DENCE ADDRESS: DANN, DORFMAN, HERRELL AND SKILLMAN	APPLICANT: YEN, TIMOTHY J. APPLICANT: RATTNER, JEROME B. TITLE OF INVENTION: NUCLEIC ACID ENCODING A TITLE OF INVENTION: TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN,	മാരധ	Db 3663 GNADK 3667	1428 VN-DK 1431	QY 1368 IKDSIDTDINFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKT 1427 : : : : : : :	Qy 1313 -DILNSRFNKRENFKNYLESDLIPYKDLTSSNYYVKDPYKFLNKEKRDKFLSSYNY 1367	3492DKINDISSRATNEEKQIFVSKLKALINRTHKQIDEAETFVSVETIVRNFKVE	Db 3436 NELEQALKSAINHIHQSQNNESVSAALKESISLIDSIEIQAHKKLEAKAYIDGYSD 3491 Qy 1260 VTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVK 1312	1207 LEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQV	UD 3399 ALKKREALAELQELAUKKENKFKQSQEAT-IEEKQSAI 3435
Qy	Db .	Db	Qy	Db	 0v	Db Qy	Db Q3	S B S	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Qy	Qy	Db	Ov B	Qy	Qy	D Qy	Db	٥٧
1019 FDKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVLQN 1058	979 -NSLNDESKRKK		934 KNKNIYQELIGQKSSENFYEKILKDSDTFYN-ESFTNFVKSKADDI- 978	:	-PLSLTPODKPEVSANDDTSHSTNLNNSLKLFENILSLG	844 -NNSLSQLFMEIYEKEMYCNLYKLKDNDKIKNLLEEAKKVSTSVKTLSSSSMQ 895	1397 -DKEVQMHFAELQEKFLSLQSEHKILHDQHCQMSSKMSELQTYVDSLK 1443	AQAGEQKOAQPVPVPVPEAKAQVPTPPAFVNNKTENVSKLDYLEKLYEFUNTSYL 	INEEKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQ:	0	615VKVQVQKVLLMNKIDELKKTQLILKNVELKHNIHV 649 : :: ::: : : : : : 1191 KPQMDLEVKEISLDSYNAQLVQLEAMLRNKELKLQESEKEKECLQHELQTIRGDLETSNL 1250	567 YKNLISKIENEIETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDI 614 : : : : : : : :	510 EKMMGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKALK-YMEDYSLRNIVVEKELKY 566 	457 KEKIKIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNF 509 :: : : :	397 STEPNEYPNGYTYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEI 456 : : : : :	- NDKVETEQAEIQELKKSNHLLEDSLKELQLLSETLSLEKKEMSSIISLN-KREIEE	342 DKNKKTERHEKETKETAKTTKENTDSIFTDDLELEVYLREKNKNIDTSAKVETKE 396	811 RSECRLEADQSPKNSAILQNRVDSLEFSLES-QKQMNSDLQKQCEELVQIKGEIEENLMK 869 292 LEEAH-NLISVLEKRIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLL 341	KDNVGKMEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQ	180 KLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNI 231		125 YADLKHRVRNYLLTIKELKYPOLFDLTNHMLTLCDNIHGFKYLIDGYEEINELLY 179

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1744 1059 В

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Sequence 1, Application PC/TUS9516216 GENERAL INFORMATION:
                  COUNTRY: USA
ZIP: 19103-2307
COMQUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                           APPLICANT: Yen, Timothy J.
APPLICANT: Rattner, Jerome B.
TITLE OF INVENTION: Nucleic Acid Encoding a Transiently
TITLE OF INVENTION: Expressed Kinetochore Protein, and
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENP-NPTCNENN 1578
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  Release #1.0,
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Version
#1.30
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REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS: |
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Best Local Similarity
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APPLICATION NUMBER: PC'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLNEYEDLLRAKLNDVCAND -----YCQIPFNLKIRANELDVLKKLVFGYRKPLDNI 231
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18.9%; Pred. No. 1.2
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PCT-US95-16216-1

CORRESPONDENCE ADDRESS:

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SEPSTEGEITGQATTKPGQQ 720	IDKYNKQVNDYPKYSQKYRDAIKKEIKALQ 1373	EPYYLIVLKKEIDKLK 675	IVKVQVQKVLLMNKIDELKK 633 	LEEKMLQPGGYSNSQIE 1	NFEKMMGKRYSYKVEKLTH :: ; ; ; ; NADTLRIDSL	IYTDNERKKFINEIKEKIKIEKKK 466 : : : :: : : ::	EKNKNIDISAKVETKESTEPNEYPNGVTYPL 411 :	ANSGNTPNTLLDKNKKIEEHE 351 :	KKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQ 291 	VFGYRKPLDNI 2 : NL 9	CDNIHGFKYLIDGYEEI 174 	BH 4; Length 2285; 10; 546; Indels 443; Gaps 73	e Organisms	CVENP-NPTCNENN 1578 	FKSLLEEKEQAEI 2344

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                                                                                          Sequence 8, Application Patent No. 6191270 GENERAL INFORMATION:
                 APPLICANT: DRUILHE, PIERRE
APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC
FILE REFERENCE: 0660-0125-0 PCT
CURRENT APPLICATION
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NUMBER: US/08/973,462B
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EARLIER APPLICATION NUMBER: PCT/FR96/00894
EARLIER APPLICATION NUMBER: FR 95/07007
EARLIER FILING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
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Best Local Similarity
Matches 269; Conserv
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ORGANISM: Artificial
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                                                                                       -SH--STNLNNSLKLFENILSLGKNKNIYQELIGQKSS-ENFYEKILKDSDTFY
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US-08-328-254-6
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GENERAL INFORMATION:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/141,239
FILING DATE: 22-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REFISTRATION NUMBER: 31,815
REFERSTRATION NUMBER: P-CJ 1191
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                               STREET: 45.
CITY: San Diego
STATE: California
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                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Zhu, Xueliang
APPLICANT: Lee, Wen-Hwa
TITLE OF INVENTION: A NO.
NUMBER OF SEQUENCES: 8
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                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                     FILING DATE: 24-OCT-1994
                                                                                                                                                                                                                     APPLICATION NUMBER:
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INFORMATION FOR SEQ ID NO: (
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                      FQGDLVKEMQLGLEEGLVPSLSSSCVPDSSSLSSLGDSSFYRAL---LEQTGDMSLLSNL
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19.8%; Pred. No. 1.8e-10;
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                                                                                                                                      Sequence 1, Application US/09310187A Patent No. 6358751
GENERAL INFORMATION:
APPLICANT: Benichou, Gilles
APPLICANT: Fedoseyeva, Eugenia
TITLE, OF INVENTION: Involvement of Autoantigens
TITLE OF INVENTION: Graft Rejection
FILE REFERENCE: UCSF-090
CURRENT APPLICATION NUMBER: US/09/310,187A
CURRENT FILING DATE: 1999-05-12
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; NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
LENGTH: 1939
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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                                    QLEE-----KEALISQLTRGKLSYTQQMEDLKRQLEEEGKAKNALAHALQSAR 1339
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   --CDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKD-NDKIKNLL
                                                                                                       KVSR-----TLEDQANEYR-----VKLEEAQRSLNDFTTQRAKL--QTENGELAR 1291
                                                                                                                                                                              RKKHADSVAELGEQIDNLQ ----RVKQKLEKEKSEFKLE--LDDVTSNMEQIIKAKANLE
                                                                                                                                                                                                  NKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEPSTEGEITGQATTK 716
                                                                                                                                                                                                                                                   RELEEISERLEEAGGATSVQIE----MNKKREAEFQKMRRDLEEATLQHEA----TAAAL 1194
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ilarity 19.7%; Pred. No. 3.4e-10;
Conservative 267; Mismatches 563;
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RESULT 14
US-08-938-105-3
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Patent No. 6353151
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite
                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1232
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                   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Crook, Wannell M.
REGISTRATION NUMBER: 31,071
                                                                                                                      CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Leinwand, Leslie A. APPLICANT: Vikstrom, Karen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1785
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                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                  COUNTRY: U.S.A. ZIP: 80203
                                                                                                                                                                                                                                                                                                                         STREET: 1700
CITY: Denver
  REFERENCE/DOCKET NUMBER:
                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HDCDLLREQYEEETEAKAELQRVLSKANSEVAQWRTKYETDAIQRTEELEEAKKKLAQRL 1399
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
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LENGTH: 1886 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                              534
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                   PVNNKTEN----VSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEESKL 817
                                                         HMEQIIKAKANLEKVSR-----TLEDQANEYR-----VKLEEAQRSLNDFTTQRA 1227
                                                                                                 STEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQAQPPVPVPEAKAQV----PTPPA 760
                                                                                                                                                                               KHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEP
                                                                                                                                                                                                                       ARAKVEKLRSDLTRELEEISERLEEAGGATSVQIE----MNKKREAEFQKMRRDLEEATL
                                                                                                                                                                                                                                                                                                                                            ENSKHNLEKLTKALKY-----MEDYSLRNIVVEKELKYYKNLISKIENEIETLVENI 585
                                                                                                                                                                                                                                                                                                                                                                                                                        RSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYKVE---KLTHHNTFASY
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                                                                                                                                         QHEA----TAAALRKKHADSVAELGEQIDNLQ----RVKQKLEKEKSEFKLE--LDDVTS 1182
                                                                                                                                                                                                                                                           KKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNK--IDELKKTQLILKNVEL
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US-09-104-324B-4
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09104324B Patent No. 6232460 GENERAL INFORMATION:
                                                 COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/09/104,324B
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                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS
ADDRESSEE: Fulbright & Jaworski LLP
STREET: 666 Fifth Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1056
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                                                                                                                                                                                          STREET: 666
CITY: New Y
STATE: New
ZIP: 10103
                 FILING DATE: 2 CLASSIFICATION:
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APPLICATION DATA:
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Methods For Diagnosis And Treating Cance
And Methods For Identifying Pathogenic M
No. 6232460mal Cells
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FILING DATE: 15-July-1097
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 62324601
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                                                                                                                                                                                                                            GSALEGDSVQAQAQEQKQAQPPVPVPVPVPEAKAQVPTPPAPVNNKTENV-SKLDYLEKLYE
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PLSLTPQDKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQELIGQKSSENFYEKI 955
                                       ----ESAKQKFGEITDTYQKEI------EDKKISEENLLEEVEK----AKVIADEAV-
                                                           DSLNNSLSQLFMEI---YEKEMVCNLYKLKDNDKI--KNLLEEAKKVSTSVKTLSSSSMQ
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20.7%; Pred. No. 5
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RESULT 17 US-09-134-001C-4820 ; Sequence 4820, Application US/09134001C	THHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENE 577 R :: :: :: : :	Oy 525 THHNT
Db 1019 VMKKLNQIHVIINAKFNVEPSLVDTALLQIELK QY 1456 KIKELNY-LKTIQDKLADFKKNNNFVGIADLS7 ;; ; ; Db 1076 QVHIANQTLELLQDDLNSLRRQLN	KFMKRINEVGIPIIFVINQIDKH-NEEEITFETFK 216 DRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKL 524	Db 172 DYNHVQSALNF Qy 465 KKIESDKKSYE 1: : Db 217 SRVEKSIKDW-
961 1417	DPLELEYYLREKNKNIDISAKVET-KESTEDNEY-PNGVTYPL 411 :	Qy 360 TIKENIDSLET
Qy 1315LNSRFNKRENFKNVLESDLIPYKDLES Db 905 DNAKLSAROHKLNHYKNOTILNGELIDTTAGRI	RIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAK 359 :	Qy 305 RIDTLKK : Db 69 Q-DILP-
1260 V 845 I	TIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEK 304 :: :	
Qy 1207 LEQSQPKKPASTHVGAESNTITTSQNVDDEVDI	3.7%; Score 314.5; DB 4; Length 1151; rity 19.7%; Pred. No. 5.8e-09; nservative 225; Mismatches 485; Indels 379; Gaps 63;	Query Match Best Local Similarity Matches 268; Conser
Qy 1152HLIAELKEVIKNKNYTGNSPSENNTDVI	ylococcus epidermidis	LENGTH: 1: TYPE: PRT ORGANISM: S-09-134-0010
QY 1100 SPLKTLSBESIQTEDNYASLENFKVLSKLI : : : : : : : :	APPLICATION NUMBER: US 60/055,779 . Q EILING DATE: 1997-08-14 R OF SEQ ID NOS: 5674 D NO 3242	
Qy 1050 NNPKHYLQNFSVFFNKKKEAEIAETENTLI ::: :::::::: 	BER: US/09/134,001C 998-08-13 -11-08	
Qy 991 EEDIN-KLKKTLQLSFDLYNKYKLKLERLFDKI 	e-Stamm et al LEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS IDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS	
Qy 932 LGKNKNIYQELIGQKSSENFYEKILK-DSDTF	plication US/09134001C 0 0N:	S-09-134-(Sequence Patent No GENERAL 1
Db 510 SHNYKHYYIHLDDSLDKLIGRTETHFELKQEN	DOUBLE LEADING TO BELLEVIET VALUE OF STANDED SELL STO	RESULT 16
465	1229	Qy 1188
Qy 812 EEESKLSSCDPLDLLFNIQNNIPVMYSMFDSL	GISKDKRDYLWTSAKNTLSTPLPKAYTVKTPTKPKLQQRENLNIPIEESKKKR 882	Db 830GIS
752 KAQVPT	FTSVDH	800
75	LLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKD 1134	1075
Db 336DILDNAYIMTYDMRESLRNYLESMATI	ERLFDKKKTVGKYKMQIKKLT-LLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAET 1074 DRIEEKEKLKREAKENTATLKEKKDKK	Qy 1016 ERLFDK :: Db 770 EREE
Qy 638 LKNVELKHNIHVPNSYKQENKQEPYYLIVLKKI	LGLYKSKEQEQSSLRASLEIELSNLKAELLSVKKQLEI 769	Db 732
Qy 578 IETLVENIKKDEEQLFEKKITKDENKPDEKILI ::::::::::::::	KHQYDKIIEERDSE 731 KLKKTLQLSFDLYNKYKLKL 1015	4 6
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5 ----LNSRFNKRENFKN--VLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYI 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 IYSVSSRQSLNGNNIGINELRESIQYFAKVESRTILEQQMTYQLQQMNNSFKKMIKDFHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 LNENQAFK------MIINAVDLAEDKQDI-----QAVEDYVADALGQVNLHSD 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0 IVKDVPLF----DRTKQDITDTILRLDNQITKVGVFGTFSAGKSSLINALLGDN---YL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 LGKNKNIYQELIGQKSSENFYEKILK-DSDTFYNESFTNFVKSKADDINSLNDESKRKKL 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .0 SHNYKHYYIHLDDSLDKLIGRTETHFELKQENSTAYHRKHETQHRNEFVTSNQDIKRALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 IKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFENILS 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 EEBSKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKDNDK 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 -----ILNQEYDVVPSL--ISELYQ--TQTSISNTYVL----TFSDEVIKALNKKI 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 SDNSEPSTEGEITGQATTKPGQQAGSALEGDS-----VQAQAQEQKQAQPPVPVPVPEA 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 ----DILDNAYIMTYDMRESLRN--YLESMATDF-----KVNGFFNKRKK-----
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                                                                                                                                                                                                                                             7 FLNNIETLYKTVNDK------IDLFVIHLE-----AKVLNYTYEKSNVEV 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLIHTVSLEEIKKWSAEDEYATF--VKTV-----HLKLPLDWLKGKIIIDSLGLHSNNQR 761
QVHIANQTLELLQDDLNSLRRQLN------DYIH 1103
                                                                           KIKELNY-LKTIQDKLADFKKNNNFVGIADLSTDYNH 1491
                                                                                                                                                              VMKKLNQIHVIINAKFNVEPSLVDTALLQIELNSMLQSLPKQLTKRKIVN---PKSQKDI 1075
                                                                                                                                                                                                                                                                                                                            KSVFNSQMTQNNDFNEEKKISTKIYLDQIHQRLFLEQSLITERIKKYFNSQL--EEQILP 1018
                                                                                                                                                                                                                                                                                                                                                                                                            KDSIDTDINFANDVLGYYKILSEKYKSDL------DSIKKYINDKQGENEKYLP 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTGEAVTPSVIDNILSKIENEYEVLYLKPLAG---VYRSLKKQLENNVMTFNVNVKDI-- 1314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEQSOPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDY--DDLGQV----- 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTNETEQILTSSDLILYVTYFNHSFTDND------KAFIEHMKDM------NQ 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----HLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSESGSDT 1206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEDIN-KLKKTLQLSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNSL 1049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MQSILDTLQINEEQFEEAYIQFQQNQ-----EVSAEAQLLNDSNQLFNYLKQXRX----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNAKLSARQHKLNHYKNQTLLNQELIDTTAQRTFNEVEEQVY-HLNERLKLQLLDE---V 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSSPNPTTAATTELSYGKESQITLK----- 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         904
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Qy 322 INEIKNPPPANSGNTPNTLLDXNKKIEEHEKEIKEIAKTIKFNIDSLETDPLELEYYLRE 381 Db 327 L	CO IN HZ TPTPHHEOOP Z
RESULT 18 US-08-687-080-51 Sequence 51, Application US/08687080 Patent No. 5965427 GENERAL INFORMATION: APPLICANT: Gregory Dolganov TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof INVENTION: Human RAD50 Gene and Methods of Use Thereof INVENTION: Human RAD50 Gene and Methods of Use Thereof INVENTION: Human RAD50 Gene and Methods of Use Thereof INVENTION: Human RAD50 Gene and Methods of Use Thereof INVENTION: Human RAD50 Gene and Methods of Use Thereof INVENTION: ASSOCIATES STREET: 350 Cambridge Associates STREET: 350 Cambridge Avenue, Suite 250 STATE: CA INVENTE: Palo Alto STATE: CA INVENTE: Palo Alto INVENTE: Floppy disk COMPUTER READABLE FORM: MEDIOM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATION TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATION NUMBER: US/08/687,080 FILING DATE: 17-JUL-1996 CLASSIFICATION NUMBER: US/08/687,080 FILING DATE: 17-JUL-1996 FILING DATE: 26-JAN-1996 ATTORNETYAGENT INFORMATION: NAME: Sholtz, Charles K. REGISTRATION NUMBER: 38,615	Db 700 DELSTMRNOLEDYOROTA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: N
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1312 amino aci
                                   1033 K-KLTLLKEQLESKLNSLNNPKH------VLQNFSVFFNKKKEAEIAETENTLENTKI 1083
 702
                                                                                                                                                                                        937
                                                                                                                                                                                                                                                                                                         494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 3.7%; Score 308; DB 2; Local Similarity 19.4%; Pred. No. 1.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNLISKIENEIETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQK-----V 622
                                                                                                                                                                                                                                                                                                                        NIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKDNDK-----IKNLLEEAKK 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRYIKALETLRQVRQTQGQKVKEYQME-----LKYLKQYKEKACEIRDQITSKEAQLTSS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EIDREMISSLGVSKAVLNNVIFCHQEDSNWPLSEGKALKQKFDEIFS------A 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESDKKSYEDRSKS---LNDITKEYE------KLLNEIYDSKFNNNIDLTNFEKMMG 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOFRDVN-----GELIAVQRSMVCTQKSKKTEFKTLEGVITRTKHGEKVSLSSKCA 134
QSKLRLAPDKLKSTESELKKKEKRRDEMLGLVPMRQSII--DLKEKEIPELRNKLQNVNR 759
                                                                        LDRLKEEIEKSSKQRAMLAGATAVYSQFITQLTDENQSCCPVCQRVFQTEAELQEVISDL 701
                                                                                                              RKKLEEDINKLKK---TLQLSFDLYNKYKLKL------ERLFDKKKTVGKYKMQI 1032
                                                                                                                                                 EINOTRDRLAKLNKELASSEQNKNHINNELKRKE----EQLSSYEDKLFDVCGSQDFESD
                                                                                                                                                                                     NIYQ-----ELIGQKSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDESK 986
                                                                                                                                                                                                                          LNH--HTTTRTQMEMLTKDKADKDEQIRKIKSRHSDELTSLLGYFPNKKQLEDWLHSKSK 585
                                                                                                                                                                                                                                                               VSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFENILSL-----GKNK 936
                                                                                                                                                                                                                                                                                                   ------NSNVETLKMEVISLQ-----NEKADLDRTLRKLDQEMEQ
                                                                                                                                                                                                                                                                                                                                                                             ILSK-----KQNELKNV-----KYELQQLEGSSDRILELDQELIKAERELSKAEK-----
                                                                                                                                                                                                                                                                                                                                                                                                                 NVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLF 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                      HKLVRERQEGEAKTANQLMNDFAEKETLKQKQ-----IDEIRDKKTGLGRIIELKSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTKPGQQAGSA-----LEGDSVQAQAQEQKQAQPPVPVPVPEAKAQVPTPPAPVNNKTE 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLLNQEKSELLVEQGRLQLQADRHQEHIRARDSLIQSLATQLELDGFERGPFSERQIKNF 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKMEKVFQGTDEQL----NDLYHN-HQRTVREKERK-----LVDCHRELEKLN----KES 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVE 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEIVKSYENELDPLKNRLKEIEHNL--SKIMKLDNE----IKALDSRKKOMEKDNSELE 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYMEDY----SLRNIVVEKE--LKYY 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248; Conservative
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, 324-0960
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RESULT 19
US-08-592-126-148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5821091 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 148, Application US/08592126
TELEFAX: (415) 324-0960 INFORMATION FOR SEQ ID NO: 1. SEQUENCE CHARACTERISTICS: LENGTH: 1312 amino acids
                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Transcri
TITLE OF INVENTION: Polypept
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1172
                                                                                                REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94306
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                               TELEPHONE:
                                                                                                                                                                                                                                             APPLICATION NUMBER:
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350 Cambridge Avenue, Suite
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1204 SDTLEQSQPKKPASTHVGAESNTITTS----QNVDDEVDDVIIVPIFGESEEDYDDLGQV 1259
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                                          AQQAAKLQGI--DLDRTVQQVNQEKQEKQHKLDTVSSKIELNRKLI--------
                                                                                     SYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSESG 1203
                                                                                                                                DIQRLKNDIE---EQETLIGTIMPEE---ESAKYCLTDVTIMERFQMELKD----VERKI 809
                                                                                                                                                                                                                     QSKLRLAPDKLKSTESELKKKEKRRDEMLGLVPMRQSII--DLKEKEIPELRNKLQNVNR 759
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OY 476 DRSKSLNDITKEYEKLLNETYDSKFNNNIDLTNFEKM	Db 337 TNNGQRSSMAPNDQTNGIYIQNLQEFHITNAMEGLNLLQKGLKHRQVASTKMNDFS 392	QY 422 ELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKEKIKIEKKKIESDK-KSYE 475	272 TETE	QY 323 NEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLFTDP 372	Db 174 YTMTGDEKLYNGELSDAAGIPRVLLKLFDTLELQQNDYVVKCSFIELYNEELKDLLD 231	KNENIKELL	QY 221 VEGYRKPIDNIKUNVGKMEDYLKKNRKTILENLNELLEESKKTIDKNRKMATREEEKKKL 2/8	Query Match 3.6%; Score 303.5; DB 4; Length 1038; Best Local Similarity 21.2%; Pred. No. 2e-08; Best Local Similarity 21.2%; Pred. No. 2e-08; Matches 229; Conservative 169; Mismatches 395; Indels 287; Gaps 5	ORGANI S-09-541-	Ų	CURRENT FILLING DATE: 2000-04- NUMBER OF SEQ ID NOS: 10 SOFTWARE: FastSEQ for Windows	FILE REFERENCE: 1015 CURRENT APPLICATION NUMBER: US/09/54	; GENERAL INFORMATION: ; APPLICANT: Nislow, Corey ; APPLICANT: Sakowicz, Roman ; APPLICANT: Beraud, Christophe ; TITLE OF INVENTION: Antifungal Assay	ESULT 20 IS-09-541- Sequence Patent N	QY 1480 - VGIADISTDYNHUNLIFK 1497 O	DLDIYYKTLDQAIMKFH	1431 KIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNF	Db 1060 LEENIDNIKRNHNLALGROKGYEEEIIHFKKELREPQFRDAEEKYREMMIVMRTTELVNK 1119	QY 1393 YKSDLDSTKKYINDKQGENEKY	Db 1000 DMRLMRQDIDTQKIQERWLQDNLTLRKRNEELKEVEEERKQHLKEMGQMQVLQMKSEHQK 1059	Qy 1364 SYNYIKDSIDTD	DDYKKQKETE	Qy 1320 NKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLS 1363	Db 908 -AKEQVSPLETTLEKFQQEKEELINKKNTSNKIAQDKLNDIK 948	PSVIDNILSKIENEYEVLYLKPLAGVYRSLKK	Db 854 QDQQEQIQHLKSTTNELKSEKLQISTNLQRRQQLEEQTVELSTEVQSLYREIKD- 907
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APPLICANT: NISLOW, Corey
APPLICANT: Sakowicz, Roman
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal Assay
FILE REFERENCE: 1015
CURRENT APPLICATION NUMBER: US/09/723,82/
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/541,782
PRIOR APPLICATION NUMBER: 09/541,782
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.
; ORGANISM: Saccharomyces cerevisiae US-09-723-820-4
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US-09-723-820-4
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LENGTH: 1038
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QFEQLINKHNMLKDNIKNSITSTHSHITNVDDIYNTIENIMKNYGNKENATKDEMIENIL 983
                                                                                                                                                                     ADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGK-----YK 1029
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                                                                                                  MQIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENT - - - LENTKILLK 1086
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                                                                   -ESISVM-----KGQVEESENAISLLKNNTKFND
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Qy 85 GGSVASGGSVASGGSVASGGSQNSRRTNPSDNSSDSDAKSYADLKHRVRNYLLTIKELKY 144	Query Match 3.6%; Score 302.5; DB 4; Length 3169; Best Local Similarity 18.7%; Pred. No. 8.8e-08; Matches 392; Conservative 277; Mismatches 596; Indels 829; Gaps 97; Oy 25 YQELVKKLEALEDAVLTGYSLFOKEKMVLNEGTSGTAVTTSTPGSKGSVASGGSGSVAS 84	SEQUENCE CHARACTERISTICS: LENGTH: 3169 amino acids TYPE: anino acid STRANDEDNESS: <unknown> TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 257: US-09-453-702B-257</unknown>	ATTORNEY/AGENT INFORMATION: NAME: Seay, Nicholas J. REGISTRATION NUMBER: 27386 REFERENCE/DOCKET NUMBER: 960296.95017 TELECOMMUNICATION INFORMATION: TELEPHONE: (608) 251-5000 TELEPHONE: (608) 251-9166 INFORMATION FOR SEQ ID NO: 257:	; OPERATING SYSTEM: PC-DOS ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/09/453,702B ; FILING DATE: 03-Dec-1999 ; CLASSIFICATION LONGER: CUNGNOWN> PRICASSIFICATION NUMBER: 60/110,955 ; FILING DATE: 04-DEC-1998	ADDRESSEE: Quarles 6 Brady STREET: 1 South Pinckney Street CITY: Madison STATE: WI COUNTRY: US ZIP: 53701-2113 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage COMPUTER: IBM PC compatible	APPLICANT: Blattner, Frederick R. Burland, Valerie Perna, Nicole T. Plunkett, Guy Welch, Rod TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157 NUMBER OF SEQUENCES: 265 CORRESPONDENCE ADDRESS:	Db 984 KEIPNLSKKMPLRLSNINSNSVQSVISPKKHALEDENKSSENVDNEGSRKML 1035 RESULT 22 US-09-453-702B-257 ; Sequence 257, Application US/09453702B ; Patent No. 6365723 ; Patent No. 6365723	YLSSGLHHLI
Db 1020 ESFDIIRSNOHEWGDLSTVEOFKKFEFYVKSELSSAKSIFDDIKNKYITDPETKRNVLVH 1079 Qy 888 TLSSSSMQPLSLTPQDKPEYSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQELI- 943	964 778 979	Qy 633 KTQLILKNVELKHNIHVENSYKQENKQEPYYLIVLKKEIDKL	LPTSLYYEIDSRSFF LMNKIDELK : : ::	512 633 552 692	Db 453 KFGDRFQLRDINTLESFKKPQDYFFYQQEMLLRWNYAAASDQVRINILKEYGGIYTDTDI 512 Qy 423 LNSFGDLINPFDYTKEPSKNIYTDNERKKFINE-IKEKIKIEKKKIESD 470	LKIQNIQNETIEFKETRERLKELENRYKSLTSETKEKKNVFFLESMIGDSLET	DNKGNKQ DTLK : : NTYKDYT	OY 251 NINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLI 299

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RESULT 23
US-08-290-919-3
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ZIF: 2000 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1162
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                                                                                                                                                                                                                                                     APPLICANT: HOLDER, ANTHONY A.
APPLICANT: BLACKMAN, MICHAEL J.
APPLICANT: CHAPPEL, JONATHAN A.
TITLE OF INVENTION: IMPROVEMENTS
TITLE OF INVENTION: VACCINE
NUMBER OF SEQUENCES: 19
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                                                                                    ZIP:
                                                                                                                                                    STREET: 1100 NEW CITY: WASHINGTON
                                                                                                      COUNTRY:
                                                                                                                                    STATE:
                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --DIDTRVIGLTFKEGINSLSEALEHMNIDAIMSVIGLVQYARMI------KMNDNISA 1844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NDKIDLFVIHLEAK----VLNYTYEKSNVEV---KIKELNYLKTIQDKLADFKKNNNFVG 1481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIVDFLGIQDNTIKVKLESDIKPISEIQOPLHSILSROKEHVKNLLSGLLDEFSNKLRKQ 1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IENEYEVLYLKPLAGVYR----SLKKQLENNVMTFNVN------VK 1312
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                                                                                 RY: U.S.A.
20005-3918
                                                                                                                                  D.C.
                                                                                                                                                                                1100 NEW YORK AVENUE,
                                                                                                                                                                                                       CUSHMAN DARBY & CUSHMAN, L.L.P.
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RESULT 24
US-08-480-604A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08480604A Patent No. 5736139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
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TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,604A
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, NISHA V.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1570 PNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSSN 1621
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 53 amino acids
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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APPLICATION NUMBER: (
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                                                                                                                COMPUTER: LBm...
COMPUTER: LBm...
OPERATING SYSTEM: PC-DO5/PL-
OPERATING SYSTEM: PC-DO5/PL-
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OPERATING S
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LOCATION: LOCATION: /label= X
OTHER INFORMATION: /note= "X = M and N, or
                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.0%; es 52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                            UNITED STATES
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                                                                                                                                                                                  Version
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FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/405,496
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/161,907
FILING DATE: 04-DEC-1993
PRIOR APPLICATION UNMBER: US 07/985,321
FILING DATE: 04-DEC-1992
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TELEFAX: (415) 397-833!
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME: INCOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPHD-01763
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
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APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
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  KLTKALK---YMEDYS--LRNIVVEKELKYYKNLISKIENE-----
                                                                     TKEYEKLLNEIYDSKFNN----NIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSKHNLE
                                                                                                                              Y---ELKK-LNNLDEKYLISFEDISKNNSTYSVRFINKSNGESVYVETEKEIFSKYSEHI 927
                                                                                                                                                             YTDNERKKFINEIKEKIKIEKKKIESDKKSYEDR-----
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                                             TKEISTIKNSIITDVNGNLLDNIQLDHTSQVNTLNAAFFIQSL-----IDYSSNKDVLN 981
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1481 1904	1422 ETLYKTVNDKIDLFVIHLEÄKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVG :: : : : : : : : : :	Qy Db
1421 1850	1384 GYYKILSEKYKSDLDŠIKKYINDKQGENEKYLPFLNNI 	Qy Db
1383 1790	1332 DLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLS-SYNYIKDSID-TDINFANDVL 	Qy Db
1331 1732	1286 LKPLAGYYRSLKKQLENNVMTFNVNVKÖILN-SRENKRENFKNVLES	Qy Db
1285 1676	1226 TITTSQNVDDEVDDVIIVPİFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIENEYEVLY :	Qy Db
1225 1638	1172 SENNTDVNNALESYKKFLPEGTDVATVVSESGSDTLE-QSQPKKPASTHVGAESN : : : : : : : : : :	Qy db
1171 1579	1124 VLSKLEGKLKDNLNLEKK-;-KLSYLSSGLHHLIAELKEVIKNKNYTGNSP:::: :: ::: :::: :::::::::::::::::::	<u>р</u> ъ
1123 1520	1068 EAEIAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFK :: : :	Qy Db
1067 1470	1008 YNKYKLKLERLEDKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHYLQNESVFFNKKK	Оу
1007 1425	948 SENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDL	Qy Db
947 1389	891 SSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQELIGQKS	Qy Db
890 1364	831 NNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKDNDKIKNLLEEAKKVSTSVKTLS 	Qy
830 1310	773 DYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLFNIQ	Qy Db
772 1253	718 GQQAGSALEGDSVQAQAQAQAQAQPPVPVPVPEAKAQVPTPPAAPVNNKTENVSKL 	Qy Db
717 1200	679 PKVESLINEEKKNKTEGQSDNSEPSTEGEITGQATTKP :	Оу
678 1147	624LMNKIDELKKTOLILKNVELKHNIHVPNSYKQENKQEDYYLIVLKKEIDKLKVFM	Qy Db
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US-08-405-496A-6
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GENERAL INFORMATION:
APPLICANT: WILLIA
                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                       Query Match
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FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                    Local Similarity
mes 339; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
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                     K - - NKKTIE - -
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                                                        ---NKY-RIPERLKNK----EKVKVTFIGHGKDEFNTSEFARLSVDSLSNEISSFLDTIK 685
                                                                                          VCANDYCQIPFNLKIRANELDVLKKLVFGY-----
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IVENTION: VACCINE FOR CLOSTRIDIUM

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                                                                         - INTITGKYYVDNNTDKSIDFSISLVSKNQVKVNGLYLNESVYSSYLDFVKNSDGHHNTS
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APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, NISHA V.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
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                                                                                                                  APPLICATION NUMBER: US 0 FILING DATE: 25-OCT-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                             PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
FILING DATE: 04-DEC-
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STREET: 22:
CITY: SAN
STATE: CAL
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                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release ""
                                                                                        APPLICATION NUMBER: US 08/161,907 FILING DATE: 02-DEC-1993
                                                                                                                                                                                     APPLICATION NUMBER: US 0 FILING DATE: 16-MAR-1995
                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
APPLICATION NUMBER: US 07/429,791 FILING DATE: 31-OCT-1989
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                                           JMBER: US 07/985,321
04-DEC-1992
                                                                                                                                                                                                                                                                                                                                         Release #1.0, Version
                                                                                                                                                      US 08/329,154
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS: LENGTH: 2710 amino acids
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TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E
REGISTRATION NUMBER: 40,
REFERENCE/DOCKET NUMBER;
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hes 339;
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GQQAGSALEGDSVQAQAQEQKQAQPPVPVPVPEAKAQV----PTPPAPVNNKTEN---VSKL 772
                                                                                                                                                                                                                                                                                                              DLSTSVKVQLYAQLFSTGLNTIYDSIQL---VNLISNAVNDTINVLPTITEGIPIVSTIL 1038
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                                                             PIDDLYISEIDFNNNSIKLGTCNILAMEGGSGHTVTGNIDHFFSSPSISSHI-----P
                                                                                                    PKVESLINEEKKN----
                                                                                                                                            LPIAGISAGIPSLVNNELILHD-KATSVVNYFNHLSESKKYGP-----LKTEDD--KILV 1147
                                                                                                                                                                                -----LMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFM 678
                                                                                                                                                                                                                               DGINLGAAIKELLDEHDPLEKKEL - - - EAKVGVLAINMSLSIAATVASIVGIGAEVTIFL
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                                                                                                        ----IKTEGOSDN-----
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RESULT 27
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                                                                                                                                                                   Sequence 6, Application US/08957310 Patent No. 6365158
                                                                                                                   GENERAL INFORMATION:
APPLICANT: Williams, James A.
APPLICANT: Kink, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         1384
                                                                    TITLE OF INVENTION: IDENTIFICATION TITLE OF INVENTION: OF TOXIN A AND TITLE OF INVENTION: DISEASE
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                                    NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
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                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                    ETLYKTVNDKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVG 1481
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 220 Montgomery Street,
                    Medlen & Carroll
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia Dinna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 04-DEC-1992
PRIOR APPLICATION UNMBER: US 07/470 707
FILING DATE: US 07/470 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2710 amino aci
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0: FILING DATE: 23-OCT-1997 CLASSIFICATION: 424 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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                    444
                                                   841
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STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 24-OCT APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 SGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDSDAKSYADLKHRVRNYLLTIK--E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                              GNTP-----NTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKN
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                                                                      KNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNI 443
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California
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24-OCT-1994
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1421	1384 GYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNI :
1383	-TDINFANDVL : FKDIKKLSL
1331 ·	1286 LKPLAGVYRSLKKQLENNVMTFNVNVKDILN-SRFNKRENFKNVLES:
1285	1226 TITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIENEYEVLY
1225 1638	1172 SENNTDVNNALESYKKFLPEGTDVATVVSESGSDTLE-QSQPKKPASTHVGAESN : : : : : : : : : :
1171 1579	1124 VLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSP : : : : : : : : : :
1123	1068 EAEIAETENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFK
1067	1008 YNKYKLKLERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVLQNPSVFFNKKK
1007	948 SENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDL:
947 1389	891 SSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQELIGQKS (
890	831 NNIPVMYSMFDSLNNSLSQLFMEIVEKEMVCNLYKLKDNDKIKNLLEEAKKVSTSVKTLS 8 : : : : : : : : :
830 1310	773 DYLEKLYEFLNTSYICHKYILVSHSTMNEKILKOYKITKEEESKLSSCDDLDLLENIQ 8
772	718 GQQAGSALEGDSVQAQAQEQKQAQPPVPVPVPVPEAKAQVPTPPAPVNNKTENVSKL 7
717	679 PKVESLINEEKKNIKTEGQSDNSEPSTEGEITGQATTKP 7
678 1147	624LMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFM (
623 1095	583 ENTKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVOKVL (; ; ; ; ; ; ; ; ; ;
1038	542 KLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEIETLV 982 DLSTSVKVQLYAQLFSTGLNTIYDSIQLVNLISNAVNDTINVLPTITEGIPIVSTIL 1
541 981	485 TKBYEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSKHNLE 5
927	872 YELKK-LNNLDEKYLISFEDISKNNSTYSVRFINKSNGESVYVETEKEIFSKYSEHI

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TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION: FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3135 amino acids
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                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 347; Conserv
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APPLICANT: Willlamson, Kim C.

APPLICANT: Willlamson, Kim C.

APPLICANT: Kaslow, David C.

TITLE OF INVENTION: Cloning and Expression of Plasmodium

TITLE OF INVENTION: faliciparum Transmission-Blocking Target Antigen, Pfs230

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UMMBER: US 08/
FILING DATE: 29-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Quine, Jonathan, A.
REGISTRATION NUMBER: P-41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,170B
FILING DATE: 13-CCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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  1654 QLEEVIYNDIESLELK---
                                                                                                                                                                                                                                                                          1502 LKNNLANF -- TYKHQFNYMEIPALMDNDISFKCICVDLKKKKYNVKSPLGPKVLRALYKK 1559
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                                                                                                                                                                            181 LNEYFDLLRAKLNDVCAND'--YCQIPFNLKIRANELDVLKKLV--FGYRKPLDNIKDNV 235
                                      291 QLEEA-HNLISVLEKRIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTL----LDKNK 345
                                                                                                                                                                                                                                                                                                                   128 LKHRVRNYLLTIKE----LKYPQLFDLTNHMLTLCDNIHGFKYLID---GYEEINELLYK 180
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CITY: San Francisco
STATE: California
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                                                                                                                  GKMEDYIKKNKKTIENINELIEESKKTIDKNKNA---TKEEEKKKLYQAQYDL--SIYNK 290
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                                                                                           -TDANPESII-ESLSINESNESGPFPTGDVDAEHLILEGYDTWESLYDE
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19.6%; Pr
ative 270;
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----DIEQYVLQVN-LKAPKLMMSAQIHNNRHVCDFSKNN 1704
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                                                                                                                                                                                                                                                                                                                                                              Score 298; DB 1; Length 3135;
Pred. No. 1.5e-07;
0; Mismatches 575; Indels 58
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INFORMATION FOR SEQ ID NO:
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UMBER: 38,440
ET NUMBER: 015280-113110US
N INFORMATION:
15) 576-0200
) 576-0300
O ID NO: 2:
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or compatible
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tIn Release #1.0, Version #1.30
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, David C.
: Cloning and Expression of Plasmodium
: faliciparum Transmission-Blocking Target Antigen, Pfs230
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-JAN-1993
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-OCT-1997
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Best Local S
Matches 347
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LENGTH: 3135 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                      2094 KNVE------EGVQNEEY-----KKFSLKPSLVFDDNNNDIKVIGKE 2129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1820 KFFEKVINEYDDTEEEKDLESILPGAIVSPMKVLKKKDPFTSYAAFVVPPIVPKDLHFKV 1879
                                                                                                                                                                                                                                                                                                                                                                                     2053 VHLCNFFDNPELTFDNNK----------IVLCKIDAELFSEVIIQLPIFGT 2093
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---NDKIKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLN-NSLK 924
                                                                                                                                                                                                                           KN-----EVSISLALK------GVYGNRIFTFDKNGKKGEGISFFIPPI-----
                                                                                                                                                                                                                                                                DNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQAQ-----PPVPVPVPVPEAK 752
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                                                          KKCTVKIKKGD----IFGLK--CPKGFAIFPQACFSNVLLEYYKSDYEDSEHINYYIHKD 2280
                                                                                                                                         -KQDTDLKFIINETIDNSNIKQRGLIYIFVRKNVSENSFKLCDFTTGSTSLMELNSQVKE
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                                                                                                                                                                                                                                                                                                                                                                                                                           ----LFEK-KITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLIL-----
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                                                                                                EES--KLSSCDPLDLLFNIQNNIPVMYSMFDS--LNNSLSQLFMEIYEKEMVCNLYKLKD 868
                                                                                                                                                                               AQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKE 812
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IES AND USES	/TUS9307261 MP3 MALARIA ANTIGEN, ANALOGS, ANTIBOD Blasdale	US93-07261-11 quence 11, Application p quence 11, Application p TITLE OF INVENTION: Pf NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: ADDRESSE: John H. C STREET: One Giralda CITY: Madison STATE: New Jersey COUNTRY: USA ZIP: 07940-1000 COMPUTER READABLE FORM:	RESU PCT- Se- G
	KCVENPNPTCNENNG 1579	1546 HLDEREECKCLLNYKQEGD	Qу Db
GCFR 1545 : GKYS 2993	NSLSLTK-QNQNIIYGNVAKTUFIHINQGYKEIHGCDFTGKY	1491 HNNLLTKFLSTGMVFENLA :: : :: : 2953 NSLSLTK-QNQNIIYGNVA	Ф
TDYN 1490 :: :LEFN 2952	VKIKELNYLKTIQDKLADFKKNNNFVGIADLS	1447 TYEKS-NVE	Qу Db
KVLNY 1446 KVL-Y 2903	NDKIDLFVIHLEA 	1417 FLNNIETLYKTV	Оу
LP 1416 ; TKVA 2844	KDSIDTDINFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYL ::	1369KDSIDTDINFANDVI :: 2787 EKFEEELIDTKKVLACTCI	Qу Db
I 1368 : LILP 2786	SSNYVVKDPYKFLNKEKRDKFLSSYNYI :: : :: :: :: :: :: ADKYNTFSKDKIGNILKNAISINNPDEKDNTYTYL	1324 NFKNVLESDLIPYKDLTSSNY	Qу
NSRFNKRE 1323 : : NKKLNPQT 2729	LENNVMTFNVNVKDIL	1281 YEVLYLKPLAGVYRSLKKQ ; : 2670 CDFLYLENQTNDAISNNNN	Qy Db
NE 1280 : :IIHG 2669	DYDDLGQVVTGEAVTPSVIDNILSKIENE	1233 VDDEVDDVIIVPIFGESBEDYDDLGQVVTGEAVT- 	Ωу
TSQN 1232 2616	YKKELPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITT : : : : : : : : : :	1175 NTDVNNALESYKKFLPEGTDVAT	Оу
PSEN 1174	ASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSEN ::	1116 Y-ASLENFKVLSKLEGKLKDN : : :	ДУ
TEDN 1115 : TQSF 2544	NFSVFFNKKKEAEIAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDN 	1056 LQNFSVFFNKKKEAEIAET : 2502 FPNSSLITNDKK	Дy
NPKHV 1055 TPKDY 2501	KEQLESKLNSLN :::: PNDTKKIQKSICKINAKALDVVTIKCPHTKNF	1016 ERLEDKKKTVGKYKMQIKKLTLL : : : : ! 2444LYDSNEHICDYEKNESLISTL	Фр
KLKL 1015 : HTYI 2443	SLNDESKRKKLEDDINKLKKTLQLSFDLYNKYKLKL : : : 	964 NESTINFVKSKADDINSLNDESKRKKL 	Qy Db
DTFY 963 : NVIK 2387	NILSLGKNKNIYQELIGQKSSENFYEKILKDSDTFY	925 LFENILSLGKN-	Оу Дъ
GNLP 2328	LMDENFRELQ - NIQQYTGISNITDVLHFKNFNLGNLP	2281 KKYNLKPKDVIE	Дb

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SEQUENCE CHARACTERISTICS:
SEQUENCE THARACTERISTICS:
LENGTH: 1588 amino acids
TYPE: amino acid
TYPE: amino acid
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APPLICATION NUMBER: PCT/US93/CFILING DATE: 19930805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 201-822-7398
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  488
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                                                                                                                                                                                                                             689 KKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQ------AQA
                                                                                                                                                                                                                                                                                                                   636 LILKNVELKHNIHVPNSYKQENKQEPYYL-----IVLKKEIDKLKVFMPKVESLINEE 688
                                                                                                                                                                                                                                                                                                                                                                      306 ---KLKEDK----EKKLIAAEEPDDEKKIKLKDSDDKVVVPVN-----------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 KKNKKTIENINE--LIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLIS 300
                                                                                                                                                                                                                                                                                                                                                                                                               581 LVENIKKDEEQLFEKKITKDENKPDEKILEVSD-----IVKVQVQKVLLMNKIDELKKTQ 635
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REGISTRATION NUMBER: 31,895
REFERENCE/DOCKET NUMBER: DX0288K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 LKEKENKETLKKKELENQKEKEEKNKIKDNNDEALKNKGNDKDDKKIVPKKPESVEKDLK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 EKNEKARNALKEKKLKEQKKNDAQKAKDLTKKESQD-----SSSEKSLKEKVNGEA 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 201-822-7039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEIVETKFYGMRENALGEL-DEYEE------
DYQL-EHEPPTKLPEYEKGHVSREYQLDHEPPTKLPEYE---
                                        KYILVSHSTMNE-----KILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDS 842
                                                                                                                                    QEQKQAQPPVPVPVPEAKAQVPTPPAPVNNKTENVS-----KLDYLEKLYEFLNTSYICH 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----EDGEGDLKDVEEKLEETGYGFREKFPTTRILVKRK----RNKEQK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ED------RSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLT 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKEKIKIEKKKIESDKKSY 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMELKEKEFIKQHLKDYEE----RKEKRRNWILRSLRRDKLREIEQLEKLNA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EIAKTIKFNIDSLFTDPLELEYYLREKNKN-IDISAKVETKESTEPNEYPNGVTYPLSYN 414
                                                                                        REKRENPDGEPLNTPEIHV----IRPSDLMDKGENKSAGHPFKYQPTKGLKEY-EESHVSK 487
                                                                                                                                                                                                                                                                          -----KNKSSFPDKFRAPDKKRTMFYRLSELFPIVPRKD-NELAVCGDSMDSKVNGK 392
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07-AUG-1992
                                                                                                                                                                                 -----KSTFNPFKRRNKLKERKMQELHKFKKNYKKYQKLLE 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.5%; Score 296; DB 5;
20.3%; Pred. No. 8.3e-08;
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-KGHVSREYQLDNE 538
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COUNTRY:

Madison New Jersey USA

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305

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RESU PCT- Se ; Se ; ;	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Оу	Qy Db	Qy Db	Qy Db	Qy Db	Qý	Qy Db	Qy Db
RESULT 31 PCT-US93-07261-16 ; Sequence 16, Application PC/TUS9307261 ; GENERAL INFORMATION: ; TITLE OF INVENTION: PfEMP3 MALARIA ANTIGEN, ANALOGS, ANTIBODIES AND USES THEREO ; NUMBER OF SEQUENCES: 23 ; CORRESPONDENCE ADDRESS: ADDRESSEE: John H. C. Blasdale ; STREET: One Giralda Farms ; CITY: Madison	1587 CTEEDSGSNGKKIT 1600 :::: :: 1311 ERQONTGLKNTPSEGQONT 1329	1532 CVKKQCPQNSGCFRHLDEREECKCLLNYKOEGDKCVENPN-PTCNENNGGCDADAK 1586	1475 -KNNNFVGIADLSTDYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQ 1531	1433 DLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFK- 1474 	1377 NFANDVLGYYKILSEKYKSDLDSIKKYINDKOGENEKYLPFLNNIETLYKTVND-KI 1432 	1330 ESDLIPYKDL-TSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDI 1376 : : : :	1291 GVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFKNVL 1329 	1234 DDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTDSVIDNILSKIENEYEVLYLKPLA 1290 	1175 NTDVNNALESYKKF-LPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNV 1233	1118 SLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSEN 1174 	1058 NFSVFFNKKKEAEIAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYA 1117 	1001 LQLSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVLQ 1057 	946 KSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKT- 1000 :: : :: : ::: : ::: : ::: :	903 DKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQELIQQ 945 : : : ::	843 LNNSLSQLFMEIYEKEMYCNLYKLKDNDKIKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQ 902 ::: :: :: : : : : : : :::::::::::::::

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PCT-US93-07261-16
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TELEPANE: 201-822-7039
TELEFAX: 201-822-7039
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1663 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.5%; Score 296; DB 5; Length 1663; Best Local Similarity 20.3%; Pred. No. 8.8e-08; Matches 308; Conservative 248; Mismatches 601; Indels 362; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US93/07261
FILING DATE: 19930805
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,531
FILING DATE: 07-ÄUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Blasdale, John H. C.
REGISTRATION NUMBER: 31.895
REFERENCE/DOCKET NUMBER: DX0288K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-822-7398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 07940-1000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0
SOFTWARE: Microsoft Word 5.1a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1663 amino
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: pepti
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Microsoft WO CURRENT APPLICATION DATA:
432 REKRENPDGEPLNTPEIHV---IRPSDLMDKGENKSAGHPFKYQPTKGLKEY-EESHVSK 487
                                       735 QEQKQAQPPVPVPVPEAKAQVPTPPAPVNNKTENVS-----KLDYLEKLYEFLNTSYICH 789
                                                                                                                                                                              342
                                                                                                                                                                                                                     636 LILKNVELKHNIHVPNSYKQENKQEPYYL-----IVLKKEIDKLKVFMPKVESLINEE
                                                                                                                                                                                                                                                                 306 ---KLKEDK----EKKLIAAEEPDDEKKIKLKDSDDKVVVPVN------
                                                                                                                                                                                                                                                                                                        581 LVENIKKDEEQLFEKKITKDENKPDEKILEVSD-----IVKVQVQKVLLMNKIDELKKTQ 635
                                                                                                                                                                                                                                                                                                                                                           265
                                                                                                                                                                                                                                                                                                                                                                                  526 HHNTFASYENSKHNLEKLTKALK----YMEDYSLRNIVVEKELKYYKNLISKIENEIET 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                231 EEIVETKFYGMRENALGEL-DEYEE------RYEK---KRYYLK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               415 DINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKEKIKIEKKKIESDKKSY 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    356 ETAKTIKFNIDSLFTDPLELEYYLREKNKN-IDISAKVETKESTEPNEYPNGVTYPLSYN 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 VLEK-RIDTLKK----NENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIK 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 KKNKKTIENINE--LIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLIS 300
                                                                                         393 KL----
                                                                                                                                689 KKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
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                                                                                                                                                                            -----KNKSSFPDKFRAPDKKRTMFYRLSELFPIVPRKD-NELAVCGDSMDSKVNGK 392
                                                                                                                                                                                                                                                                                                                                                           -----EDGEGDLKDVEEKLEETGYGFREKFPTTRILVKRK----RNKEQK-----
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	ation US/09572191 N: H; Christophe icz, Roman	2-191-2 Per 2, Applicat. No. 635466 INFORMATION: ANT: Beraud, ANT: Sakowic	SOLT 32 -09-572-191 Sequence 2, Satent No. SENERAL INI APPLICANT: APPLICANT:	7 CO CO CO CO CO CO CO CO CO CO CO CO CO	
	LKNTPSEGQQNT 1329	ERQQNTGLKI	1311	Db	
	SNGKKIT 1600	CTEEDSG	1587	Qy	
131	QQNTGLKNTPNERQQNTGLKNTPSEGQQNTGLKNTPN	TGLKNTPSKG	1251	Дb	
158	GCFRHI	CVKKQCP	1532	Qy	
125	MKNKELLNKDISNKDMKNKELLNKDLSNEDMKNKELLNKDIRNKDLKSIGNMEQQN	MKNKELLNKI	1195	Db	
153	IADLSTDYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQ	-KNNNFVGI	1475	Qy	
119	NAELKNKELRNKGSDGLKENAELKNKELRNKGSEGLKENVYTNNDLKNNDIQNKDLSNKD	NAELKNKELF	1135	Дb	
147	YEKSNVE	DLFVIHLEAKVLNYT	1433	Qy	
113	3SEGLKENAEQKNKELQNKGSEGLKENAELKNKELRNKGSDGLKE	ELKNKELQNKG	1080	Db	
143	GYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVND-KI	NFANDVL	1377	Qy	
107	ELR-	ENAELKNKEI	1020	Db	
137	TSS	ESDLIPYKDL-	1330	Qy	
101	LKENAELKNKELRNKGSDGLKENAELKNKELRNKGSDGLKENAELKNKELRNKGSEGLK	GLKENAELKN	960	Db	
132	LENNVMTFNVNVKDILN		1291	Qy	
959	TDLAKGKEVTNKARENLEEYNET-DLAKGKEVTNKARENLEEYEEKDYMKNNELQNKGSD	TDLAKGKEVT	901	Db	
129	IFGESEEDYDDLGQVVTGEAVTPSVIDN	DDEVDDVIIVP	1234	Qy	
900	LEEYNETDLAKGKEVTNKARENLEEYNETDLAKGKEVTNKARENLEEYNE		851	Db	
123	YKKF-LPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNV	NTDVNNALESYKKF-	1175	Оу	
850	EYNETDLAKGKEVTNKÅRENLEEYNETDLAKGKEVTNKAREN	NLEEYNETDI	806	Db	
117	EKKKLSYL	. K	1118	Qy	
805	NETDLA	NLEEYN	762	Дb	
111	TENTLENTKILLKHYKGLVKYYNGESSPLKTLSEE	NESVEENKKKEAEIAE	1058	Ωу	
761	KGKEVTNKARENLEEYNETDLAKGK-EVTNKARENLEEYNETDLAKGKEVTNKAHE	LAKGKEVTNE	705	Db	
105	DKKKTVGKYKMQIKKLTLLKEQLE	LQLSFDLYNKYKLKLERLE	1001	Qy	
704	-YNETDLAKGKEVTNKPHESVDEYDQ-SELAKGKDITNKPHESVDEYDQTE	KPHENLEE	648	DЬ	
100	EKILKDSDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKT-	KSSENFYEKI	946	Qy	
647	ITNKPHESVDEYDQ-SELAKGKDITNKPHESVDEYDQTELAKGKEVTN	DQTELAKGKDITNKP	591	Db	
945	DKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQELIGQ	DKPEVSANDI	903	Qy	
590	YEKGHVSREYQL-DNEGPSTLKEYDQTELAKGKDITNKPHESVDEY	VRDELPE	539	Дb	
902	LKDNDKIKNLLEEAKKVSTSVKTLS	LNNSLSQLFN	843	Qy	
538	TKLPEYEKGHVSREYQLDHEPPTKLPEYEKGHVSREYQLDNE	 DYQL-EHEPPT	488	Дb	
842	KILKQYK	KYILVSHSTMNE	790	Qy	

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; ORGANISM: Human
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SEQ ID NO 2
LENGTH: 13
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CURRENT APPLICATION NUMBER: US/09/572,191
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 SVASGGSVASGGSGNSRRTNPSDNSSDSDAKSYADLKHRVRNYLLTIKEL-KYPQLFDLT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 19.4
nes 292; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTRDKKKTNYMEYFQEAMLFFKKSEQEKKSLIEKVTQLED------LTLKKEKF 452
                          KQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLY 864
                                                                                                                                                                INEEKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQAQPPV 744
                                                                                                                                                                                                         QAKLDE -
                                                                                                                                                                                                                                                                                                      NLISKIENEIETLVENIKKDEEQLFEKKITKDENKPD--EKILEV--SDIVKVQVQKVLL 624
                                                                                                                                                                                                                                                                                                                                                                                                                                              KIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYK 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----ENINELIEESKKTIDKNKATKEEEKKKLYQAQYDLSIYNKQLEE-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAAEAYQVLSGGWRNRRVASTSMNRESSRS------HAV--FTITIESMEKSNEIVNIR 257
                                                                                                 PVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKIL
                                                                                                                                      FSSERID--
                                                                                                                                                                                                                                         MNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESL 684
                                                                                                                                                                                                                                                                          RPVPKLSPEMGSF-GSLYTQNSSILDNDILNEPVPPEMNEQAFEAISEELRTVQEQMSAL
                                                                                                                                                                                                                                                                                                                                             --QLELESELQSLQKANLNLENLLEATKACKRQEVSQLNKIHAETLKIITTPTKAYQLHS
                                                                                                                                                                                                                                                                                                                                                                             VEKLTHHNTFASYENSKHNLEKL---TKALKYMEDYSLRNIVVE-----KELKYYK 568
                                                                                                                                                                                                                                                                                                                                                                                                               KSDKNQQGFSPKAQKEPCLFAN--TEKLKAQLLQIQTELNNSKQEYEEFKELTRKR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -HHPRVAKYAME----NHSLREENRRLRLLEPVKRAQE--MDAQTIAKLEKAFSEISGME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEYPNGVTYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKEKI 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IQSNKMI-----VKFREDQIIRLEKLHKESRGGFLPEEQDRLLSELRNEIQTLREQIE- 505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RCFGETLSTLNFAQRAKLIKNKAVVNEDTQGNVSQLQAEVKRLKEQLAELASGQTPPESF 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SKLTF-----LLRDSLG-----GNAKTAIIANVHPGS 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.5%; Score 294; DB 4
19.4%; Pred. No. 9e-08;
htive 240; Mismatches 5
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                                                                                                                                      -----WTKQQEELLSQL--NVLEKQLQE------
-VKLEYSSF---KTNQEKEFNKLSERHMHVQL-
                                                                                                                                                                                                       -EEHKN-----LKLQQHVDKLEHHSTQMQEL
                                                                   -DFLKSE--VHDLRVVLHSA-----
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JS-(; SEQ ; SEQ	; PRIOR ; PRIOR ; PRIOR	; FILE ; CURR	; TITLE	; APF	; GENE	; Patent	RESULT US-09-	Db 1	0у 1	Db´ 1	0у 1	Db 1	0у 1	Db 1	0у 1	Db 1	Qy 1	Db 1	0у 1	քե 1	Qy 1	Db 1	0у 1	Db	Qy 1	Db	Оу	Db	Qy	Db	Qy
RT M: H 62-2	FastSEQ for 2	PPLICATION NUMBER: US 0 LING DATE: 2000-05-17 DE SEC ID NOS: 6		OF INVENTION	APPLICANT: Sakowicz, Roman APPLICANT: Wood, Kenneth	Beraud, Chr	sequence 2, Application 05/09/23202 Patent No. 6379912 Convent Theoremseron.	33	1346HQNLHQK 1352	1489 YNHNNLLTK 1497	1303 QEKEQLRSKLEEMYEERERTSQEMEMLRKQVECLAEENGKLVG 1345	KIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFK	1246 QEESIKERLAKSKIVEEMIKMKADLEEVQSALYNKEMECIRMTDEVERTQTLESKAF 1302	1372 IDTDINFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLDFLNNIETL-YKTV 1428	1199REMENLRLESQULIEKNWLLQGQLDDIKRQKENSDQNHPDNQQLKNE 1245	VVKDPYKELNKEKRDKELSSYNY	1166GRASKTS-LEHLVTKLNEDREVKNAEILRMKEQL 1198	GVYRSLK	131 VMDSAAEDPQSPKTPPHFQTHLAKLLETQEQEIED- 1165	LEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDY	1092 ELTKKEALIQELQHKLNQKKEEVEQKKNEYNFKMRQ-LEH 1130	AELKEVI	1049	TLSEESIQTEDNYASLENFK	994 LRSSVCEKTETIDTLKQELKDINCKYNSALVDREESRVLIKKQEVDILDLKETLR 1048	EQLESKLNSLNNPKHVLQNFSVFFN	951QMAKVQKLEESLLATEKVISSLEKSRDSDKKVVADLMNQIQE 993	EEDINKLKKTLQLSFDLYNKYKI	899 LNNLMELLEAEKERNNKLSLQFEEDKENSSKEILKVLEAVRQEKQKETAKCE 950	919 LNNSLKLFENILSLGKNKNIYQELIGQKSSENFYEKILKDSDTFYNESFTNFYKSKADDI 978	845QLDNLRLENEKLLESKACLQDSYDNLQEIMKFEIDQLSRNLQNFKKENETLKSD 898	VSTSVKTLSSSSMQPLSLTPQDKP

Query Best I Matche Qy 9	ery Mast Loc t Loc ches 93	y Match 3.5%; Score 294; DB 4; Length 1388; Local Similarity 19.4%; Pred. No. 9e-08; hes 292; Conservative 240; Mismatches 510; Indels 467; Gaps 70; 93 SVASGGSVASGGSGNSRRTNPSDNSSDSDAKSYADLKHRVRNYLLTIKEL-KYPQLFDLT 151 1 1 1 1 1 1 1 1 1 1	
} 6	י ני זיי	SONO	
₽ Q	258	TSLLNLVD-LAGSERQKDTHAEGMRLKEAGNINRSLSCLGQVITALVDVGNGKQRHVCYR 316	
Qy	199	DYCQIPFNIKIRANELDVIKKLVFGYRKPLDNIKDNVGKMEDYIKKNKKTI 249	
B	317	DGNAKTAIIANVHPGS 344	
Qy	250	ENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEE 294	
망	345	RCFGETLSTLNFAQRAKLIKNKAVVNEDTQGNVSQLQAEVKRLKEQLAELASGQTPPESF 404	
Qy	295	AHNLISVLEKRIDTLKKNENIKE-LLDKINEIKNPPPANSGNTPNTLLDKNKKI 347	
Dβ	405	LTRDKKKTNYMEYFQEAMLFFKKSEQEKKSLIEKVTQLEDLTLKKEKF 452	
Qy	348	EIAKI	
Db	453	GGFLPEEQDRL	
Qγ	401	DINNALNELNSFGDLINPFDYTKEPS	
Db	506	PRVAKYAME	
Оу	461	KIEKKKIESDKKSYEDRSKSINDITKEYEKILNEIYDSKFUNNIDLTUFEKMMGKRYSYK 520	
, ב	9 0	SURNQUGESPRAQREPCHEANTERKRAQLHQTELNNSRQETEEFRELTRKK o	
B 5	613	OLELESELOSLOKANI NI ENIL FATKAOKROEKSOLINK THAETIKTITTPTKAVOLIS 670	
ογ	569	ISKIENEIETLVENIKKDEEOLFEKKITKDENKDDEKILEVSDIVKVOVOKVLL	
D _b	671	: ::	
Qy	625	KKTQLILKNVELKHNIHVPNSYKQENKQEPYYL	
ДĎ	730	QAKLDE	
Qγ	685	IKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALEC	
Db	761	FSSERID 788	
Qy	745	SKLDYLEKLYEFLNTSY	
Db	789	TQTKNBFLKSEVHDLRVVLHSA 810	
Qy	805	SCDPLDLLFNIQNNIPVMYSMFDSL	
Ъ	811	DKELSSVKLEYSSFKTNQEKEFNKLSERHMHVQL- 844	
Qy	865	KLKDNDKIKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTN 918	
Db	845	QLDNLRLENEKLLESKACLQDSYDNLQEIMKFEIDQLSRNLQNFKKENETLKSD 898	
Qy	919	VILSLGKNKNIYQELIGQK	
DЬ	899	LNILMELLEAEKERNNKLSLQFEEDKENSSKEILKVLEAVRQEKQKETAKCE 950	
Qy	979	KLEEDINKLKKTLQLSFDLYNKYKLKLERLFDK-KKTV	
Ъ	951	KVQKLEESLLATEKVISSLEKSRDS	
Qy	1038	LKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAETAETENTLENTKIL 1084	

ОУ 19	Db 258			Query M Best Lo Matches		Qy 1489	Db 13(Qy 1429	Qy 1372 Db 1246	Db 1199		Db 1166	Qy 1257	Qy 1199 Db 1131		. Qy 113	Db 104	ОУ 1085	Db 994
9 DYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMEDYIKKNKKTI 249	TSLLNLVD-LAGSERQKDTHAEGMRLKEAGNINRSLSCLGQVITALVDVGNGKQRHVCYR	NAME OF COUNTY OF STREET O	SVASGGSVASGGSGNSRTNPSDNSSDSDAKSYADLKHRVRNYLLTIKEL-KYPQLFDLT	Match 3.5%; Score 294; DB 4; Length 1388; Local Similarity 19.4%; Pred. No. 9e-08; Indels 467; Gaps 70; es 292; Conservative 240; Mismatches 510; Indels 467; Gaps 70;	HQNLHQK 1352 HQNLHQK 1352 2. Application US/09723219 3. Capalication US/09723219 3. Application US/09723219 3. Application US/09723219 INT: Beraud, Christophe INT: Sakowicz, Roman INT: Wood, Kenneth Wood, Kenneth Sakowicz, Roman INT: Wood, Kenneth US/09/09/09/09/09/09/09/09/09/09/09/09/09/	9 YNHNNLLTK 1497	03 QEKEQLRSKLEEMYEERERTSQEMEMLRKQVECLAEENGKLVG 1345	NDKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDK	2 IDTDINFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETL-YKTV 1428 :	REMENTRLESQ	SRENKRENEKNYLESDLIPYKDLTSSNYVYKDPYKFLNKEKRDKFLSSYNYIK	6GRASKTS-LEHLVTKLNEDREVKNAEILRMKEQL	GQVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSL	9 VSESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDDV11VPIRGESEEDYDDL 1256 : ::	ELTKKEALIQELQHKLNQKKEEVEQKKNEYNFKMRQ-LEH	39 EKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATV 1198	H-	5 LKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNL 1138	: : :: : :

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PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5178
LENGTH: 1010
TYPE: PRT
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US-09-134-001C-5178
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERWIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 Match 3.5%; Score 293.5; DB 4 Local Similarity 20.0%; Pred. No. 6.5e-08; les 240; Conservative 201; Mismatches 417
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                                                                      SLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSKHN 539
  LEKLTKALKYMEDYSLRNIVVEKELKYYKNL--ISKIENEIETLVENIKKDEEQL-----
                                                                                                                                  DIDTFNN--DELALYKE-LESSQTDKMIEKFPQFNDYGCKI-----LKSFEE---
                                                                                                                                                                           ELNSFGDLINPFDYTKEPSKNIYTDNERKKF--INEIKEKIKIEKKKIESDKKSYEDRSK 479
                                           AKNKITKELDDL----NHKYKVNVELSENTKKL----KAEKI----KFDDLKKEQNY 300
                                                                                                                                                                                                                                                       KFNIDSLFTDPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALN 421
                                                                                                                                                                                                                                                                                                                                                                                                  STKTRKEGDLRSHFADGKSPMSVIYQFKVNNQTFKIHREAPFIKEGNITKTQAKLNIYEL 116
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                                                                                                                                                                                                                         -FNSERFD----EIRHLLVENVKQEKV--QIENR-----
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                                                                                                                                                                                                                                                                                                                                       LDKINEIKNPPPANSGNTPNTLL--------DKNKKIEEHEKEIKEIAKTI 361
                                                                                                                                                                                                                                                                                                                                                                                                                                           KNATKEE----EKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKEL 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---REMENUR--LES-----QQLIEKNWLLQGQ---LDDIKRQKENSDQNHPDNQQLKNE 1245
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                                                                                                                                                                                                                       YTQIENLWN 211
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RESULT 36
US-08-446-855A-2
                                                                                                                                                                                                                              Sequence 2, Application US/08446855A
Patent No. 5849573
GENERAL IMFORMATION:
APPLICANT: Stewart, Thomas S
                                                                                                                                  APPLICANT: Flores, Maria V
APPLICANT: O'Sullivan, William J
TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
TITLE OF INVENTION: phosphate synthetase II
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                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                            NUMBER OF SEQUENCES:
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FILING DATE: 06-7u1-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.009
REFERENCE/DOCKET NUMBER: 47-8
TELECOMMUNICATION INFORMATION:
TREFERENCE. 73-816-1000
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA
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COMPUTER READABLE FORM:
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                                                                                                           KTVNDKIDLFVIHLEAKVLNYT--YEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIA 1483
                                                                                                                                                                                   -----FANDVLGYYKILSEKYKSDLDSIKKY---INDKQGENEKYLPFLNNIETLY 1425
                                                                       EKESNHEKGHRRNGLNKKNKEKNMEKN-KGKNKD-KKNYHYVN-H 1701
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Sequence 2, Application US/09150741 Patent No. 6183996 FITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoy1 PATENTE OF INVENTION: Nucleotide Sequence Encoding Carbamoy1 PATENTE OF INVENTION: Synthetase II FILE REFERENCE: CURRENT FILING DATE: 1998-09-10 EARLIER FILING DATE: 1998-09-10 EARLIER FILING DATE: 1995-07-06 EARLIER FILING DATE: 1995-10-02 EARLIER FILING DATE: 1995-10-02 EARLIER FILING DATE: 1995-10-02 EARLIER FILING DATE: 1995-10-02 EARLIER FILING DATE: 1995-10-02 EARLIER FILING DATE: 1995-10-02 EARLIER FILING DATE: 1995-10-02 EARLIER FILING DATE: 1995-10-06 EARLIER FILING DATE: 1995-10-06 EARLIER FILING DATE: 1995-10-06 EARLIER FILING DATE: 1995-10-06 EARLIER FILING DATE: 1995-10-06 EARLIER FILING DATE: 1995-10-06 EARLIER FILING DATE: 1995-10-06 EARLIER FILING DATE: 1995-10-06 EARLIER LANGER DATE: 1995-10-06 EARLIER FILING DATE: 1995-10-06 EARLIER LANGER: 1995-10-06 EAR				
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	SYENSKHNLEKLTKALKYMEDYSLRNI : : : : : : DYDAVLLSNGPGDPKKCDFLIKNLKSUTKNK ILISTIANULLSNGPGDPKKDEPCLDEKKK :		33.5; DB 4; Length 2391; 5. 1.9e-07; 7. 1.9e-07; 8. 1.9e-07; 9. 1.	ling Carbamoyl

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                                                                        KTVNDKIDLFVIHLEAKVLNYT--YEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIA
                                                                                                                                CSNYNNASAFVNGKDRNDNLENDCIEKNMDHTYKHYNRLNNRRSTNERMMLMVNN-----
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                                             ---EKESNHEKGHRRNGLNKKNKEKNMEKN-KGKNKD-KKNYHYVN-H
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US-08-755-587-44
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Best Local Sin
Matches 382;
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Patent No. 6
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APPLICANT: Stratton, Michael R
TITLE OF INVENTION: Materials an
TITLE OF INVENTION: identification
TITLE OF INVENTION: susceptibili
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 0
FILING DATE: 23-NOV-1
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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 228
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STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Kenneth D Sibley REGISTRATION NUMBER: 31 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 14-DE0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: GB 9617961.9 FILING DATE: 28-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                        7 LCSFLF----FIINTQCVTH--ESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGT 60
                                                                                                                                                                                                            AVTTSTPGSKGSVASGGSVASGGSVASG----SGNSRRTNPS
LDNIKDNVGKMEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSI
                                       KTRKKIFHEAN-----
                                                         EEINELLYKLNFYFDLLRAKLNDVCANDYCQI----PFNLKIRANELDVLKKLVFGYRKP
: :: :: | | | | | :: | : | | :: | | :: | |
                                                                                                                                                                                VFPHDTTANVKSYFSNHDESLKKNDRFIASVTDSENTNQREAASHGFGKTSGNSFKVN--
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                                                                                                           -SCKDHIGKSMPNV---
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Plaza, 3605 Glenwood
                                                                                                                                                                                                                                                                                                                          3.5%; Score 292.5;
18.6%; Pred. No. 3.3e
ative 288; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Materials and methods relating to the identification and sequencing of the BRCA2 cancer susceptibility gene and uses thereof.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17
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                                       - - ADECEKSKNOVKEKYSFVSEVEPNDTDPLDSNV-AHQKP
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nes 717;
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)y 1171 PSENNTDVNNALESYKKFLPEGTDVATVVSESGSDTLEQS 1210	Qy
	NY , 1111 QTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNS 1170	pb Qy
	NY 1072 AETENTIENTKILIKHYKGLVK	DP QA
	PY 1037 LLKEQLESKLNSLNNPKHVLQNESVFFNKKKEAEI 1071	pb qq
	NY 986 KRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKLT 1036	ф
	NY 943 IGOKSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLN-DES 985	Д
	PY 887 KTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQEL 942	QУ
)Y 827 FNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKDNDKIKNLLEEAKKVSTSV 886	D 04
	NY 767 ENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLL 826	Db Oy
	NY 708 EITGOATTKPGQQAGSALEGDSVQAQAQAQAQAQPPVPVPVPEAKAQVPTPPAPVN-NKT 766	Db Oy
	PY 648 HVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEPSTEG 707	Дb
	NY 597 ITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELKHNI 647	рь
	NY 547 LKYMEDYSLRNIVVEKELKYYKNLISKIENEIETLVENIKKDEEQLFEKK 596	ОУ
	NY 498 SKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKA 546 ::	Db Oy
:	NY 438 EPSKNIYTDNERKKFINEIKEKIKIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIYD 497 : :: : : : :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	Db Oy
	NY 379 LREKNKNIDISAKVETKE-STEPNEYPNGVTYPLSYNDINNALNELNSFGDLINPFDYTK 437	dq Qy
	NY 347 IEEH	DP OA
	NY 288 YNKQLEEAHNLISVLEKRIDTLKKNENIKELLDKINEI-KNPPPANSGNTPNTLLDKNKK 346	Ωу
<u>.</u>	; : : : : : : : : : :	DВ

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RESULT US-08-6 Seque Paten GENN AN AN AN AN AN AN AN AN AN AN AN AN A	р _р	Qy Db	ОУ	Вρ	ОУ	Qу	ОУ	Qу	О У	Qy Db	Фр	Db Qy	В
SULT 39 Sequence 4, Patent No. 5 GENERAL INF APPLICANT TITLE OF	1611 1973	1567 1914	1531 1857	1519 1797	1470 1739	1439 1679	1437 1619	1413 1559	1360 1514	1309 1460	1258 1402	1211 1342	1283
USON TO SOLUTION: 103-753D-4 LUCANT: APPLICATION: APPLICANT: HOLT, JEFFREY T. APPLICANT: HOLT, JEFFREY T. APPLICANT: KING, MARY-CLAIRE APPLICANT: KING, MARY-CLAIRE APPLICANT: SZABO, CSILLA I. APPLICANT: ROBINSON-BENION, CHERYL L. APPLICANT: THOMESON, MARILYN E. APPLICANT: THOMESON, MARILYN E. APPLICANT: THOMESON, MARILYN E. APPLICANT: THOMESON, MARILYN E. APPLICANT: THOMESON, MARILYN E. APPLICANT: THOMESON, MARILYN E. APPLICANT: THOMESON, MARILYN E. APPLICANT: THOMESON, MARILYN E. APPLICANT: THOMESON CHARACTERIZED BRCA1 AND BRCA2 TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 TOTICLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS. UMMBER OF SEQUENCES: 29 CORRESPONDENCE ADDRESS: ADDRESSEE: ARLES A. TAYLOR, JR. STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER STREET: BOULEVARD CITY: DURHAM	LFDGIFCSSS 1620 :: NTCGIFSTAS 1982	VENDNDTCNDNNGGCDADAKCTEEDSGSNGKKITCECTKPDSYP 1610	QCVKK	GNLQGMLNISQH 1530 	-LADFKKNUNFVGIADLSTDYNHUNLLTK-FLSTGMVFENLAKTVLSNLLD 1518 	LEAKVLNYTYE-KSNVEVKIKELNYLKTIQDK 1469 	NLCRQTENLKTSKSIFLKVKVHENVEKETAKSPATCYTNQSPYSVIENSALAFYTSCSRK 1678		KFLSSYNYIKDSIDTDINFANDVLGYYKILSEKYKSDLDSIKKYINDK-QGENE 1412 	VNVKDILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRD 1359:	QVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFN 1308 	QPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLG 1257	VSEKNNKCQLILQNNIEMTTGTFVEEITENYKR-NTENEDNKYTAASRNSHNLEFDGSDS 1341

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; PAGES: 789-792
; DATE: 1995
; RELEVANT RESIDUES IN
; RELEVANT RESIDUES IN
US-08-603-753D-4
                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                        Query Match
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HYPOTHETICAL: r
ANTI-SENSE: nc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/2
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
TELEFAX: (919) 419-0383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUBLICATION INFORMATION:
AUTHORS: Wooster, R. et al.
TITLE: Identification of the breast cancer
TITLE: susceptability gene BRCA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 17 JAN 1995
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S.
FILING DATE: 17 JAN 1995
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                                                                                                                                                                 160
  278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: .BRCA2 protein
LOCATION: 1 to 3418; Genbank locus HSU43746
IDENTIFICATION METHOD:
OTHER INFORMATION: BRCA2 protein has a negative
OTHER INFORMATION: regulatory effect on growth (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEVELOPMENTAL STAGE: adult
TISSUE TYPE: female breast
CELL TYPE: normal breast tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 20 FE
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                                                                                                                    AVTTSTPGSKGSVASGGSVASGGSVASG----SGNSRRTNPS 114
                                    DNSSDSDAKSYADLKHRVRNYLLTIKELKYPQLFDLTNH-MLTLCDNIHGFKYL--IDGY 171
                                                                              VFPHDTTANVKSYFSNHDESLKKNDRFIASVTDSENTNQREAASHGFGKTSGNSFKVN--
                                                                                                                                                                 VCGSLFHTPKFVKGRQTPKHISESLGAEVDPDMSWSSSLATPPTLSSTVLIVRNEEASET
-SCKDHIGKSMPNV---
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                                                                                                                                                                                                                                              3.4%; Score 288.5; DB 2;
18.6%; Pred. No. 5.4e-07;
vative 287; Mismatches 718;
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- LEDEVYETVVDTSEEDSFSLCFSKCRTKNLQKVRTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KFLSSYNYIKDSIDTDINFANDVLGYYKILSEKY---KSDLDSIKKYINDK-QGENE--- 1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VNVKDILNSRFNKRENFKNVL---ESDLIPYKDLTSS-----NYVVKDPYKFLNKEKRD 1359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------LEAK------
                                      INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09099753
         INVENTION:
                                                                                                                                                                                    PAGE, DAVID L.
KING, MARY-CLAIRE
SZABO, CSILLA I.
JETTON, THOMAS L.

ROBINSON-BENION, CHERYL L.

THOMPSON, MARILYN E.

THOMPSON, MARILYN E.

VENTION: CHARACTERIZED BRCA1 AND BRCA2

VENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS

VENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.
                                                                                                                                                                                                                                                                                JENSEN, ROY A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -KYLPFLNNIETLYKTV--------NDK----IDLFV-----
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; RELEVANT RESIDUES
; RELEVANT RESIDUES
US-09-099-753-4
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                           Q
                                                              Matches
                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/60
FILING DATE: 20 FEB 1996
APPLICATION NUMBER: U.S.
FILING DATE: 17 JAN 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: ARLES A. TAYLOR, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: WORD PERFECT 6.1 and ASCII CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                               PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: SUITE 1401, UNIVERSITY TOWER, STREET: BOULEVARD CITY: DURHAM
160 VCGSLFHTPKFVKGRQTPKHISESLGAEVDPDMSWSSSLATPPTLSSTVLIVRNEEASET 219
                                                                                                                                                                     VOLUME: 379
PAGES: 789-792
DATE: 1995
                                                                                                                                                                                                                              AUTHORS: Wooster, R. et al.
TITLE: Identification of the breast
TITLE: susceptability gene BRCA2
                                                                                                                                                                                                                                                                                               OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                          NAME/KEY: BRCA2 prote LOCATION: 1 to 3418; IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                     CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVELOPMENTAL STAGE: adult TISSUE TYPE: female breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: ARLES A. TAYLOR, JR. REGISTRATION NUMBER: 39,395 REFERENCE/DOCKET NUMBER: 12
                                                                                                                                                                                                                                                                                                                                                                                     ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens sapiens INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
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ZIP: 27707
                                                                                                                                                                                                                  JOURNAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                7
                    CCSFLF----FIINTQCVTH--ESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                   Nature
                                                            Conservative 287;
                                                                                                                                                                                                                                                                                                                                     BRCA2 protein
1 to 3418; Genbank locus HSU43746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC/XT/AT compatible SYSTEM: Windows 3.1
                                                                                                                                                                                                                                                                                                                                                                                                     normal breast tissue HMEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
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                                                                        3.4%;
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                                                                                                                                                                                                                                                                                           BRCA2 protein has a negative regulatory effect on growth o
                                                                                                                                        SEQ
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                                                                           Score 288.5; DB 4; Length Pred. No. 5.4e-07;
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                                                            Mismatches
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domain at amino
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                                                            Indels
                                                                                                                                                                                                                                                                                               of human mammary cells.
                                                                                                                                        acids 3334-3344
                                                                                           3418;
                                                            663;
                                                           Gaps
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RESULT 41

US-08-986-106-4

; Sequence 4, Application US/08986106
; Patent No. 6177410
; GENERAL INFORMATION:
; APPLICANT: HOLT, JEFFREY T.
; APPLICANT: JENSEN, ROY A.
; APPLICANT: KING, MARY-CLAIRE

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PAGES: 789-792
DATE: 1995
RELEVANT RESIDUES IN SEQ ID
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US-08-986-106-4
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APPLICATION UNMBER: 08/603,753

FILING DATE: 20 FEB 1996

ATTORNEY/AGENT INFORMATION:

NAME: ARLES A. TAYLOR, JR.

REGISTRATION UNMBER: 39,395

REFERENCE/DOCKET NUMBER: 1242/3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 49-8000

TELEPHONE: (919) 49-8000

TELEPHONE: (919) 49-8000

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TELEPHONE: (919) 49-8000

TELEPHONE: (919) 49-8000

TELEPHONE: (919) 419-0383

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 3418
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.4%; Score 288.5; DB 4; Length 3418; Best Local Similarity 18.6%; Pred. No. 5.4e-07; Matches 382; Conservative 287; Mismatches 718; Indels 663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: BRCA2 protein
PUBLICATION INFORMATION:
AUTHORS: Wooster, R. et al.
TITLE: Identification of the breast cancer
TITLE: susceptability gene BRCA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage
COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: ARLES A. TAYLOR, JR.
ADDRESSEE: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER
STREET: BOULEVARD
CITY: DURHAM
STATE: NORTH CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: STEINER, MITCHELL S.
APPLICANT: ROBINSON-BENION, CHERYL L.
APPLICANT: THOMESON, MARILYN E.
TITLE OF INVENTION: THERAPBUTIC METHODS
TITLE OF INVENTION: PROSTATE CANCER
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                         115
327 KTRKKIFHEAN------ADECEKSKNQVKEKYSFVSEVEPNDTDPLDSNV-AHQK
                                              172 EEINELLYKLNFYFDLLRAKLNDVCANDYCQI----PFNLKIRANELDVLKKLVFGYRK
                                                                                                                                                                                                        220 VFPHDTTANVKSYFSNHDESLKKNDRFTASVTDSENTNOREAASHGFGKTSGNSFKVN-
                                                                                                                                                                                                                                                                                                                 160 VCGSLFHTPKFVKGRQTPKHISESLGAEVDPDMSWSSSLATPPTLSSTVLIVRNEEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sind
TOPOLOGY: unknown
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                                                                                                                                                                                                                                                          61 AVTTSTPGSKGSVASGGSGGSVASGGSVAS--GGSVASGGSVASGG----SGNSRRTNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL: Nature VOLUME: 379
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                                                                                                                                                                                                                                                                                                                                                                     7 LCSFLF----FIINTQCVTH--ESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSG
                                                                                                                                                    DNSSDSDAKSYADLKHRVRNYLLTIKELKYPQLEDLTNH-MLTLCDNIHGFKYL--IDG
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QTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNS 1170	1111 ОТЕ	Qy	
AGTENTLENTKILLKHYKGLVKYINGESSPLKTLSEESI 1110 :: : : : : : :	1072 AET	Qy Db	:
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IGQKSSENFYEKILKDSDTEYNESFTNFVKSKADDINSLN-DES 985	942 943 IGC	ργ	
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		Db	
HVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEPSTEG 707	648 HVF	Qy	
EGQCENDPKSKKVSDIKEEVLAAACHPVQHSKVEYSDTDFQSQKSLL 760	714 EGC	Db V	
GTILRKCSRNETCSNNTVISQDLDYKEAKCNKEKLQLFITPEADSLSCLQ 713		2: B	
LKYMEDYSLRNIVVEKELKYYKNLISKIENEIETLVENIKKDEEQLFEKK 596		Qy	
AQFEANAFEAPLTFANADSGLLHSSVKRSCSQNDSEEPTLS 658	618 AQE	ДЪ	
YSYKVEKLTHH	498 SKE	Qy	
KKKTNKFIYAIHDETFYKGKKIPKDQKSELINCS 617	584	Db	
EPSKNIYTDNERKKFINEIKEKIKIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIYD 497	438 EPS	Qγ	4
TEASESGLEIHTVCSQKEDSLCPNLIDNG-SWPATTTQNSVALKNAGLISTL 583	533 TE	Db	
LREKNKNIDISAKVETKE-STEDNEYPNGVTYPLSYNDINNALNELNSEGDLINDEDYTK 437	379 LRE	Qy	
LESHTDCILAVKQAISGTSPVASSFQGIKKSIFRIRESPKETFNASFSGHMTDP-NFKKE 532	474 LES	DЪ	
TDPLELEYY 378	347 IEEH-	Qy	
SEKDLLDTENKRKKDFLTSENSLPRISSLPKSEKPLNEETVVNK-RDEEQH 473	424 SEF	ДĎ	
YNKQLEEAHNLISVLEKRIDTLKKNENIKELLDKINEI-KNPPPANSGNTPNTLLDKNKK 346	288 YNF	Оу	
FESGSDKISKEVVPSLACEWSQLTLSGLNGAQMEKIPLLHISSCDQNI 423	376 FES	Db	
LDNIKDNVGKMEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSI 287	228 LD	Qy	

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US-08-290-919-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08290919 Patent No. 5720959
                                                                                                                                                                                                                                                                                      GENERAL INFORMATION: APPLICANT: HOLDER
                                                                                                                                                                                                                                                APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1797
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                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                   STREET:
                                                         COUNTRY: U.S.A. ZIP: 20005-3918
                                                                                                STATE:
                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LFDGIFCSSS
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                                                                                                               WASHINGTON
                                                                                              D.C.
                                                                                                                                                                                                                                              BLACKMAN, MICHAEL J.
CHAPPEL, JONATHAN A.
                                                                                                                                  CUSHMAN DARBY & CUSHMAN, L.L.P. 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                      HOLDER,
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                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12,
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                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 4
                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,7
                            CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                           APPLICANT: CHAPPEL, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1570 PNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 22-FEB-PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: IFILING DATE: 04-OCT-CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                 STREET: LIVE CITY: WASHINGTON
               APPLICATION NUMBER:
                                                            APPLICATION NUMBER: FILING DATE: 04-OC
                                                                                                                                                                                                 COUNTRY: U.S.A. ZIP: 20005-3918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION:
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TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 PNPTCNENNGGCDADATCTEEDSGSSRKKITCECTKPDSYPLFDGIFCSSSN
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5720959
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DATE:
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                                                              04-OCT-1994
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JMBER: GB 9203821.5
22-FEB-1992
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                                                                                                                                                                                                                                                                                                                                               IMPROVEMENTS
                                                                                                              Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= x
/note= "X = M and N, or
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                                                                             US/08/290,919
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Pred. No. 7.1e-09;
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                                                                                                                Version
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; LENGTH: 48 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-290-919-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-356-952-4
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US-09-356-952-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 4
LENGTH: 1589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09356952 Patent No. 6117663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.3%; Score 280; DB 1; Length 48; Best Local Similarity 100.0%; Pred. No. 8e-09; Matches 48; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Boriack-5jodin, Ann
APPLICANT: Margarit, S. M.
APPLICANT: Morarit, S. M.
APPLICANT: Morarit, S. M.
APPLICANT: Cole, Philip
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 600-1-228N
CURRENT APPLICATION NUMBER: US/09/356,952
CURRENT FILING DATE: 1998-07-21
EARLIER APPLICATION UMMBER: 60/093,631
EARLIER FILING DATE: 1998-07-21
NUMBER OF SEQ. ID NOS: 14
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TELEFAX: (202) 822-0944
TELEX: 6714677 CUSH
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/A
FILING DATE: 22-FEB-1993
                                                                                          127
                                       226 KPLDNIKDNVGKMEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDL 285
                                                                                                                                      188
187 AETSSGHNNT-----VSMNNSPFSAPNDASHITPQSSNFNSNASLSQDMTKSADGSSEM 240
                                                                                                                                                                                                                     140 KELKYPOLFDLTNHMLT------LCDNIHGF---KYLIDGYEEINELLYKLNEYFDL 187
                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                                           81 SVASGGSVASGGSVASGGSGNSRRTNPSDNSSDSDAKSYADLKH-RVRNYLLTI 139
                                                                                                                                                                                                                                                                   7 SIPNTSSAREAGNASQTPSISSSSNTSTTNTESSSASLSSSPSTSELTSIRPIGIVVAA 66
                                                                                     RDSHLRKHSHPMKKYSSSKSSRRSSLNSLGNSAYLHVPRNPSKSRRGSSTLSASLSNAHN 186
                                                                                                                                                                             YDFNYPIKKDSSSOLLSVOQGETIYILNKNSSGWWDGLVIDDSNGKVNRGWFPQNFGRPL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
                                                                                                                                 ----LRAKLNDVCANDYCQIPFN-LKIRANELDVLKKLVFGYR 225
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                                                                                                                                                                                                                                                                                                                                                                                                Length 1589;
                                                                                                                                                                                                                                                                                                                                                       Indels 429;
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                                                                                                                                                                                                                                                                                                                                                       Gaps
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1100	AELLKGEQEKWFDIYSEDYSDDDSENDEAIIDDELGSEDYIERKAANIEKN	1050	Db
1272	AESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDN	1222	Qy
1049	LEFLNNSDDFKDACEKYVEISNLACIIVDQLIEERENLLNYAARMMKNNLT	999	Db
1221	KNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHVG	1164	Qy
998	TLDDPYLFSSMRSNFPVGHHEPFKNISNTPLVKGPFHKKNEQLALSLFHVLVSQDVEFNN	939	Db
1163	QTEDNY ASLENFKYLSKLEGKLKDNLNLEK KKLSYLSSGLHHLIAELKEVIKN	1111	Оу
938	NLIKTPSILLDLESEEFLVHAMSSVSSVLTEFFDIKQAFHDIVIRLIMTTQQT	886	σь
1110	AEIAETENTKILLKHYKGLVKYYNGESSPLKTLSEESI	1069	Qy
885	LNNATGEHLKIISKPKSRIRNLEINSSTYEQINQNVLLLEILENLDLSIFINLK	832	DЬ
1068	KTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKE	1022	Qy
831	ASGSVFTPFNRPSHNRTFSRARVSKRKKKYPLTVDTLNTMKKKSSQIFEK	782	Db
1021	FYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDK	962	Qy
781	VTSNEVTASSSKNSSISRIPPKMADAIASASGYSANSETNSQIDLKASSA	732	Дb
961	SANDDTSHSTNLNNSLKLFENILSL-GKNKNIYQELIGQKSSENFYEKILKDSDT	908	Qy
731	VQLLYFVLQSSVFSDDNTLPQLLPRFFKGSFSGGSWTNPFSTFITDEFGNATKNKA	676	рь
907	TLSSSSMQPLSLTPQDKPEV	854	
675	ENFSYLGPRNSVNSVYTPRTSIQNSTLEDFSPSNKNFKSAKSIYEMVDVEFSKFLRH	619	Db
853	KQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFME	805	Qy
618	SVPL-SGKRNVSTSTTDTLTPMRSSFSTVNENDM	586	Db
804	PVPVPEAKAQVPTPPAAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKIL	745	Qy
585	KKMDTMNDKDNDNQENNCSRTEGDDGKIEVDSVHDLV	549	Db
744	EKKNIKTEGOSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQAQPPV	688	Qy
548	VFTQLGCRLMQHEIKAKŞCSKEIKKIFKGLISSLSRISINSHLYFDSAFHR	498	Db
687	KKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINE	632	Qy
497	IKLWTELQDLTVYYTKTAHKMFLKENRLNFTKYFDLISDSI	457	дь
631	SKIENEIETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDEL	572	Qy
456	GPSSLNSLSAPDLTQNIQSRVVAPSRSSILAKSDIFYHYSRD	415	DЬ
571	MMGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLI	512	Qy
414	LRKNANIEDSSTRSKQSESEQNRSSLLMEKQDSKETDGNNNSINDDDNNNENNKNEFNEA	355	DЪ
511	IKEKIKIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNF-EK	456	Qy
354	ELPLISNSIMESDDICDSEPKFPPNDHLVNLYTRD	320	Db
455	YPNGVTYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINE	403	Оу
319	KTSDYKLVYYNKDLDIYCS	301	Db
402	KNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKNKNIDISAKVETKESTEPNE	343	Qy
300	THAIMNNNETNLQTSGEKAGPPLVAEETIKILPLEEIEMIINGIRSNIASTWSPIPLIT	241	Db
342	SIYNKQLEEAHNLISVLEKRIDTLKKNENIKEL-LDKINEIKNPPPANSGNTPNTLLD	286	Qy

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US-08-755-587-16
                                        APPLICATION NUMBER: US/08/755,587
FILING DATE: 25-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9523959.6
FILING DATE: 23-NOV-1995
PRIOR APPLICATION NUMBER: GB 952555.0
FILING DATE: 14-DEC-1995
PRIOR APPLICATION NUMBER: GB 9617961.9
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kenneth D Sibley
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405-135
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2329 amino acids
TYPE: amino acid
TYPE: amino acid
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US-08-755-587-16
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APPLICANT: Futreal
APPLICANT: Wooster
APPLICANT: Ashwort
APPLICANT: Stratto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Materials and methods relating to the TITLE OF INVENTION: identification and sequencing of the BRCA2 cancer TITLE OF INVENTION: susceptibility gene and uses thereof.
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                   MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: N
COUNTRY:
                                    TYPE: amino acid
TOPOLOGY: linear
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310 UCB Plaza, 3605 Glenwood Avenue,
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Stratton, Michael R
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US-08-639-501-2
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Patent No. 5
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                                                                                                                                                                                                                                                                                                  APPLICANT: Simard, Jacques
APPLICANT: Couch, Fergus
APPLICANT: Rommens, Johanna
APPLICANT: Weber, Barbara
TITLE OF INVENTION: Chromosome 13-Linked Breast Cancer
TITLE OF INVENTION: Susceptibility Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1536
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                                                                                          SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer,
STREET: 1201 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1683
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              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                           FILING DATE: 2
CLASSIFICATION:
                                                                                                                                                                                                                              STREET: 1201 New CITY: Washington
                                                                                                                                                                                                    COUNTRY:
                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEQSQPKKPASTHYGAESNTITTSQNYDDEYDDVIIVPIFGESEEDYDDLGQVYTGEAVT
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                                                             29-APR-1996
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                                                                                                       Release #1.0, Version
                US 08/585,391
                                                                          US/08/639,501
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N.W., Suite 1001
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ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
PEGISTRATION NUMBER: 28,957
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REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                         1215
                                                                                                                                                                                                                                                                1103
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Local Similarity 21.0%; Pred. No. 1.6e-05;
nes 330; Conservative 225; Mismatches 569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid TOPOLOGY: linear
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                                                      GFRGFYSAHGTKLNVSTEALOKAVKLFSDIENISEETSAEVH-----PISLSSSKCHDSV 1269
                                                                                                                                                                                                                                                                LTPSQKAEITELSTILEESGSQF----EFTQFRKPSYILQ----KSTFEVPENQMTILKT 1154
                                                                                                                                                                                                                                                                                                                                                                       VE--IVNTLALDNQKKLSKPQSINTVSAHLQSSVVVSDCKNSHITPQMLFSKQDFNSNHN 1102
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDYSLRNIVVEKELKYYK-NLISKIENEIETLV----ENIKKDEEQLFEKK-ITKDEN 602
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PTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYK-ITKEEE 814
                                                                                                  STEGEITGQAT-----TKPGQQA----GSALEGDSVQAQAQEQKQAQPPVPVPVPEAKAQV 755
                                                                                                                                                           TSEECRDADLHVIMNAPSIGQVDSSKQFEGTVEIKRKFAGLLKNDCNKSASGYLTDENEV 1214
                                                                                                                                                                                                            -KQENKQEPYYLIVLKK---EIDKLKVFMPKVE----SLINEEKKNIKTEGQSDNSEP 703
                                                                                                                                                                                                                                                                                                                 -KPDEK--ILEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELKHNIHVPNSY-----
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                               Sequence 2, Application US/09044946
Patent No. 6033857
GENERAL INFORMATION:
APPLICANT: Tavtlgian, Sean V.
APPLICANT: Kamb, Alexander
   APPLICANT:
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' Tavtigian, Sean '
Kamb, Alexander
Simard, Jacques
Couch, Fergus
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Best Local Similarity
Matches 330; Conserv
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INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08
FILING DATE: 18-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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APPLICANT: Weber, Barbara
TITLE OF INVENTION: Chromosome 13-Linked
TITLE OF INVENTION: Susceptibility Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
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tive 225; Mismatches 569;
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                                                    --VISN--VKDA---
                                                                                                                      -YLS-----
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                                                                                                                    -KNKLDSGIEPVLKNVEDQKNTSFSK----
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                                                    NAYPOTVNEDICVEELVTS - -
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US-09-044-908-2
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                                                                                                      TELEFAX: 202-962-8300 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                        REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                              FILING DATE: 21-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 20-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                  TYPE: ami
                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/573,779 FILING DATE: 18-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1201 New CITY: Washington
                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                              NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                      LENGTH:
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                                                  amino acid
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1201 New York Avenue N.W., Suite 1001
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                                                                      3418 amino acids
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Weber, Barbara
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Kamb, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version
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Query Match

3.3%;

Score 279.5;

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Length 3418;

OY 654 -KOENKOEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGOSDNSEP 703 Db 1155 TSEECRADALHTINAAPSIGOVDSKOFEGTVEIKRKFAGLLKNDCNKSASGYLTDENEV 1214 OY 704 STEGEITGOATTKPGOQAGSALEGDSVQAQAQEQKQAQPPVPVPVPEAKAQV 755 Db 1215 GFRGFYSAHGTKLAVSTEALQKAVKLESDIENISEETSAEVHPISLSSSKCHDSV 1269 OY 756 PTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYK-ITKEEE 814 Db 1270 VSMEKIENHNDKTVSEKNNKCQLILQNNIEMTTGTFVEEITENYKKNTEEND 1321 OY 815 SKLSSC	Hest Local Similarity 21.0%; Pred. No. 1.6e-06; Watches 330; Conservative 225; Mismatches 569; Indels 449; Gaps 81; Oy 187 LLRAKLNDVCAN
US-08-480-604-10 Sequence 10, Application US/08480604A Patent No. 5736139 GENERAL INFORMATION: APPLICANT: FIRCA, JOHN A. APPLICANT: FIRCA, JOSEPH R. APPLICANT: FIRCA, JOSEPH R. APPLICANT: FIRCA, JOSEPH R. APPLICANT: FIRCA, JOSEPH R. APPLICANT: FIRCA, JOSEPH R. APPLICANT: FIRCA, JOSEPH R. APPLICANT: FIRCA, JOSEPH R. APPLICANT: FIRCA, JOSEPH R. APPLICANT: CONCINC ACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE NUMBER OF SEQUENCES: 32 CORRESPONDENCE ADDRESS: ASCARROLL, LLP STREET: 220 MONTGOWERY STREET, SUITE 2200 CITY: SAN FRANCISCO STRIE: C20 MONTGOWERY STREET, SUITE 2200 CITY: SAN FRANCISCO STRIE: 94104 COMPUTER: 1BM PC COMPATIBLE FORM: MEDIUM TYPE: FIDOPY disk COMPUTER: IBM PC COMPATIBLE OF AMERICA ZIP: 94104 COMPUTER: IBM PC COMPATIBLE OF AMERICA SOUTMARE: PO-DOS/MS-DOS SOUTMARE: PO-DOS/MS-DOS SOUTMARE: PO-DOS/MS-DOS SOUTMARE: NOT-JUN-1995 CLASSIFICATION NUMBER: US/08/480,604A FILING DATE: 107-JUN-1995 CLASSIFICATION NUMBER: US 08/422,711 PRIOR APPLICATION NUMBER: US 08/422,711 PRIOR APPLICATION NUMBER: US 08/422,711 PRIOR APPLICATION NUMBER: US 08/422,711 PRIOR APPLICATION NUMBER: US 08/422,711	ON 1581 ETTEITAAPKCKEMQNSLNINGKNLYSIETVPPFKLLSDNLCROTENLKTSKSIFLK 1636 OY 1091 LVKYNGESSPLKTLSEESIOTEDNYASLENFKYLSKLEGKLKDNLALEKKKLSYL 1146 1

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3.3%; Score 270.3, 222., 223.

Best Local Similarity 18.5%; pred. No. 1.2e-06;

Matches 347; Conservative 292; Mismatches 595; Indels 643;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2366 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION NUMBER: US 07/985,321
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
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TOPOLOGY: linear
MOLECULE TYPE: protein
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FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: TEXALS
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                                                                         555 IVVDKE--YLLEKISSLARSSERGYIHYIVQLQGDKISYEAACNLFAKTPYDSVLFQKNI 612
                                                                                                                                                                                                                                                 510 QSTEQEMASLWSFDDARAK-----AQFEEYKRN-----YFEGSLGEDDNLDFS-QN 554
                                                                                                                                                                                                                                                                                                                                  510 ---EKMMGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYME------DYSLRN 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               403 YPNGV--TYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKE-- 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               341 EVQSSFESVLASKSDKSEIFSSLGDMEASPLEVK--IAFNSKGIINQGLISVKDSYCSNL 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 -----IDGYEEINELLYKLNFYFD------LLRAKLNDVCANDYCQIPFNLKIRANELD 215
598 TKDE-----NKPDEKILE------VSDIVKVQVQKV-------LLM 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               399 IVKQIENRYKILNNSLNPAISEDNDFNTTNTFIDSIMAEAN--ADNGR--FMMELGKYL 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281 GGMYLDVDMLPGIQPDLFESIEKPSSVTVDFWEMTKLEAIMKYKEYIPEYTSEHFDMLDE 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 YIEESLNKITONSGNDVRNFEEFKNGES---FNLYEQELVERWNLAAASDILRISALKEI 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENI----KELL-----DKINEIKNPPPANSGNTPNTLLDKNKKIEEH------EK 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EIKE-----IAKTIKFNIDSLFTD----PLELEYYLREKNKNIDISAKVETKESTEPNE 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----KIKIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNF- 509
                                                                                                                                                               IVVEKELKYYKNLISKIENEIET----LVENIKKD-------EEQLFEKKI 597
                                                                                                                                                                                                                                                                                                                                                                                                                    RVGFFPDVKTTINLSGPEAYAAAYQDLL-----MFKEGSMNIHLIEADLRNFEISKTNIS 509
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Query Match 3.3%; Score 278.5; DB 2; Length 2366; Best Local Similarity 18.5%; Pred. No. 1.2e-06; Matches 347; Conservative 292; Mismatches 595; Indels 643; Gaps 92; Qy 121 DAKSYADLKHRVRNYLL-TIKELKYPQLFDLTNHMLTLCD-NIHGFKYL 167	TELEFAX: (415) 397 INFORMATION FOR SEQ ID SEQUENCE CHARACTERISS LENGTH: 2366 amino TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: prote 15-08-405-496A-10	APPLICATI FILING DA ATTORNEY/AG NAME: IN REGISTRAT REFERENCE TELECOMMUNI TELEPHONE	PILING DATE: PRIOR APPLICATION NU APPLICATION NU FILING DATE: PRIOR APPLICATION NU APPLICATION NU FILING DATE: PRIOR APPLICATION	OPERATING SYSTEM: OPERATING SYSTEM: SOFTWARE: Patent: CURRENT APPLICATION NUMBE: FILING DATE: 16-1 CLASSIFICATION: PRIOR APPLICATION: APPLICATION NUMBE: APPLICATION NUMBE:	ADDRESSEE MEDIEN & CARROLL, LLP STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: USA ZIP: 94104 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk MEDIUM TYPE: Floppy disk	ESUL S-08 Seq Pat GE	Db 1627 ENDNIQPYFIKFNTLETNYTLYVGNRQNMIVEPNYDLDDSGDISSTVINFSQKYLYGIDS 1686 Qy 1566 CVENPNPTCNENN 1578	QY 1539 QNSGCFRHL
933 1010 992	Qy 857 KBMVCNLXKLKDNDKIKNLLEEAKKVSTSVKTLSSSSMOPLSLTPODK 904	737 QKQAQPPVPVPVPEAKAQVPTPPAPVNIKTENVSKLYLEKLYLEKLYELNTSYICHKYILVSH	NKIDELKKTOLILKNVELKHNIHVPNSYKOE-NKQETYLIVLKKELIKKVMPKV	558 IVVEKELKYYKNLISKIENEIETLVENIKKDEEQLFEKKI	TYNGLENNIALDNING DER FALSE DER KELLNIELEGEN KOM FRIEDOM KELLNIELEGEN KELLNEIYDSKFUNNIDLTNF	Qy 313 ENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEH	Db 168 YNKFFRKRMEIIYDKQKNFINYYKAQREENPELIIDDIVKTYLSNEYSKEIDELNT 223 Qy 255 LIEESKKTIDKNK-NATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISYLE-KRIDTLKKN 312	Db 51 DINSLTDIYIDTYKKSGRNKALKKFKEYLVTEVLELKNUNLTPVEKNLH-FVWIGGQIND 109 Qy 168IDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQIPENLKIRANELD 215

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1094 1112 1055 1052 1037

1169

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APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, NISHA V.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                          CVNKVVISPNIYTDEIN 1703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CVE----NPNPTCNENN 1578
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                                           SAN FRANCISCO
    UNITED STATES OF AMERICA
                                                                                   MEDLEN & CARROLL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---ILTGYYLKDDIKISLS-----LTLQDE-KTIKLNSVHLDESGVAEILKFM
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                                                              SUITE
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OF
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
FILING DATE:
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APPLICATION NUMBER: US/08/915,13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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YPNGV--TYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKE--
                                                                                                                                                                       ENI---KELL-----DKINEIKNPPPANSGNTPNTLLDKNKKIEEH------EK
                                                                                                                                                                                                                                                                                                                                                      TAINYINQWKDVNS-DYNVNVFYDSNAFLINTLKKTVVESAINDTLE-SFRENLNDPRFD
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                                                            EVQSSFESVLASKSDKSEIFSSLGDMEASPLEVK--IAFNSKGIINQGLISVKDSYCSNL
                                                                                                                                              GGMYLDVDMLPGIQPDLFESIEKPSSVTVDFWEMTKLEAIMKYKEYIPEYTSEHFDMLDE
                                                                                                                                                                                                                                                                  LIEESKKTIDKNK-NATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLE-KRIDTLKKN
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                                                                                                     ---IAKTIKFNIDSLFTD----PLELEYYLREKNKNIDISAKVETKESTEPNE
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02-DEC-1993
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92;

RESULT 51 US-08-915-136-10

Sequence 10, Patent No. 6

INFORMATION:

CORRESPONDENCE ADDRESS:

STREET:

ADDRESSEE:

COUNTRY:

CALIFORNIA

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1687

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1627 1539 1570 1486 1525 1433 1484 1377 1429 1340 1388 1282 1337 1232 1288 1179 1229 1142

	38	SESDVWIIDVDNVVRDVTISDKIKKGDLIEGILSTLSIEENKIILNSH.	(a)	В
	1281	NVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIENEY	1232	Qy
	1336	NMGINI	1288	рь
	1231	SYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQ	1179	ρ
*	1287	:	1229	DЪ
	1178	NYTGNSPSENNTDV	1142	Qγ
	1228	SAPSITYREPHLSIYDVLEVQKEELDLSKDLMVLPNAPNR	1169	DЪ
	1141	SIQTEDNYASLENFKVLSKLEGKLKDNLNLEKK	1094	Qy
	1168	DLVISEIDFNNNSIVLGKCE	112	Db 4
	1003	AKENETAERENTIENRKTIIKUVKCIVK		Ş
	1111	:::: : SDPLLRQEIEAKIGIMAVNLTTATTAIITSSLGIASGFSILLVPLAGISAGIPSLVNNEL	1052	рь
	1054	SLNNPKH	1037	Qγ
	1051	QLFSTGLNTITDAAKVVELVSTALDETIDLLPTLSEGLPIIATIIDGVSLGAAIKELSET	992	DЪ
	1036	KYKMQIKKLT	1010	Qy
	991	KGTIFDTVNGKLVKKVNLDTTHEVNTLNAAFFIQSLIE-YNSSKESLSNLSVAMKVQVYA	933	Db
	1009		959	Qy
	932	TSFEDISETDEGFSIRFINKETGESIFVETEKTIFSEYANHITEEISKI	878	DЬ
	958	IGQKSSENFYEKILKD	905	Qy
	877	KVMLTECEINVISNIDTQIVEERIEEAKNLTSDSINYIKDEFKLIESISDALCDLKQQNE	818	DЪ
	904		857	γ
	817	NLPELSTLLQEIRNNSNSSDIELEE	783	Db
	856	KLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYE	797	Qy
	782	INKEESIIK-DISSKEYISFNPINKEESIIK-DISSKEYISFNP	762	DЪ
	796	ICHKYILVSH	737	Qy
	761	SQDSIIVSANQYEVRINSEGRRELLDHSGEW	731	DЬ
	736	ITGQATTKPGQQAGSALEGDSVQAQAQE	682	Qy
	730	TEIEAAIDLAKEDISPKSIEINLLGCNMFSYSINVEETYPGKLLLKVKDKISELMPSI	673	Db
	681		626	Qy
	672	EDSEIAYYYNPGDGEIQEIDKYKIPSIISDRPKIKLTFIGHGKDEFNTDIFAGFDVDSLS	613	рь
	625	LLM	598	Qy
	612	AACNLFAKTPYDSVLFQKNI	555	Ор
	597	LVENIKKDEEQLFEKKI	558	Qy
	554	: : GSLGEDDNLDFS-QN	510	Db
	557	HNTFASYENSKHNLEKLTKALKYMEDYSLRN	510	Qγ
	509	FPDVKTTINLSGPEAYAAAYQDLLMFKEGSMNIHLIEADLRNFEISKTNIS	455	Db
	509	IYDSKENNNIDLTNE-	459	Qy
	454	IVKQIENRYKILNNSLNPAISEDNDENTTTNTEIDSIMAEANADNGRFMMELGKYL	399	Db

				US RE	Qy Db	Qу	Фр	Db Qy	Db Qy	Qy Db	Qy Db
2 07 9 10	FILING DATE: 23-OCT-1997 CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/329,154 FILING DATE: 24-OCT-1994 APPLICATION NUMBER: US 08/161,907 FILING DATE: 02-DEC-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/985,321	ABI IBM IBM Pat Pat	DISEASE: 22 ESS: Carrol gomery Str	SULT 52 -08 -957-310-10 -08 -957-310-10 -08 -967-310 -08 -967-310 -08 -	/ 1566 CVENPNPTCNENN 1578	1539 QNSGCFRHL	1486STDYNHNNLLTKFLSTGMVFENL : :: : : 1570 NRKGNTNTSDSLMSFLESMNIKSIFVNF	/ 1433 DLFVIHLEAKVLNYTYEKŚNYEVKIKELNYLKTIQDKLADFKKNNNFVGIADL 1485 : :	1377 NFANDVLGYYKILSEKYKŚDŁDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKI 1432 	1340 TSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDI 1376 	1282 EVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFKNVLESDLIPYKDL 1339

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TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2366 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-957-310-10
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                               797 STMNEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYE 856
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                                                                                                    QKQAQPPVPVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSH
                                                                                                                                                                 --ESLI---NEEKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQE
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                                                                                                                                           SQDSIIVSANQYEVRINSEGRRELLDHSGEW------
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                                                                                                                                                                                                                                                                                                                                                          IVVDKE--YLLEKISSLARSSERGYIHYIVQLQGDKISYEAACNLFAKTPYDSVLFQKNI 612
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 -KENKITVKSK-----
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Db 1627 ENI Qy 1566 CVF	1539	Qy 1486 9	Db 1525 N	1484		Qy 1377 NF	1340 T 1429 I 1377 N	1388 E 1340 T 1429 I 1377 N	1282 1388 1340 1429 1377	1337 1282 1388 1340 1429 1377	1232 1337 1282 1388 1340 1429 1377	1288 1232 1232 1337 1282 1388 1340 1429	.1229 1179 1288 1232 1337 1388 1388 1340	1142 .1229 1179 1288 1232 1337 1282 1388 1340 1429	1094 1169 1142 11229 1179 11288 1232 1232 1232 1337 1282 1388 1340	1112 1094 1169 11142 1142 11229 1179 11288 1232 1337 1388 1340	1055 1112 11094 11094 11169 11142 11229 11279 11288 1232 1232 1337 1282 1388 1340 1429	1052 1055 11112 1094 11169 11142 1129 1179 11288 1288 1232 1337 1388 1340	1037 1052 1055 1112 1094 11169 1142 1142 11288 11288 11232 11288 11282 11388 1337 11388 1340	992 1037 1052 1055 1112 1104 11169 1142 1128 1128 11288 11288 11337 11388 11340	1010 992 1037 1052 1055 11112 1094 11169 11142 1129 1129 11288 1288 1232 1337 1388 1340	933 1010 992 1037 1052 1055 1112 1114 11094 11169 11142 11288 1232 1288 1233 1337 1282 1337	959 933 1010 992 1037 1055 1055 11112 1104 11169 11142 11288 11288 11337 11388 11340	878 959 933 1010 992 1037 1052 1055 1112 1114 11094 11169 11179 11288 1232 1337 1388	905 878 959 933 1010 992 1037 1052 1055 1112 1014 11169 11142 1128 1128 1232 1337 1340
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PYFIKENTLET	NISUSEMSFEEFRHL	STDYNHNNLLTKFLST : :: : KGNTNTSDSLMSFLES	ILTGYYL	י האשעוו ווושתם	;	LGYYKILSEKY :	SNYVVKD	EVNG SNYVVK ::: LMLNSNHIQQ LGYYKILSEKY ::	PLAGVYRSLKK : EVNG EVNG ILMLNSNHIOO LGYYKILSEKY : : : :	VWIIDDNVVR PLAGVYRSLKK :	NVDDEVD	NTRSFINVDDEVDNVDDEVD WIIDVDNVVR PLAGVYRSLKK :	GWTPGLRSLEN YKKFLPEGTDV : : NTRSFINVDDEVDNVDDEVD VWIIDVDNVVR PLAGVYRSLKK EVNG FLWG ILMLNSNHIQQ LGYYKILSEKY : :	-LSSGLHHLI- GWTPGLRSLEN YKKFLPEGTDV : NTRSFINVDDEVD : : VWIIDVDNVVR PLAGVYRSLKK EVNG EVNG [::: ILMLNSHIYO LGYYKILSEKY C	SPLKILSEE GSGHTVTDDID -LSSGLHHLI- :	TKVVDYFK SPLKTISEE GSGHTVTDDID -LSGLHHLI GWTPGLRSLEN YKKFLPEGTDV YKKFLPEGTDV YKKFLPEGTDV YKKFLPEGTDV YKKFLPEGTDV YKKFLPEGTDV YKKFLPEGTDV YKKFLPEGTDV YKKFLPEGTDV YKKFLPEGTDV YKFLPEGTDV YKFLPEGTDV '''' I''' I''' EVNGSFI	VFYKKK TKVVDYFK SPLKTLSEE GSGHTVTDDID -LSGLHHLI- GWTPGLRSLEN YKKFLPEGTDV WTRSFINVDDEVD VWIIDVDNVVR PLAGVYRSLKK PLAGVYKILSEKY	QEIEAKIGIMA VFFNKKK IKVVDYFK SPLKTLSEE GSGHTVDDID -LSSGLHHLI GWTPGLRSLEN YKKFLPEGTDV ::::::::::::::::::::::::::::::::::::	EQLESKLN ::: : : C::: : : VF-NKKK VF-NKKK SPLKTLSEE :::: GSGHTVTDDID -LSSGLHHLI ::: GWTPGLRSLEN YKKFLPEGTDV YKKFLPEGTDV YKKFLPEGTDVNVDDEVD :: : VWIIDVDNVVR PLAGVYRSLKK SNYVVK EVNG EVNG ILMLNSNHIOO LGYYKILSEKY CGYYKILSEKY CGYYKILSEKY	LNTITDAAKVV EQLESKLN ::: : QEIEAKIGIMA VFINKKK IKVVDYFK SPLKTLSEE GSGHTUSEI: GSGHTUSEI:	LERLFDKKKTV	TVNGKLVKKVN LERLFDKKKTV : CNTITDAAKVV EQLESKLN :: : : QEIEAKIGIMA VFNKKK TKVVDYFK SPLKTLSEE : : : GSGHTVTDDID -LSSGLHHLI : : : GWTPGLRSLEN YKKFLPEGTDV YKKFLPEGTDV YKKFLPEGTDV YKKFLPEGTDV YKFLPEGTDV YKFLPEGTDV '' : : '' VWIIDVDNVVR PLAGVYRSLKK : : : EVNG EVNG EVNG EVNG EVNG EVNG EVNG EVNG EVNG EVNG EVNG EVNG EVNG EVNG EVNGSNYVVK : : : ILMLNSNHIOQ LGYYKILSEK	ESFTNEVK I	ISFEDISETDE ISFEDISETDE ESFTNFVK TVNGKLVKKVN LERLFDKKKTV LNTITDAAKVV EQLESKLN SI QEIEAKIGIMA VFNKKK VFNKKK TKVVDYFK SPLKTLSEE CWTPGLRSLEN YKKFLPEGTDV YKKFLPEGTDV INTRSFINVDDEVD YKKFLPEGTDV YKKFLPEGTDV INTRSFINVDDEVD YKKFLPEGTDV INTRSFI VWIIDVDNVVR PLAGVYRSLKK LGYYKILSEX ILMLNSNHIOO LGYYKILSEX ILMLNSNHIOO LGYYKILSEX ILMLNSNHIOO LGYYKILSEX	VSAND-DTSH
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RESULT 53 US-09-336-447A-76 ; Sequence 76, Application US/09336447A

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GENERAL INFORMATION:

APPLICANT: HANSEN, ERIC J.

APPLICANT: AEBI, CHRISTOPH

APPLICANT: COPE, LESLIE D.

APPLICANT: MACIVER, ISOBEL

APPLICANT: FISKE, MICHAEL J.

APPLICANT: FREDENBURG, ROSS A.

ITITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS

FILE REFERENCE: AMCY:024

CURRENT APPLICATION NUMBER: US/09/336,447A

CURRENT FILING DATE: 1999-06-21

NUMBER OF SEQ ID NOS: 98

SOFTWARE: PACENTIN Ver. 2.1

SEQ ID NO 76

LENGTH: 3788

TYPE: PRT

ORGANISM: MORAXEL1a Catarrhalis
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NAME/KEY: MOD_RES

LOCATION: (1036)..(3786)

OTHER INFORMATION: Xaa = any
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1475	FVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKK		1419	Qy
2483	EINLINEARNAXANYATPSITINSLLHEQQLXGKSEQIDNPRTEINLINEA	⊣	2432	망
1418	-LDSIKKYINDKQGENEKYLPFL	ß	1363	Qy
2431	-RTEINLINEARNAAGDTIIPLDDDXXPSEQIDNPR	P	2396	DЪ
1362	IPYKDLTSSNYVVK		1303	Qy
2395	-MILGDTAIVSNSQDNKTQLKFYKSEQIDN		2367	DЪ
1302	VIDNILSKIENEYEVLYLKPLAGVYRSLKKQLEN	ŲΡ	1243	Qy
2366	AKASSENTQNIAKSEQIDNPRTEINLINEARNA	EARN	2330	рь
1242	ESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVII		1183	Qy
2329	ELQSEQIDNPRTEINLINEARNAATHDYNERQTEASEQIDNPRTEINLIN		2280	DЬ
1182	-LNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNAL	KLEGKLKDN	1127	Qy
2279	ATPSITINNQA-DIAQNQTDIQDLAAYN	QDQKSEQIDNPRTEINLINEARNAXANY	2225	DЪ
1126			1067	Qy
2224	DNPRTEINLINEARNANQAHIANNINXIYELAQQ	: : :	2180	DЪ
1066			1014	Qy
2179	SGRSEQIDUPRTEINLIN-EARNAALESNVEEGLLELS	EGLLDL	2137	Db
1013	KILKDSDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKL		954	Qy
2136	ILGDTAIVSNSQDSEQIDNPRTEINLINEARNAKALESNVE	NPRTEINLINEARNAILGDTAIVSNSQDS	2081	DЪ
953	DDTSHSTNLNNSLKLFENILSLGKNKNIYQELIGQKSSENFYE	KPEVSAN	904	Qy
2080	I	NNIYELAQQQDQSEQI	2031	ДЪ
903	NLLEEAKKVSTSVKTLSSSSMQPLSLTPQD	- z	845	Qy
2030	IANNI		2026	Дb
844	ICHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLN	YS	785	Qy
2025	NSNQADIAQNQTDIQDLAAYNELQSE-QIDNPRTEINLINEARNANQAD		1978	DЪ
784	AQVPTPPAPVN		728	Qy
1977	EQIDNPRTEINLINEARNAAKAXAANXDRSEQIDNPRTEINLINEARNAXANYATPSITI		1918	Вρ
727	SLINEEKKNIK-TEGQSDNSEPSTEGEITGQATTKPGQQAGSALEG	LKVEMPKVE-	674	Qy
1917	: : : : : : : : :	: : IDNPRTE	1862	Дb

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 52, Application US/09315793 Patent No. 6221597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ROBerts, Christopher J.
TITLE OF INVENTION: ESSENTIAL GENES OF YEAST AS TARGETS FOR ANTIFUNGAL
TITLE OF INVENTION: AGENTS, HERBICIDES, INSECTICIDES AND ANTI-PROLIFERATION
TITLE OF INVENTION: DRUGS
FILE REFERENCE: 9301-048
CURRENT APPLICATION NUMBER: US/09/315,793
CURRENT FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 62
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DNDKIKNLLEEAKKVST---SVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSLK 924
                                                                                                                                                                                                                                    TEGQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQAQPPVPV--PVPEA
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                                                                                                                                                 KAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILV----SHSTMNEKILKQY 807
                                                                                                                                                                                                                                                                          ---LISEIDAKAN-----
                                                      KVNLRELSSADTTPP-------VPA-----ETVRDLGFEGYLSDFITG----
                                                                                        KITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLK
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                                                                                                                            KDKILEPPI-MTVSAINAQFAAYLAQCVDY-NTS----KALTVVDSDSYKLFANPILDKF
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18.0%; Pred. No. 6.5e-07;
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US-08-290-919-1
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GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BLACKMAN, MICHAEL J.
APPLICANT: CHAPPEL, JONNTHAN A.
TITLE OF INVENTION: IMPROVEMENTS
TITLE OF INVENTION: VACCINE
NUMBER OF SECURE
                                                                  APPLICATION NUMBER: PCT/
FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                        APPLICATION NUMBER: GB 9: FILING DATE: 22-FEB-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                CLASSIFICATION:
                                NAME: KOKULIS, PAUL N. REGISTRATION NUMBER: 1
                                                                                                                                                                                                               APPLICATION NUMBER: US/08/290,919
FILING DATE: 04-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1100 NEW CITY: WASHINGTON
                REFERENCE/DOCKET
                                                                                                                                                                                                                                                                                                             COMPUTER:
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                                                                                                                                                                                                                                                                                                          IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CUSHMAN DARBY & CUSHMAN,
                                                                                      JMBER: PCT/GB93/00367
22-FEB-1993
 INFORMATION:
                NUMBER:
                                16,773
               212242/HCM/MJL/6BC8/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IN OR RELATING
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1014

900

1194

737

691

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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1354 amino acids
TYPE: amino acid
TOPOLOGY: Linear
MOLECULE TYPE: protein
US-08-685-871-2
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US-08-685-871-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08685871
Patent No. 6013499
GENERAL INFORMATION:
APPLICANT: NARUMIYA, Shuh
APPLICANT: IWAMATSU, Akihiro
TITLE OF INVENTION: RHO TARGET PROTEIN KINASE P160
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
CTREFER. 2000 Fetalal No. 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.3%;
Best Local Similarity 100.0%;
Matches 47; Conservative (
                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/685,871
FILING DATE: 24-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-184102
FILING DATE: 25-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-262553
FILING DATE: 14-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BERT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                   RAME: BENT Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16887/845
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1527 ISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPT 1573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
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TELEFAX: \___
SEC
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LOCATION: 1
OTHER INFORMATION: /label= X
OTHER INFORMATION: /note= "X = M and N, or N"
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CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 48 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: D.C.
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20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                               1354 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Best Local Similarity
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OY 327 NPPPANSGNTPNTLLDKNKK-IEEHEKEIKEIAKTIKFNIDSL 368	Qy 267 KNATKEBEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLDKINEIK 326	Query Match 3.2%; Score 272; DB 3; Length 1535; Best Local Similarity 19.2%; Pred. No. 1.5e-06; Matches 258; Conservative 223; Mismatches 520; Indels 344; Gaps	; LENCTH: 1535 amino acids ; TYPE: amino acid ; TOPOLOGY: linear US-08-755-587-185	; REGISTRATION NUMBER: 31,665 ; REFERENCE/DOCKET NUMBER: 5405-135 ; INFORMATION FOR SEQ ID NO: 185: ; SEQUENCE CHARACTERISTICS:	; APPLICATION NUMBER: GB 9617961.9 ; FILING DATE: 28-AUG-1996 ; ATTORNEY/AGENT INFORWATION: ; NAME: Kenneth D Sibley	O NO	V-1996 A: GB 95 V-1995	Patenti Patenti LICATION	H		OF INVENTION: identification and sequencing of t op INVENTION: susceptibility gene and uses there R OF SEQUENCES: 222	Wooster, Richard F Ashworth, Alan Stratton, Michael R NVENTION: Materials and methods relatin	pplication US/087 997 ATION: Futreal, Phillip	RESULT 57 US-08-755-587-185	Qy 1555 CLLNYKOEGDKCVENPN 1571 : Db 1149 KILFYNDEQDKEOSNPS 1165	QY 1500 STGMVFENLAKTVLSNLLDGNLQGMLNTSQHQCVKKQCPQNSGCFRHLDEREECK 1554	OY 1444 LNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFYGIADLSTDYNHNNLLTKFL 1499	Db 1011 NRKDFKIDRKKANTQDLRKKEKENRKLQLE 1040
Db 1060 NNSSMSNSYSYLSDEVYSDSGYLSKNKLD	Qy 1148 Db 1014	1092 956	ы — ы	QY 1003 LSEDLYNKYKLKLERLEDKKKTVGKYKMQIKKLTLLK	QY 943 IGQKSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQ : : : :	Qy 893 SMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQEL : : : : : : :	Qy 840 FDSLNNSLSQLFMEIYEKEMVCNLYKLKDNDKIKNLLEEAKKVSTSVKTLSSS	Qy 810 TKEEESKLSSC	Qy 752 KAQVPTPPAPVNNKTENVSKLD-YLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKI- 	OY 700 NSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQAQAQAQAQAQPPVPVPVPEA	Qy 651NSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSD	OY 597 ITKDEN-KPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELKHNIHVP	Qy 552 DYSLRNIVVEKELKYYKNLISKIENEIETLVENIKKDEEQLFEKK- : : : : : : : : :	OY 506 LTWEKMMGKKYSYKVEKUTHHWYFASYEWSKHNLEKLTKALKYME : : : : :: :: :: :: : : : : : : : : : :	244 PIFKNSTMVLYADIGDKQATQVSIKKDLDS-SNIVYDLAEENK	Db 184 1	Oy 369 F	360

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US-08-290-919-2
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                                                                  US-08-290-919-2
                               Query Match
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   Matches
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                                                                                                                                                                                                                                            TELEPHONE: (202) 861-301
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BLACKMAN, APPLICANT: CHAPPEL, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 22-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Rel-
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                 FEATURE:
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                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                  Local Similarity
                                                                             LOCATION: 1
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 04
CLASSIFICATION:
                                                                                                                               NAME/KEY:
                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND--VLGYYKIL--SEKYKSDLDS 1399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFN-VNVKDILNSRF---NKRE 1323

    Application US/08290919
    5720959

   46;
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20005-3918
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                                                                                                                                                                                                         : 48 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLACKMAN, MICHAEL J.
CHAPPEL, JONATHAN A.
VENTION: IMPROVEMENTS IN OR RELATING TO MALARIA
   Conservative
                                                                                                                                                                           שא: single
linear
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                                                                                                                               Modified-site
                                                                                                                                                            protein
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              3.2%;
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                                                                             /label= X
/note= "X = M and N, or N"
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Score 271; DB 1;
Pred. No. 2.4e-08;
1; Mismatches (
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   0;
                            Length 48
   Indels
 0;
 Gaps
 0;
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US-08-923-992A-10
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                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                            Matches 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 371-25
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 60
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-IgA Fc Binding Forms
TITLE OF INVENTION: Streptococcal Beta Antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1527 ISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPT 1573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1164 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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 212
                                                                                                                                                141
                                                                                                                                                                                                                                                             134
                                                                        153
                                                                                                                                                                                     187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington STATE: D.C.
                                                                                                                                                                                                                         91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Esmond, Robert W. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 05-SEF
                                                                                                                                                                                                                                                                                                   32 GSVAHASELVKHDSVKT-TEVAAKPYPSMAQTDQGNNSSSSELETTKIEIPTTDIKKAVE 90
                                                                                                                                                                                                                                                                                                                                      80 GSVASGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDSDAKS-----YADLKHRVR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                         PLEKTAGETSATDTGKREKQLQQWKNN---LKNDVHN---TILSHEQKNEFKTKID---- 140
 LGI--TNEDKDSMLKKIEDIR---
                                  IDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKT-IKFN 364
                                                                    NQFNETNRLLHIKQHEEVEKDKKA-KQQKTLKQSDTKVDLSNIDKELNHQKSQVETNAEQ
                                                                                                       KTIENINELIE-ESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKR 305
                                                                                                                                                                                     LLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMEDYIKKNK 246
                                                                                                                                                                                                                                                             NYLLTIKEL-----KYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYKLNFYFD 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1164 amino acids
                                                                                                                                                                                                                                                                                                                                                                          Conservative
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05-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              371-2540
                                                                                                                                                                                                                                                                                                                                                                                           3.2%; Score 271;
18.2%; Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          us 60/024,707
                                                                                                                                                ----ETNDSDALLEL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32,893
                                                                                                                                                                                                                                                                                                                                                                          242;
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                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
1.2e-06;
-KQAQQADK - -KEDAEVKVREE
                                                                                                                                                                                                                                                                                                                                                                                                          Length 1164;
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 249
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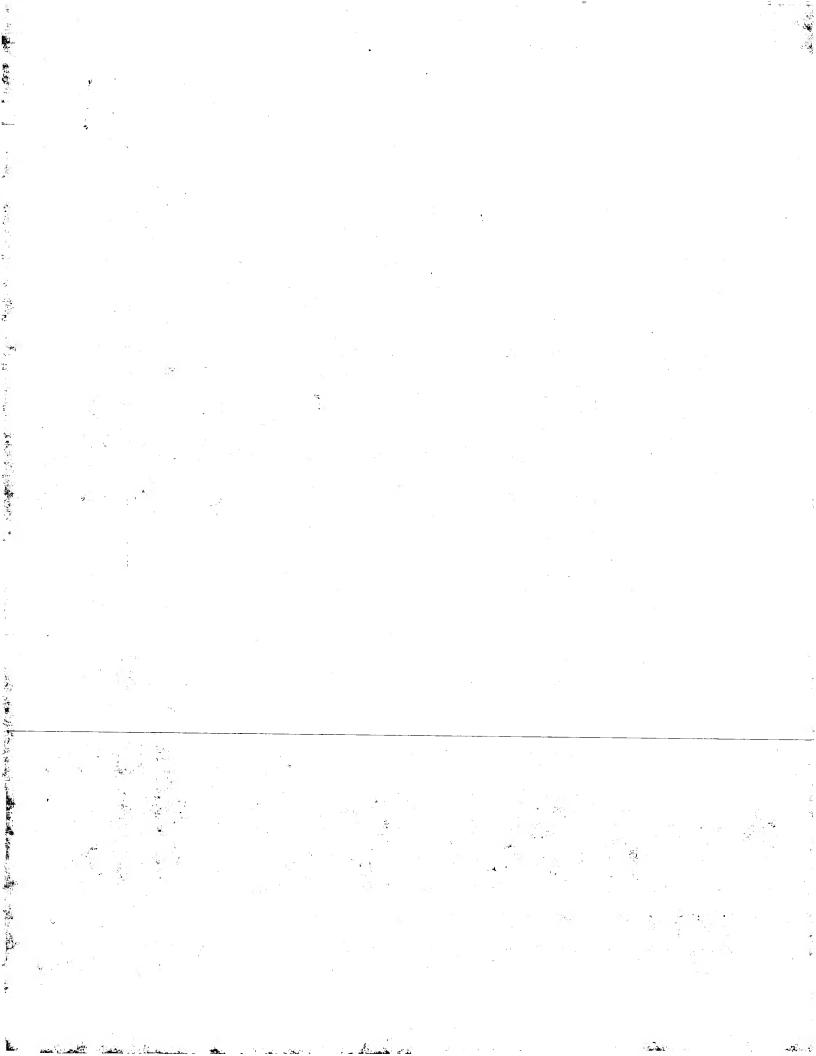
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M64681 Plasmodium
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4]181 4]40) rd,H. rd,H. rd,H. rd,H. recombinants intended for USE IN A E [GP190,MSP1 583-A 2 09-APR-1998;); BUJARD HERMANN (DE) on/Qualifiers 40 on/Qualifiers 7 c 1060 g 1054 t 7 c 1060 g 1054 t 00.0%; Score 4940; DB 6; Length 4940; ve 0; Mismatches 0; Indels 0;	ALIGNMENTS 4940 bp DNA Patent WO9814583.	A64813 6 A01099 6 E01429 6 E01429 6 E01429 6 E01429 7 AP199405 7 AP199405 8 AP199405 8 AP199409 8 AP199409 9 AP199410 8 AP199410 8 AP199410 8 AP199410 8 AP199410 8 AP199410 8 AP199410 8 AP199410 8 AP199401 8 A64818 6 A64804 6 A64805 6 AXZ78285 6 AXZ78285 6 AXZ78286 6 AXZ78287 8 AP199403
4]181 4]40) rd,H. rd,H. rd,H. rd,H. recombinants intended for USE in Elepi90,MSP1 583-A 2 09-APR-1998; 583-A 2 09-APR-1998; 583-A 2 09-APR-1998; 583-A 2 09-APR-1998; 583-A 2 09-APR-1998; 583-A 2 09-APR-1998; 583-A 2 09-APR-1998; 583-A 2 09-APR-1998; 583-A 2 09-APR-1998; 583-A 2 09-APR-1998; 583-A 2 09-APR-1998; 583-A 2 09-APR-1998; 583-A 2 09-APR-1998; 7 c	ALIGNMENTS 4940 bp DNA linear Patent W09814583.	の の の い い い い い の の の の の の の の の い

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900	1 TTGTACCAGGCCCAGTACGACCTGTCCATCTATAACAAACA	841	Db Qq
424		8	Db
<u>~</u>	GAATCCAAAAAGACCATAGACAAAAATAAGAATGCAACCAAGGAGGAAGAAAAGAAGAAG		0 1
780 780	ATGGAAGATTATATTAAAAAGAATAAGAAGACCATCGAGAACATTAACGAGCTGATCGAA	721	용 성
720		661	Db
720	. AAGAAGTTGGTCTTCGGATATCGCAAGCCTCTCGACAACATCAAGGACAATGTGGGAAAG	661	γO
660	AATGACTATTGTCAAATTCCATTCAATTTGAAGATCAGAGCCAACGAGTTGGACGTATTG	601	B 8
0	TGTACAAGTTGAATTTCTACTTCGACTTGCTAAGGGCCAAACTGAATGACGTTTGCGCC		DЬ
600	TGTACAAGTTGAATTTCTACTTCGACTTGCTAAGGGCCAAACTGAATGACGTTTGCGCC		Qy
540	TGTGATAACATTCATGGCTTCAAATATCTGATTGACGGTTACGAAGAGATCAATGAACTC	481	Ъ
540	GTGATAACATTCATGGCTTCAAATATCTGATTGACGGTTACGAAGAGATCAATGAACTC	481	Qy
480 480	. ACTATCAAGGAGCTGAAGTACCCACAGTTGTTCGACCTCACTAATCATATGCTGACACTG	42 <u>1</u> 421	Db Qy
420	AGCGATTCCGACGCCAAGTCCTACGCCGACCTCAAGCACCGAGTGAGAAACTATCTCCTC	ō,	Db
420	GCGATTCCGACGCCAAGTCCTACGCCGACCTCAAGCACCGAGTGAGAAACTATCTCCTC	36:	Qy
		0	망
360	GCTCAGTGGCAAGCGGCGGTTCCGGGAACAGTCGAAGAACCAATCCATCTGACAACTCT	30:	Qy
300	. TCCGGTGGGTCTGTGGCCTCTGGGGGTTCCGTCGCCCTCCGGCGG	241 241	Db Qq
240	AGTGGCACGGCTTACAACCAGCACACCCGGTTCTAAAGGGTCTGTGGCTAGCGGTGGC	181	Db
240	1 AGTGGCACGGCCGTTACAACCAGCACACCCCGGTTCTAAAGGGTCTGTGGCTAGCGGTGGC	181	Qy
180			DЬ
180	CCGTCCTTACCGGATACAGCCTGTTCCAGAAGGAGAAGATGGTGCTGAATGAA	121	Qy
120 120	CAGTGCGTGACCCACGAATCCTATCAGGAGCTGGTTAAGAAACTGGAAGCTTTGGAAGAT	61	DB 04
60	CGCACGCGTATGAAAATCATTTTCTTCCTCTGTTCATTTTTTTT		Db
60	GCGTATGAAAATCATTTTCTTCCTCTGTTCATTTCTGTTTTTTTATCAATAACT		Qy

2220	GGACAACAGGCCGGTTCAGCTCTCGAAGGCGATAGCGTGCAAGCTCAAGCACAAGAGCAG	2161	Qy
2160	TCAGATAACTCCGAGCCTTCCACAGAAGGAGAGATAACCGGACAGGCTACCACCAAGCCC	2101	Db
2160	CAGATAACTCCGAGCCTTCCACAGAAGGAGAGATAACCGGACAGGCTACCACCAAGCC	2101	Qy
2100	ATGCCCAAAGTCGAGAGCCTGATCAACGAAGAGAAGAAGAACATTAAAACTGAAGGACAG	2041	dd
2100	CCCAAAGTCGAGAGCCTGATCAACGAAGAAGAAGAAGAACATTAAAACTGAAG	2041	Qy
2040	AAGCAGGAACCATACTACCTCATCGTACTCAAGAAAGAGATAGACAAACTGAAAGTGTTC	1981	Db
2040	AGGAACCATACTACCTCATCGTACTCAAGAAAGAGATAGACAAACTGAAAGTGTT	1981	Оу
1980	CTGAAGAACGTGGAGTTAAAACATAATATACATGTGCCGAATAGTTATAAAGCAGGAGAAT	1921	дь
1980	AACGTGGAGTTAAAACATAATATACATGTGCCGAATAGTTA:	1921	Qy
1920	CAAGTGCAGAAGGTGCTCCTCATGAACAAGATTGATGAACTCAAGAAGACTCACTC	1861	Db
1920	AAGTGCAGAAGGTGCTCCTCATGAACAAGATTGATGAACTCAAGAAGACTCAACTC	1861	Qy
1860	ACAAAAGACGAAAATAAACCAGATGAGAAGATCCTGGAGGTCTCCGATATTGTTAAAGTC	1801	Db
1860	ACAAAAGACGAAAATAAACCAGATGAGAAGATCCTGGAGGTCTCCGATATTGTTAAAGTC	1801	Qy
1800	ATCGAGACGCTTGTTGAGAACATTAAGAAGGATGAAGAACAGTTGTTTGAGAAGAAGATT	1741	Db
1800	TCGAGACGCTTGTTGAGAACATTAAGAAGGATGAAGAACAGTTGTTTGAGAAGAAC	1741	Qy
1740	ATTGTTGTGGAGAAGAACTAAAGTATTACAAGAATCTCATAAGTAAG	1681	Db
1740	AACTAAAGTATTACAAGAATCTCATAAGTAAGATCGAAAAC	1681	Оу
1680	CATAATCTTGAGAAGCTCACCAAAGCTCTTAAGTATATGGAGGACTATTCTCTGCGGAAC	1621	Db
1680	ATAATCTTG	1621	Оу
1620	TCTTACAAAGTGGAGAAACTGACACCACCATAATACCTTTGCATCCTATGAGAATTCTAAG	1561	Db
1620	CTTACAAAGTGGAGAAACTGACAC	1561	Qy
1560	TCCAAATTCAACAATAACATCGACCTGACCAACTTCGAGAAAATGATGGGAAAACGGTAC	1501	Db
1560	TCCAAATTCAACAATAACATCGACCTGACCAACTTCGAGAAAATGATGGGAAAACGGTAC	1501	Qy
1500	AGCAAAAGTCTAAACGATATCACTAAAGAGTATGAAAAGCTGCTGAACGAGATCTATGAT	1441	Db
1500	AGCAAAAGTCTAAACGATATCACTAAAGAGTATGAAAAGCTGCTGAACGAGATCTATGAT	1441	Qy
1440	GAGAAGATCAAAATTGAGAAGAAAATTGAGAGTGACAAGAAAAGTTACGAAGACCGC	1381	Db
1440	AGAAGATCAAAATTG	1381	Оу
1380	GAACCCTCTAAGAATATCTACACAGACAATGAGGAGAAGGAAG	1321	Db
1380	\AGAATATCTACACAGACAATGAGAGAAAGAAGTT	1321	Qy
1320	ACGCTCTCAACGAGCTCAATAGCTTCGGTGACTTGATTAACCCCTTCGATTATACGAAA	1261	Db
1320	AACGCTCTCAACGAGCTCAATAGCTTCGGTGACTTGATTAACCCCTTCGATTATACGAAA	1261	Qy
1260	ACCGAACCTAATGATATCCCAATGGTGTGACGTACCCTCTGTCTTATAACGATATCAAC	1201	Db
1260	CGAACCTAATGAAT	1201	Qy
1200	TACTTGAGAGAGAATAAGAATATAGACATCTCCGCCAAAGTCGAGACAAAGGAATCA	1141	DЬ
1200	TACTTGAGAGAGAAGAATAAGAATATAGACATCTCCGCCAAAGTCGAGACAAAGGAATCA	1141	Qy
1140	GCCAAAACCATTAAGTTCAACATAGATTCTCTCTTTACTGATCCCCTTGAGCTGGAGTAC	1081	DЬ
1140	GCCAAAACCATTAAGTTCAACATAGATTCTCTCTTTACTGATCCCCTTGAGCTGGAGTAC	1081	Оу

ω.	рь	241 CTGGAGAACACCAAGATTCTTCTCAAACACTACAAAGGCCTCGTCAAGTATTATAATGGC 3300	Оу 324
4321	Qy	81 AACTTCTCAGTGTTCTTCAACAAGAAGAAGGAAGCCGAGATCGCCGAGACAGAGAA	מם מו
4261	Db	I AACTICICAGIGITECITCAACAAGAAGAAGGAAGCCCGAGATCGCCGAGACAGAGGAACACT 32	<u>ب</u>
4261	Оу	1 CTCAAGGAGCAGCTTGAAAGCAAACTCAACTCAACTCAA	ں د با د
420	da	21 CTCAAGGAGCAGCTTGAAAGCAAACTCACTGAACAATCCGAAACACGTACTGCAG 31	. ω
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396	Qy	21 ATCTACCAAGAACTTATTGGACAGAAATCGTCCGAGAACTTCTACGAGAAAGATACTGAAA 288	2 2
390	Db	21 ATCTACCAAGAACTTATTGGACAGAAATCGTCCGAGAACTTCTACGAGAAGATACTGAAA 28	28
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3841	Db	AACCTTAATAACTCACTGAAACTGTTTGAGAACATCCTGTCTCTGGCAAGAATAAGAAC 282	. 27 27
384	Qy	1 CTCTCMCMCCTCMMGMCMMGCCCGMMGTGMCCTCTMMCGMCGMCMCCTCTCMCTCGMCC 2/0	
378	dd	TCTCTCACACCTCAAGACAAGCCCGAAGTGAGCGCTAACGACGACACCTCTCACTCGACC 276	J N
3781	Оу	41 GAAGCTAAGAAGGTCTCCACCTCTGTTAAAACTCTCTTCCAGGTCCATGCAACCACTG 2/0	
3721	Db	CANAGE TANGAMOGICI CANCINCISTI MAMAKITI CICI CITI CANCINCATO CANCI	۸ د
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3661	Db	S81 GAGARGGTUGCAACCTGTARAACTCAAAGACAACGACAAGATTAAGAACCTTCTGGAG 2640 	Dh 258
3661	Qy	21 ICINIBIICBAINBCCICAACAAIICICICICICICAACIBIICAIBBABAIAIAIBBABAAB 23) N
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3541	Db		, , ,
3541	. Qy	UI ACTATUANCGAGAAGATTCTTANACAGTACAAGATAACCAAGGAAGAAGGAGGAGGTANACTG 24	
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3361	Db		22
3361	Qy	81 CCACCAGCTCCTGTGAATAACAAGACCGAGAATGTCAGCAAACTGGACTACCTTG	Оу 228
ū	Db		22
330:	Qy	21 AAGCAGGCACAGCCTCCAGTGCCAGTGCCGTTTCCAGAGGCTTAAAGCTCAAGTGCCTTACA 2	2
324	Db		Db 216

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4380	ACCTGGAGGCCAAGGTCCTCAACTATACTTACGAGAAGAGCAATGTGGAAGTTAA	w	DЬ
	CACCTGGAGGCCAAGGTCCTCAACTATACTTACGAGAAGAGCAATGTGGAAGTTAAAATC	4321	Qy
4320	GAATAACATCGAAACCCCTGTACAAGACAGTGAACGACAAAATCGACCTCTTCGT	N	Db
4320	- G	2	у
4260	GACTCTATTAAAAAAGTATATCAACGATAAGCAAGGCGAGAATGAAAAATATCTGCCCTTC	N	Дb
4260	ACTCTATTAAAAAGTATATCAACGATAAGCAAGGCGAGAATGAAAAATATCTGCC	N	Qy
4200	TTCCCTAATGTGCTGGGGTATTACAAGATCCTGAGCGAAAAATACAAGTCTGACCTT	4141	Db
4200	TCGCTAATGATGTGCTGGGGTATTACAAGATCCTGAGCGAAAAATACAAGTCTGAG	14	Qy
4140	AGGGATAAATTTCTGTCTAGTTACAACTATATCAAGGACTCCATCGACACCGATATCAAT	0	Db
4140	ATAAATTTCTGTCTAGTTACAACTATATCAAGGACTCCATCGACACCGATATC	0	Qy
4080	GACCTGACCTCTAACTACGTTGTCAAGGACCCATACAAGTTCCTCAATAAAGAGAAG	0	Db
4080	ACCTGACCTCCTCTAACTACGTTGTCAAGGACCCATACAAGTTCCTCAATAAAGAG	4021	Qy
4020	ATTCCCTA	9	Db
4020	GCTTTAATAAGAGAGAAAATTTCAAGAACGTCTTGGAGAGCGACTTGATTCCCTA1	9	Qy
3960	AAACAGCTGGAGAATAACGTGATGACCTTCAATGTCAACGTGAAGGACATTCTGAACAGC	9	Db
3960	AGCTGGA&AATAACGTGATGACCTTCAATGTCAACGTGAAGGACATTCTGAACAG	9	Ωу
3900	GAGAACGAATACGAAGTCTCTATCTGAAACCTCTGGCAGGCGTCTATAGGTCTCTCAAG	æ	Db
3900	AGAACGAATACGAAGTGCTCTATCTGAAACCTCTGGCAGGCGTCTATAGGTCTCTC	84	Qy
3840	CAGGTGGTCACCGGTGAGGCTGTCACTCCTTCCGTGATTGAT	7	ДD
3840	AGGTGGTCACCGGTGAGGCTGTCACTCCTTCCGTGATTGAT	7	Оу
3780	GATGACGTCATCTTGTGCCTATCTTCGGCGAGAGCGAGGAGGACTACGATGACCTCGGC	7	Db
3780	ATGACGTCATCATTGTGCCTATCTTCGGCGAGAGCGAGGAGGACTACGATGACCTCGG	3721	Qy
3720	ACTCATGTCGGAGCCGAGTCCAATACAATTACCACATCTCAGAACGTCGACGATGAGGTC	6	Db
3720	CATGTCGGAGCCGAGTCCAATACAATTACCACATCTCAGAACGTCGACGATGAGGT	6	Qy
3660	GTGGTGTCTGAATCTGGCTCCGACACACTGGAGCAGTCTCAACCTAAGAAGCCTGCATCT	3601	рь
3660	TGGTGTCTGAATCTGGCTCCGACACACTGGAGCAGTCTCAACCTAAGAAGCCTGCATC	9	Qy
3600	GTGAATAACGCACTGGAATCTTACAAGAAGTTCCTGCCTG	3541	DЬ
3600	TGAATAACGCACTGGAATCTTACAAGAAGTTCCTGCCTGAAGGAACAGATGTCGCCAC	5	. Qy
3540	ACCGGCAATAGCCCAAGCGAGAATAATACAG	4	DЪ
3540	GAAGTCATTAAGAACAAĠAACTACACCGGCAATAGCCCCAAGCGAGAATAATAC	3481	Qy
3480	CTGGAGAAGAAGCTCAGCTACCTCTCTAGCGGACTGCATCACCTGATCGCCGAGCTC	3421	Db
3480	TGGAGAAGAAGAAGCTCAGCTACCTCTCTAGCGGACTGCATCACCTGATCGCCGAGC	3421	Qy
3420	AGCCTCGAGAACTTCAAGGTCCTGTCTAAGCTCGAAGGCAAGCTGAAGGACCAGACCTGAAC	w	. Db
3420	CCTCGAGAACTTCAAGGTCCTGTCTAAGCTCGAAGGCAAGCTGAAGGACAACCTG	w	Qy
3360	GAGTCTTCTCCTCTGAAGACTCTCTCCGAGGAGACTCCAGACCGAGGATAACTACGCC	3301	Db
3360	AGTCTTCTCCTCTGAAGACTCTCTCCGAGGAGGAGCATCCAGACCGAGGATAACTACGC	3301	Qy
3300	CTGGAGAACACCAAGATTCTTCTCAAACACTACAAAGGCCTCGTCAAGTATTATAATGGC	3241	Db

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Submitted (14-DEC-1998) Bujard H.,
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heidelberg, BW, GERMANY
2 (bases 1 to 4940)
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Cloning vector pBSK*-MSP-1s/FCB.
Cloning vector pBSK*-MSP-1s/FCB
                                                                                                        Vaccine candidate MSP-1 from Plasmodium falciparum: a redesigned 4917 bp polynucleotide enables synthesis and isolation of
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10. .69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQNSGCFRHLDEREE
CKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="msp-1"
1156 c 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I HLEAKVLNYTY EKSNV EVK I KELNY LKT I QDKLADF KKNNNF VG I ADLSTDY NHNNL
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Pred. No. 0;
0; Mismatches
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1440 1440	GAGAAGATCAAAATTGAGAAGAAGAAAATTGAGAGTGACAAGAAAAGTTACGAAGACCGC 	1381 1381
1380 1380	GAACCCTCTAAGAATATCTACACAGAGAGAATGAGAAGAAGTTTATCAACGAAATCAAG 	1321 1321
1320 1320	AACGCTCTCAACGAGCTCAATAGCTTCGGTGACTTGATTAACCCCTTCGATTATACGAAA 	1261 1261
1260 1260	ACCGAACCTAATGAATATCCCAATGGTGTGACGTACCCTCTGTCTTATAACGATATCAAC	1201 1201
1200 1200	TACTTGAGAGAGAAGAATAAGAATATAGACATCTCCGCCAAAGTCGAGACAAAGGAATCA 	1141 1141
1140 1140	GCCAAAACCATTAAGTTCAACATAGATTCTCTCTTTTACTGATCCCCTTGAGCTGGAGTAC 	1081 1081
1080	AACACGCTGCTGGACAAGAACAAGAAGATAGAGGAGCACGAGAAAGAGATCAAAGAGATC	1021 1021
1020 1020	CTGCTCGACAAGATTAATGAAATTAAGAATCCTCCGCCAGCCA	961 961
960	CTCATCAGCGTACTGGAGAAGCGCATAGACACCCTCAAGAAGAATGAAAATATCAAAGAA	901 901
900	TTGTACCAGGCCCAGTACGACCTGTCCATCTATAACAAACA	841 841
840 840	GAATCCAAAAAGACCATAGACAAAAATAAGAATGCAACCAAGGAGGAAGAAAAAAAA	781 781
780 780	ATGGAAGATTATATAAAAAGAATAAGAAGACCATCGAGAACATTAACGAGCTGATCGAA 	721 721
720 720	AAGAAGTTGGTCTTCGGATATCGCAAGCCTCTCGACAACATCAAGGACAATGTGGGAAAG	661 661
660	AATGACTATTGTCAAATTCCATTCAATTTGAAGATCAGAGCCAACGAGTTGGACGTATTG	601
600	CTGTACAAGTTGAATTTCTACTTCGACTTGCTAAGGGCCAAACTGAATGACGTTTGCGCC	541 541
540 540	TGTGATAACATTCATGGCTTCAAATATCTGATGACGGTTACGAAGAGATCAATGAACTC 	481 481
480 480	ACTATCAAGGAGCTGAAGTACCCACAGTTGTTCGACCTCACTAATCATATGCTGACACTG	421 421
420 420	AGCGATTCCGACGCCAAGTCCTACGCCGACCTCAAGCACCGAGTGAGAAACTATCTCCTC	361 361
360	GGCTCAGTGGCAAGCGGCGGTTCCGGGAACAGTCGAAGAACCAATCCATCTGACAACTCT	301

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2461 2461	2401 2401	2341 2341	2281 2281	2221 2221	2161 2161	2101 2101	20 4 1 20 4 1	981 981	1921 1921	1861 1861	801 801	1741 1741	1681 1681	1621 1621	1561 1561	1501 1501	1441 1441
TCCTCTTGTG.	ACTATGAAC	CTCTATG:	CCACCAGO CCACCAGO	AAGCAGGG AAGCAGGG	GGACAACA GGACAACA	TCAGATAA TCAGATAA	ATGCCCAA ATGCCCAA	AAGCAGGI { AAGCAGGI	CTGAAGAAC CTGAAGAAC	CAAGTGC	ACAAAAGA ACAAAAGA	ATCGAGAC	ATTGTTGT	CATAATCT	TCTTACAAA TCTTACAAA	TCCAAATTC TCCAAATTC	AGCAAAAG AGCAAAAG
TGATCCACTGG	GAGAAC GAGAAC	AGTTCCTG AGTTCCTG	CTCCTGTG	GCACAGCCT	AGGCCGGTT	ACTCCGAGC	AAGTCGAGAGI AAGTCGAGAG	AACCATACT.	ACGTGGAGTT.	AGAAGGTGC' AGAAGGTGC'	ACGAAAATAAAC ACGAAAATAAAC	CCTTGTTG	rggagaaag <i>i</i> rggagaaag <i>i</i>	TGAGAAG TGAGAAG	3 – 3	CAACAATAACA CAACAATAACA	AAAGTCTAAACG <i>P</i> AAAGTCTAAACG <i>P</i>
CTGGACO	ATI	AATAC	AATA	CCAGTGC	TCAGCTC		AGCCTGA AGCCTGA	ACC - 20	TTAAAACATAA: TTAAAACATAA:		AAACCAG AAACCAG	AGAAC AGAAC	AC AC	CTCACC!	GGAGAAACTG <i>I</i> GGAGAAACTG <i>I</i>	AACATCG AACATCG	TATC
ACCTGCTGTT ACCTGCTGTT	CTTAAACAGTACAAGA CTTAAACAGTACAAGA	CATCCTACAI	ACAAGACCGA ACAAGACCGA	CAGTGCCO CAGTGCCO	CTCGAAGGCGI CTCGAAGGCGI	CACAGAAGGAG <i>i</i> CACAGAAGGAG <i>i</i>	TCAACO TCAACO	TCATCGTACTCI TCATCGTACTCI	CATAATAT CATAATAT	CATGAACAA CATGAACAA	ATGAC ATGAC	ATTAAGA? ATTAAGA?	PAAAGTATTAC PAAAGTATTAC	CAAAGCTCTT CAAAGCTCTT	BACACACCA BACACACCA BACACACCA	SACCTGAC	ACTAAAGAGTATGAAAAGCTG ACTAAAGAGTATGAAAAGCTG
STTCAATATCO	CAAGATAAC	ATCTGCCAC	AGAATGTC. AGAATGTC.	GTTCCA	ATAGO ATAGO	AGA7 AGA7	AAGAGAAG BAAGAGAAG	CAAGAAAG! CAAGAAAG!	TATACATGTGCCGAAT# TATACATGTGCCGAAT#	GATTGAT GATTGAT	AAGATCCTG AAGATCCTG	AAGGATGAAG AAGGATGAAG	CAAGAATC	TAAGTATATGG <i>I</i> TAAGTATATGG <i>I</i>	CACCATAATACC CACCATAATACC	CAACTTC CAACTTC	GTATGAA GTATGAA
2A – 2A	CAAGG CAAGG	AAATAT AAATAT	AGCAAAC AGCAAAC	GAGGCT GAGGCT	GTGCAAG GTGCAAG	PAACCGGAC PAACCGGAC	AAGAAC <i>I</i> AAGAAC <i>I</i>	AGATAG AGATAG	CCGAATA CCGAATA	GAACTO GAACTO	GAGGTCT GAGGTCT	AACAGI AACAGI	CTCATAA CTCATAA	5 <u></u> 5	CCTTTGCAT	GAGAAAA GAGAAAA	AAGCTGC AAGCTGC
GAACAACATTCCCGTT <i>I</i> GAACAACATTCCCGTT <i>I</i>	AAGAGGAG AAGAGGAG	ATCCTCGT	TGGACI TGGACI	PAAGCTCAA AAAGCTCAA	CTCAAGCAC	AGGCTAC AGGCTAC	NTTAAAACT TTAAAACT	ACAAACTG ACAAACTG	FAGTTATAAG FAGTTATAAG	DAAGAAGAC DAAGAAGAC	CCGATAT	TGTTTGAG	CTCATAAGTAAGATCC CTCATAAGTAAGATCC	GACTATTCTCT 	CCTATGAG	GAGAAAATGATGGGA GAGAAAATGATGGGA	3CTGAACGA 3CTGAACGA
CGTTATGT. CGTTATGT.	AGTAA! AGTAA!	CTCTCAC	PACCTTGAG	GIGCCI GIGCCI	AAGAG AAGAG	CACCAAG CACCAAG	GAAGGA GAAGGA	AAAGTG AAAGTG	CAGGAG CAGGAG	TCAACTC	TGTTAAAG TGTTAAAG	AAGAAG AAGAAG	CGAAAACG, CGAAAACG,	000 000 000	AATTCI AATTCI	AAACGG AAACGG	CGAGATCTATG CGAGATCTATG
PAT 25	CTG 24	AGC 24 AGC 24	AAG 23	ACA 22 111 ACA 22	CAG 22	CCC 21	CAG 21	TTC 20	;AAT 19 ;AAT 19	ATT 19	STC 18	ATT 18	3AG 17 3AG 17	GAAC 16 GAAC 16	AAG 16 111 AAG 16	TAC 15	3AT 15 3AT 15
520 520	460		340 340	280 280	220 220	160	100	040	ထ ထ	920	960		740 740	089	520 520	560	500

3660	GTGGTGTCTGAATCTGGCTCCGACACACTGGAGCAGTCTCAACCTAAGAAGCCTGCATCT	3601	Qy
3600		3541	DЬ
3600	GTGAATAACGCACTGGAATCTTACAAGAAGTTCCTGCCTG	3541	Qy
3540	AAGGAAGTCATTAAGAACAAGAACTACACCGGCAATAGCCCCAAGCGAGAATAATACAGAC	3481	Db
3540	AGGAAGTCATTAAGAACAAGAACTACACCGGCAATAGCCCAAGCGAGAATAATACAGAC	3481	Qy
3480 3480	CTGGAGAAGAAGCTCAGCTACCTCTCTAGCGGACTGCATCACCTGATCGCCGAGCTC	3421 3421	р 9
3420	GCCTCGAGAACTTCAAGGTCCTGTCTAAGCTCGAAGGCAAGCTGAAGGACAACCTGAAC	w	D
3420	AGCCTCGAGAACTTCAAGGTCCTGTCTAAGCTCGAAGGCAAGCTGAAGGACAACCTGAAC	w	Qy
3360	AGTCTTCTCCTCTGAAGACTCTCTCCCGAGGAGACCATCCAGACCGAGGATAACTAC	3301	р
3360	- G	3301	Qy
30		24	В
ũ	GAGAACACCAAGATTCTTCTCAAACACTACAAAGGCCTCGTCAAGTATTATAATGG	3241	QV
		3181	Db
3240	AACTTCTCAGTGTTCTTCAACAAGAAGAAGGAAGCCGAGATCGCCGAGACAGAGAACAC	3181	Qy
18	TCAAGGAGCAGCTTGAAAGCAAACTCAACTCACTGAACAATCCGAAACACGTACTGCAG	12	B 2
20	TCAAGGAGCAGCTTGAAAGCAAACTCAACTCACTGAACAATCGAACAACACTACTACT	12	Ŷ
112	CTCTTCGACAAGAAGAAGACAGTCGGCAAGTATAAGATGCAGATCAAGAAGTTGACTCTG	06	망
12	CTCTTCGACAAGAAGAAGACAGTCGGCAAGTATAAGATGCAGATCAAGAAGTTGA(0	γO
3060	ANDAMOALCIOCANCITOCANCITICONCOTOTACANCANGIACANCITGANACITGANACITGGAGAGA	3001	B 5
Š	ATCAMCTCTCTTAMCGATGAATCTAAAAGCTGGAAGAGGACATCAATAAA	9	2
00	. ATCAACTCTCTTAACGATGAATCTAAACGTAAGAAGCTGGAAGAAGAGCATCAATAAGCTG	2941	P 09
2940	GACAGCGACACTTCTATAACGAGAGCTTCACTAACTTCGTGAAATCTAAAGCCGA	88	Дb
2940	GACAGCGACACATTCTATAACGAGAGCTTCACTAACTTCGTGAAATCTAAAGCCGATGAT	2881	Qy
2880	ATCTACCAAGAACTTATTGGAC	2821	рь
2880	ATCTACCAAGAACTTATTGGACAGAAATCGTCCGAGAAACTTCTACGAGAAGATACTC	2821	Qy
2820	AACCTTAATAACTCACTGAAACTGTTTGAGAACATCCTGTCTCTCGGCAAGAATAAGAAC	2761	рь
2820	AACCTTAATAACTCACTGAAACTGTTTGAGAACATCCTGTCTCTCGGCAAGAATAAC	2761	Qy
2760	TCTCTCACACCTCAAGACAAGCCCGAAGTGAGCGCTAACGACACCTCTCACTCGACC	2701	В
2760	CTCTCACACCTCAAGACAAGCCCGAAGTGAGCGCTAACGACGACACCTCTCACTCG	2701	Qy
2700	GAAGCTAAGAAGGTCTCCACCTCTGTTAAAACTCTCTCTTCCAGCTCCATGCAACCACTG	2641	망
2700	GAAGCTAAGAAGGTCTCCACCTCTGTTAAAACTCTCTCTTCCAGCTCCATGCAACCAC	2641	Qγ
2640 2640	. GAGATGGTCTGCAACCTGTATAAACTCAAAGACAACGACAAGATTAAGAACCTTCTGGAG 	2581 2581	P Qy
2580	TCTATGTTCGATAGCCTCAACAATTCTCTCTCTCAACTGTTCATGGAGATATATGAG	52	Db
5 60	TCTATGTTCGATAGCCTCAACAATTCTCTCTCTCAACTGTTCATGGAGATATATGAGAAG	5 2	ş 9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4681 AACTACAAACAAGAAGGAGATAAGTGCGTGGAGAACCCCAAACCCTACCTGCAATGAAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCAGCTCTAATTTCCTGGGCATCTCCTTCCTGCTGATCCTCATGCTGATCCTGTACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATGGCGGGTGTGACGCCGATGCTAAATGCACCGAGGAAGACAGCGGCTCTAACGGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATGGCGGGTGTGACGCCGATGCTAAATGCACCGAGGAAGACAGCGGCTCTAACGGAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCAGCTCTAATTTCCTGGGCATCTTCTTCCTGCTGATCCTCATGCTGATCCTGTACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (06-MAR-1991) Holder A.A., National Institute Research, The Ridgeway, Mill Hill, London NW7 1AA, UK Update of published sequence Data kindly reviewed (06-MAR-1986) by R.R. Freeman.
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86014355
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigen; direct repeat; signal peptide; surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum mRNA for (P195).
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                                                                                                                       KLYGOYRKÞIÐNIKONVGKMEDYIKKNKKTIENINELIEESKKITIÓKNKNATKEBEKK
KLYGAQYDLSI YNKOLEEAHLISVILKKIENIKKNENIKELLDKINIKNATKEBEKK
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                                                                                                                                                                                                                                                                           IHGFKYLIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="P195 precursor"
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                                                                                                                                                                                                                                                                                                                                                                /db_xref="SWISS-PROT:P04933"
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Query Match
Best Local Similarity
Matches 3609; Conserv
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718
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                                                                                                                                                                                                                                                                                                             70
                                                                                                                                                                                                                                                                                                                                                               10 ATGAAAATCATTTTCTTCCTCTGTTTCATTTCTTTTTTTATCATCAATACTCAGTGCGTG
                   GCAAGCGGCGGTTCCGGGAACAGTCGAAGAACCAATCCATCTGACAACTCTAGCGATTCC
                                                                                    TCTGTGGGCTTCTGGGGGTTCCGTCGCCTCCGGCGGCAGCGTGGCATCAGGTGGCTCAGTG
                                                                                                                                    ACCCACGAATCCTATCAGGAGCTGGTTAAGAAACTGGAAGCTTTGGAAGATGCCGTCCTT 129
GCTTCAGGTGGTTCAGGTAATTCAAGACGTACAAATCCTTCAGATAATTCAAGTGATTCA
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                                                                                                                                                                    GCCGTTACAACCAGCACACCCGGTTCTAAAGGGTCTGTGGCTAGCGGTGGCTCCGGTGGG
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4750. .4752
/note="pot.
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2764. .2766
/note="pot.
2947. .2949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="region coding for 83K, antigens (aa 1-1628)" 631. 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"pot. glycosylation site"
1219. 1221
/note-"pot. glycosylation site"
2707. .2709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGLYKYYNGESSPLKTLSEESIQTEDNYASLENFKYLSKLEGKLKDNLNLEKKKLSYL
SSGLHHLIAELKEVIKNKNYGNSPSENNTDVNNALESYKFLPEGTDVATVYSESGS
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KRENEKNVLESDLIPYGDLTSSNYVYKDDPYKFLNKEGNFLSSYNYIKDSIDTDINF
ANDULGYYKILSEKYKSDLDSIKKYLDKOGENEKYLDFLNNLETLYKFVUDKIDLFU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="763..7
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475. .5334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="pot
3307. .3309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="pot. 3175. .3177
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2719. .2721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQNSGCFRHLDEREE
CKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENTLENTKILLKHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGKYKM
                                                                                                                                                                                                                                                                                                                                                                                                                                 57.0%;
73.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pot. glycosylation
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                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2816.4; DB 3; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 1321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    site"
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1449 1857	1390 AAAATTGAGAAGAAGAAATTGAGAGTGACAAGAAAAGTTACGAAGACCGCCAGCAAAAGT 	ОУ
1389 1797	1330 AAGAATATCTACACAGACAATGAGAGAAAGAAGTTTATCAACGAAATCAAGGAGAAGATC	рь
1329 1737	1270 AACGAGCTCAATAGCTTCGGTGACTTGATTAACCCCTTCGATTATACGAAAGAACCCTCT	Оy
1269 1677	1210 AATGAATATCCCAATGGTGTGACGTACCCTCTGTCTTATAACGATATCAACAACGCTCTC	Оy
1209 1617	1150 GAGAAGAATAAGAATATAGACATCTCCGCCAAAGTCGAGACAAAGGAATCAACCGAACCT	Db
1149 1557	1090 ATTAAGTTCAACATAGATTCTCTCTTTACTGATCCCCTTGAGCTGGAGTACTACTTGAGA	Qy Db
1089 1497	1030 CTGGACAAGAACAAGAAGATAGAGGAGCACGAGAAAGAGATCAAAGAGATCGCCAAAACC	Оy
1029 1437	970 AAGATTAATGAAATTAAGAATCCTCCGCCAGCCAACTCTGGGAACACCCCCTAACACGCTG	Оy
969 1377	910 GTACTGGAGAAGCGCATAGACACCCTCAAGAAGAATGAAAAATATCAAAGAACTGCTCGAC 	. B 2y
909 1317	50 GCCCAGTACGACCTGTCCATCTA 	Db Qy
849 1257	790 AAGACCATAGACAAAATAAGAATGCAACCAAGGAGGAAGAAAAGAAGAAGTTGTACCAG 	Qу
789 1197	30 TATATTAAAAAGAATAAGAAGACCATCGAGAACATTAACGAGCTGATCGAAGAATCCAAA 	Db Qy
729 1137	670 GTCTTCGGATATCGCAAGCCTCTCGACAACATCAAGGACAATGTGGGAAAGATGGAAGAT 	Db
669 1077	610 TGTCAAATTCCATTCAATTTGAAGATCAGAGCCAACGAGTTGGACGTATTGAAGAAGTTG	Оy
609 1017	550 TIGAATTICTACTICGACTIGCTAAGGGCCAAAÇIGAATGACGTTIGCGCCAATGACTAT 	ОУ
549 957	490 ATTCATGGCTTCAAATATCTGACTGACGGTTACGAAGAGATCAATGAACTCCTGTACAAG 	Db Qy
489 897	430 GAGCTGAAGTACCCACAGTTGTTCGACCTCACTAATCATATGCTGAGACACTGTGTGATAAC	Db Qy
429 837	370 GACGCCAAGTCCTACGCCGACCTCAAGCACCGAGTGAGAAACTATCTCCCTCACTATCAAG 	Db Qy

Qy	рь	Qy	рь	Qy	Db Qy	Db	Qy	рь	Qy	Db .	Ογ	Db	Qy	ДЬ	Qy	рь	Ωу	Db	Qy	Db	Qy	Db	Qy	Db	Qy	DР	ОУ	DЬ	Qy	Db	Qy	Дb	Qy	Дb	Qy
2530	2878	2470	2818	2410	2350 2758	698	2290	2638	2230	578	2170	2518	2110	2458	050	2398	990	2338	930	2278	1870	2218	810	2158	1750	2098	690	2038	630	78	570	1918	510	858	1450
GATAGCCT	GATCCATT	GATCCACT	GAAAAGAT	GAGAAGAT	TTCCTGAA	CCAGTAA	CCTGTGAAT	CAACCACC	AGCCTC		GCCGGTTC	TCGGAACC	- O	GTAGAATC	- 8	CCTTATT	CCATACTA	GTAGAATT!	GTGGAGTT	AAAGTTTTA1	AAGGTGC	GAAAATAAACCA	GAAAATA	TTAGTTGAAAATATTAAAAAAGATGAAGAAC	CTTGTTG	 GAAAAAGAATTAAAATATTAT	GAGAAAGA	GAAAAGTTAACAA	GAGAAGC	GTTGAGAAACT	GTGGAGA	AATAATAAT!	AACAATAAC	TTAAATGATATAACAAAAGAATATGAAAAATTACTTAATGAAATTTATGATAGCAAAT	CTAAACG
CAAC	CATTAGACTTATTGTTTAATATAC	GGACCTG	GATATTAAAACAATA	TCTTAAA	TACATCCTACATCTGCC	TAATAAA	TAACAAG	≥ –	- 🌣	 TGCTTTA	AGCTCTC		TTCCACA	TCATTGATAAATGAAGAAAAAAAAAACATAAAAAACAGAAGGTC	CCTGATC	TTTAATT	ACCTCATCGTACTCAAGAAAGAGATAG	AAAAC	AAAC	ATTAATG	CCTCATG	ACCAGAT	ACCAGAT	AAATATT	GAACATT	 ATTAAAA	ACTAAAG	AACAAAA	CACCAAA	TAC	GAC	TATAGAT	CATCGAC	TATAACA	TATCACT
AATTCTCTCTC	TTGTTTA	CTGTTCA	CAATATA	CAGTACAL	TACATCTO	ACTGAAA	AACAAGACCGAGAATGTCAGCAAACTGGACTACCTTGAGAAGCTCTATG	TACCAGTACCAG	GTGCCCGT	GAAGGAG <i>I</i>	GAAGGCG <i>I</i>	GAAGGAG <i>t</i>	GAAGGAG!	AATGAAG!	AACGAAG!	GTGTTGA	GTACTCA	ATAATATACATGTTCCCAATTCTTACAAACAAGAAAATAAGC	AATATAC!	ATTAATGAACAAAATTGACGAATTAAAAAAGACTC	AACAAGA	AGATGAAAAAATTTTAGAAGTATCTGACATTGTAAAAGTACAAGTT	GAGAAGAI	AAAAAAGI	AAGAAGG!	TATTATA	TATTACA	AAAAGCTCTTAAATATATGGAAGATTATTCTTTAAGGAAT	GCTCTTA	ACACCATAATACTTTTGCATCCTATGAAAATTCTAAACATAATCTT	CACCATA	ATAGATTTAACTAATTTCGAAAAAATGATGGGTAAAAGATATTCATATAAA	CTGACCA	AAAGAAT	AAAGAGTI
TCAACTG	TATACAA	TATCCAG	ATAAAATTACAAAGGAGG	GATAACC	CCACAAA TCACAAA	TGTTTCC	TGTCAGC	ACCAGAA	TCCAGAG	 TTCAGTA	NTAGCGTG	AATAACA	GATAACC	AAAAAAA	GAAGAAG	AAAAGAA	GAAAGAG	TGTTCCC	TGTGCCG	TGACGAA	TGATGAA	TTTAGAA	CCTGGAG	VTGAAGAA	TGAAGAA	AAATTTA	GAATCTC	ATATATG	GTATATG	ATACTTTT	TACCTTT	TTTCGAA	CTTCGAG	\TGAAAAA	ATGAAAAG
TTCATGG!	CAAAATAACAT	AACAACA:	AAGGAGG!	AAGGAAG	CACAAATATATCCI CACAAATATATTTI	AAATTAGA	AAACTGG!	AGTACCAGAAGCAAAAGCACAAGTCCCAAC	GCTAAAG	AGTACAAGCACAAGCACAAGAACAAAAAC	CAAGCTC	GGACAAG	GGACAGG	AACATAA	AACATTA	ATTGATA	ATAGACA	AATTCTT/	AATAGTT	TTAAAAA	CTCAAGA	GTATCTG	GTCTCCG	CAGCTTT	CAGTTGT	AAAAATTTAATAAGCAAAATAGAAAATGAG	ATAAGTA	GAAGATT	GAGGACT	GCATCCT	GCATCCT.	AAAATGA'	AAAATGA'	TTACTTA	CTGCTGA
AGATATATG	PACCTGTA	TCCCGTT	H II II BAAGAAAGC	AGGAGAGT	CCTCGTCTCICI 	ATTATCTT	ACTACCTI	CACAAGTO	CTCAAGTO	AAGCACAA	AAGCACA?	CAACTACA	CTACCACC	AAACAGA#	AAACTGAA	AATTAAAA	ACAAACTGAAAGTGTTC	ACAAACA?	ATAAGCAG	AGACTCA	AGACTCA	ACATTGT?	ATATTGTT	TTGAAAA	TTGAGAAG	AAATAGAA	AGATCGA	ATTCTTT	ATTCTCTC	ATGAAAAT	ATGAGAAT	TGGGTAA.	TGGGAAA!	ATGAAATI	ACGAGATO
AGAAGG	CATACCTGTAATGTATTCTATG	ATGTATT	AAAGCAAATTAAGTTCATG	AAACTGT	CTCAC	GAAAAAT	GAGAAGC	CCAACAC	CCTACAC	II II I	GAGCAGA	CAAAACCTGGACAAC <i>i</i>	:AAGCCCG	GGTCAATC	GGACAGT	GTGTTCA	GTGTTCA	GAAAATA	GAGAATA	TTGATTT	CTCATTC	AAAGTAC	PAAAGTCC	AGCTTTTTGAAAAAAAATTACTAAAG	AAGATTA	AATGAGA	AACGAGA	AGGAATA	CGGAACA	TCTAAAC	TCTAAGC	AGATATT	CGGTACT	TATGATA	TATGATT
AGATGGTC	CTATGTTT	CTATGTT	GTTCATGT	CCTCTTGT	CACTATGAAC	TATATGA	TCTATGAG	CACCACCAGCA	- న	AACAAGCA	AGGC	GACAACAA	GACAACA	CGGATAAT	AGAT	TGCCTAA	CATGCCCAAA	AGCAAGAA	AGG	II I III I II II CAATTGATTTTAAAAAAT	TGAAGAA	AAGTTCAA	- a	CTAAAGAC	CAAAAGA	GATTGAAACA	င်	FATAGTAGTT	TTGTTGT	ATAATCT	ATAATCT	CATATAA	CTTACAA	GCAAATTC	CCAAATTC
2589	2937	2529	2877	2469	2817	2757	3 2349	2697	2289	26	1 2229	2577	3 2169	f 2517	2109	3 2457	A 2049	A 2397	1989	r 2337	1929	A 2277	3 1869	2217	1809	A 2157	G 1749	r 2097	3 1689	r 2037	r 1629	A 1977	A 1569	1917	1509

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3669	GAATCTGGCTCCGACACACAGAGCAGTCTCAACCTAAGAAGCCTGCATCTACTCATGTC	3610
3609 4017	GCACTGGAATCTTACAAGAAGTTCCTGCCTGAAGGAACAGATGTCGCCACTGTGGTGTCT	3550
3549 3957	ATTAAGAACAAGAACTACACCGGCAATAGCCCAAGCGAGAATAATACAGACGTGAATAAC	3490 3898
3489 3897	AAGAAGCTCAGCTACCTCTAGCGGACTGCATCACCTGATCGCCGAGCTCAAGGAAGTC	3430
3429 3837	AACTTCAAGGTCCTGTCTAAGCTCGAAGGCAAGCTGAAGCACCTGAACCTGGAGAAG	3370
3369 3777	CCTCTGAAGACTCTCTCCGAGGAGGAGCATCCAGACCGAGGATAACTACGCCAGCCTCGAG	3310
3309 3717	ACCAAGATTCTTCTCAAACACTACAAAGGCCTCGTCAAGTATTATAATGGCGAGTCTTCT	3658
3249 3657	GTGTTCTTCAACAAGAAGAAGGAAGCCGAGATCGCCGAGACAGAGAACACTCTGGAGAAC	3190
3189 3597	CAGCTTGAAAGCAAACTCAACTCACTGAACAATCCGAAACACTACTGCAGAACTTCTCA	3130
3129 3537	AAGAAGAAGACAGTCGGCAAGTATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGIIIIIIIIII	3070
3069 3477	CTGCAACTGAGCTTCGACCTGTACAACAAGTACAAACTGAAACTGGAGAGAGA	3010
3009 3417	CTTAACGATGAATCTAAACGTAAGAAGCTGGAAGAGGACATCAATAAGCTGAAGAGACA 	3358
2949 3357	ACATTCTATAACGAGAGCTTCACTAACTTCGTGAAATCTAAAGCCGATGATATCAACTCT	3298
2889 3297	GAACTTATTGGACAGAAATCGTCCGAGAACTTCTACGAGAAGATACTGAAAGACAGCGAC 	2830 3238
2829 3237	AACTCACTGAAACTGTTTGAGAACATCCTGTCTCTCGGCAAGAATAAGAACATCTACCAA	2770 3178
2769 3177	CCTCAAGACAAGCCCGAAGTGAGCGCTAACGACGACACCTCTCACTCGACCAACCTTAAT	2710
2709 3117	AAGGTCTCCACCTCTGTAAAACTCTCTCTCCAGCTCCATGCAACCACTGTCTCTCACA	3058
2649 3057	TGCAACCTGTATAAACTCAAAGACAACGACAAGATTAAGAACCTTCTGGAGGAAGCTAAG 	2590 2998
2997		2938

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4749 5157	4690 CAAGAAGGAGATAAGTGCG [†] GGAGAACCCCAAACCCTACCTGCAATGAAAACAATGGCGGG 	Qy Db
4689 5097	4630 AGCGGCTGTTTCAGGCATCTGGACCAGCGCGAAGAGTGCAAGTGTCTCCTGAACTACAAA 	Qу Db
4629 5037	CTGCAGGGCATGCTGA	Qy Db
4569 4977	4510 ACTGGCATGGTGTTCGAAAACCTCGCCAAAACAGTGCTGAGCAATCTGCTCGACGGCAAC	Qy Db
4509 4917	GGAATTGCAGACCTGTCTACCGATTATAACCACAACAATCTCCTGACCAAGTTTCT	Qy Db
4449 4857	AACTACCTCAAAACAATCCAAGACAAGCTGGCAGATTTCAAGAAAAATAACAATTTCG 	Qy Db
4389 4797	GCCAAG GCAAAA	Оу
4329 4737	ATCGAAACO	Qy Db
4269 4677	AAAAAGTATATCAAC	Qу
4209 4617	GATGTGCTGGGGTAG	Ωу
4149 4557	TTTCTGTCTAGTTACAACTATATCAAGG	Qy Db
4089 4497	TCCTCTAACTAC	Qy Db
4029 4437	AAGAGAGAAATTTCAAGAACGTCTTGGAGAGCGACTTGATTCCCTATAAAGACCTC	Qy Db
3969 4377	GAGAATAACGTGATGACCTTCAATGTCAACGTGAAGGACATTCTGAACAGCCGCTT 	Фр
3909 4317	TACGAAGTGCTCTATCTGAĀACCTCTGGCAGGCGTCTATAGGTCTCTCAAGAAACAC 	Qy Db
3849 4257	ACCGGTGAGGCTGTCACTCCTTCCGTGATTGATAACATTCTGTCCA	Qy Db
3789 4197	ATCATTGTGCCTATCTTCGCGAGAGAGCGAGGAGGACTACGATGACCTCGGCCAGGTGG	Db Oy
3729 4137	GGAGCCGAGTCCAATACAA†TACCACATCTCAGA	Qy Db
4077	4018 GAAAGTGGATCCGACACATTAGAACAAAGTCAACCAAAGAAACCAGCATCAACTCATGTA	Db

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89345116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (14-APR-1989) Myler P.J., Seattle Biomedical Research Institute, 4 Nickerson Street, Seattle WA 98109-1651, U S A 2 (bases 1 to 7038)
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Plasmodium falciparum
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SKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGKYKM
QIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENTLENTKILLKHY
KGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYL
                                                                                                                                        ETKESTEPNEYPNGYTYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERK KFINELKKIKIEKKKIEDKKSYPDRSKSLNDITKEKEYKKLEDYDSKNINTDLTN FERMAGKYSYKYEKLTHNITASYEDRSKSLNDITKEKEYKKLEDYDSKNINTDLTN FEKMAGKYSYKYEKLTHNITASYENBKHLEKLTKALKYMEDYSLAUTVUEKELKY YKNLISKIENELETLVENIKKDEQLFEKIITKDENKPDEXILEVSDIVKVQVQKVLL MIKIDELKKTOLLKNELKHNIHVPNSYKQENKQEPYLIVLKEGIDKLKVEMPKVE SLINEEKKNITATEGGSUASEPSTEGETTGQAFTKPGQQAGSALEGDSVQAQAQEXQA QPPYPYPVPDEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHST
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KLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLDKINEIKNPPPANSG
NTPNTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKNKNIDISAKV
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LFQKEKMVLNEGTSGTAVTTSTPGSKGSVASGGSVASGGSVASGGSVASGGSVAS
GGSGNSRRTNPSDNSSDSDAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDN
                                                                         HSTNLNNSLKLFENILSLGKNKNIYQELIGQKSSENFYEKILKDSDTFYNESFTNFVK
                                                                                            MNEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYE
KEMVCNLYKLKDNDKIKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTS
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/protein_id="CAA33163.1"
/db_xref="GI:9897"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Plasmodium falciparum"
/strain="Palo Alto PLF-3/B11"
/db_xref="taxon:5833"
/dev_stage="trophozoite/schizont."
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                                                       TATATTAAAAAGAATAAGAAGACCATCGAGAACATTAACGAGCTGATCGAAGAATCCAAA
                                                                                                                                                                                      TGTCAAATTCCATTCAATTTGAAGATCAGAGCCAACGAGTTGGACGTATTGAAGAAGTTG
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ANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLFV
IHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLSTDYNHNNL
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CKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYP
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1929 3511	1870 AAGGTGCTCCTCATGAACAAGATTGATGAACTCAAGAAGACTCAACTCATTCTGAAGAAC	Оy
1869 3 4 51	1810 GAAAATAAACCAGATGAGAAGATCCTGGAGGTCTCCGATATTGTTAAAGTCCAAGTGCAG	ОУ
1809 3391	750 CTTGTTGAGAACATTAAGAAGGATGAAGAACAGTTGTTTGAGAAGAAGATTACAAAAGAC 	Фр
1749 3331	1690 GAGAAAGAACTAAAGTATTACAAGAATCTCATAAGTAAGATCGAAAACGAGATCGAGACG	Оy
1689 3271	1630 GAGAAGCTCAACAAAGCTCTTAAGTATATGGAGGACTATTCTCTGCGGAACATTGTTGTG	Оy
1629 3211	70 GTGGAGAAACTGACACACCATAATACCTTTGCATCCTATGAGAATTCTAAGCATAATCTT 	Db 04
1569 3151	510 AACAATAACATCGACCTGACCAACTTCGAGAAAATGATGGGAAAACGGTACTCTTACAAA	Оу
1509 3091	50 CTAAACGATATCACTAAAGAGTATGAAAAGCTGCTGAACGAGATCTATGATTCCAAATTC 	Оу
1449 3031	1390 AAAATTGAGAAGAAAATTGAGAGTGACAAGAAAAGTTACGAAGACCGCAGCAAAAGT	Оy
1389 2971	GAAATCAAGGAGAAGATC GAAATTAAGGAAAAAATT	Оy
1329 2911	1270 AACGAGCTCAATAGCTTCGGTGACTTGATTAACCCCTTCGATTATACGAAAGAACCCTCT	Фр
1269 2851	1210 AATGAATATCCCAATGGTGTGACGTACCCTCTGTCTTATAACGATATCAACAACGCTCTC	P 04
1209 2791	AAGGAATCAACCGAACCT AAGGAATCAACTGAACCC	Оу
1149 2731	1090 ATTAAGTTCAACATAGATTCTCTCTTTACTGAGTCCCCTTGAGCTGGAGTACTACTTGAGA:	рβ
1089 2671	1030 CTGGACAAGAACAAGAAGATAGAGGAGCACGAGAAAGAGATCAAAGAGATCGCCAAAACC	Ф
1029 2611	970 AAGATTAATGAAATTAAGAATCCTCCGCCAGCCAACTCTGGGAACACCCCCTAACACGCTG :	Db Oy
969 2551	910 GTACTGGAGAAGCGCATAGACACCCTCAAGAAGAATGAAAATATCAAAGAACTGCTCGAC	Ωу
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A92450 Sequence A92450 A92450.1

Patent

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GI:6741180 from RESULT A92450

LOCUS

SOURCE ORGANISM

unidentified unidentified

KEYWORDS

REFERENCE AUTHORS TITLE

unclassified.

1 (bases 1 to 4920)
Pan,W. and Bujard,H.
METHOD FOR PRODUCING RECOMB
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NG (DE); BUJARD HERMANN (DE)
Location/Qualifiers
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Pred. No. 0;
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δõ DЬ Qy Ъ δÃ Дb δÃ B Qy ДЪ Qy 밁 Qy Дb Qy Qy В δÃ QУ Ωy Qy Ф Д Дb Вþ DЬ δÃ DЬ Qγ DЬ Qγ DЬ ΔÃ В Qy DЪ Qy 1801 1810 1690 1621 1501 1510 1390 1270 1210 1141 1081 1021 1870 1090 1030 970 GAGAAGCTCACCAAAGCTCTTAAGTATATGGAGGACTATTCTCTGCGGAACATTGTTGTG GTGGAGAAACTGACACACCATAATACCTTTGCATCCTATGAGAATTCTAAGCATAATCTT AACAATAACATCGACCTGACCAACTTCGAGAAAATGATGGGAAAAGGGTACTCTTACAAA TTAAATGATATAACAAAAGAATATGAAAAATTACTTAATGAAATTTATGATAGCAAATTC AACGAGCTCAATAGCTTCGGTGACTTGATTAACCCCTTCGATTATACGAAAGAACCCTCT AAGATTAATGAAATTAAGÁATCCTCCGCCAGCCAACTCTGGGAACACCCCCTAACACGCTG GTTGAGAAACTTACACACCATAATACTTTTGCATCCTATGAAAATTCTAAACATAATCTT **AATAATATATAGATTTAACTAATTTCGAAAAAATGATGGGTAAAAGATATTCATATAAA** CTAAACGATATCACTAAAGAGTATGAAAAGCCTGCTGAACGAGATCTATGATTCCAAATTC AAGAATATCTACACAGACAATGAGAGAAAGAAGTTTTATCAACGAAATCAAGGAGAAGATC AATGAATATCCCAATGGTGTGACGTACCCTCTGTCTTATAACGATATCAACAACGCTCTC GAAAAAATAAAAATATTGATATAAGTGCAAAGGTTGAAACAAAGGAATCAACTGAACCC GAGAAGAATAAGAATATAGACATCTCCGCCAAAGTCGAGACAAAGGAATCAACCGAACCT CTTGATAAGAACAAAAAAATCGAGGAACACGAAAAAAGAAATAAAAGAAATTGCCAAAACT CTGGACAAGAACAAGAAGATAGAGGAGCACGAGAAAGAGATCAAAGAGATCGCCAAAACC CCATACTACCTCATCGTACTCAAGAAAGAGATAGACAAACTGAAAGTGTTCATGCCCAAA AATGAACTTAATTCTTTTGGTGATTTAATTAATCCATTTGATTATACAAAAGAACCAAGT AATGAATATCCAAATGGAGTTACTTATCCTTTGTCATATAACGATATTAACAATGCTTTA 1260 1980 1860 1800 1809 1740 1749 1680 1689 1629 1560 1569 1500 1440 1449 1389 1329 1269 1209 1140 1149 1080 1929 1869 1620 1509 1380 1200 1089 1029 1320 1020 960

8129	3070 AAGAAGAAGACAGTCGGCAAGTATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAG 3	Qy
3069	3010 CTGCAACTGAGCTTCGACCTGTACAAACAAGTACAAACTGAAACTGGAGAGAGTCTCTTCGAC 3	Оу
3000	2950 CITAACGATGAATCTAAACGTAAGAAGCTGGAAGAGGGACATCAATAAGCTGAAGAAGAACA 3 	Оy
2949	2890 ACATTCTATAACGAGAGCTTCACTAACTTCGTGAAATCTAAAGCCGATGATATCAACTCT 2 	Qy
2889	2830 GAACTTATTGGACAGAAATCGTCCGAGAACTTCTACGAGAAGATACTGAAAGACAGCGAC 2 	Оy
2829 · 2820	2770 AACTCACTGAAACTGTTTGAGAACATCCTGTCTCTGGCAAGAATAAGAACATCTACCAA 2 	Оy
2769 2760	2710 CCTCAAGACAAGCCCGAAGTGAGGCGCTAACGACGACACCTCTCACTCGACCAACCTTAAT 2	Оy
2709 2700	2650 AAGGTCTCCACCTCTGTTAAAACTCTCTCTCCAGCTCCATGCAACCACTGTCTCTCACA 2	Оy
2649	2590 TGCAACCTGTATAAACTCAAAGACAACGACAAGATTAAGAACCTTCTGGAGGAAGCTAAG 2 	Оy
2589 2580	2530 GATAGCCTCAACAATTCTCTCTCTCAACTGTTCATGGAGATATATGAGAAGGAGATGGTC 2 	Db
2529	2470 GATCCACTGGACCTGCTGTTCAATATCCAGAACAACATTCCCGTTATGTATTCTATGTTC 2 	Оy
2469	2410 GAGAAGATTCTTAAACAGTACAAGATAACCAAGGAAGAGGAGAGTAAACTGTCCTCTTGT 2 	Qу Дъ
2409	2350 TICCTGAATACAICCTACATCTGCCACAAATATATCCTCGTCTCTCACAGGACTATGAAC 2 	Оу
2349	2290 CCTGTGAATAACAAGACCGAGAATGTCAGCAAACTGGACTACCTTGAGAAGCTCTATGAG 2 	Db Oy
2289	2230 CAGGCTCCAGTGCCAGTGCCCGTTCCAGAGGCTAAAGCTCAAGTGCCTACACCACCAGCT 2	Оy
2229 2220	2170 GCCGGTTCAGCTCTCGAAGGCGATAGCGTGCAAGCTCAAGCACAAGAGCAGGAAGCAGGCA 2 	Qу
2169 2160	2110 TCCGAGGCCTTCCACAGAAGGAGAAGAACAGCGACAGGCTACCACCAAGCCCGGACAACAG 2	Qу
2109 2100	2050 GTCGAGAGCCTGATCAACGAAGAGAAGAAGAACATTAAAACTGAAGGACAGTCAGATAAC 2	Qу Db
2040		Db

4209 4200	GATGTGCTGGGGTATTACAAGATCCTGAGCGAAAAATACAAGTCTGACCTTGACCTCTATT	4150 4141	Qу
4149 4140	TTTCTGTCTAGTTACAACTATATCAAGGACTCCATCGACACCGATATCAATTTCGCTAAT	4090 4081	Qу Дъ
4089 4080	TCCTCTAACTACGTTGTCAAGGACCCATACAAGTTCCTCAATAAAGAGAGAG	4030 4021	Qy Db
4029 4020	AAGAGAGAAATTTCAAGAACGTCTTGGAGAGCGACTTGATTCCCTATAAAGACCTGACC	3970 . 3961	Qy
3969 3960	GAGAATAACGTGATGACCTTCAATGTCAACGTGAAGGACATTCTGAACAGCCGCTTTAAT	3910 3901	Qy Db
3909	TACGAAGTGCTCTATCTGAAACCTCTGGCAGGCGTCTATAGGTCTCTCAAGAAACAGCTG	8 8	Qy
3849 3840	ACCGGTGAGGCTGTCACTCCTTCCGTGATTGATAACATTCTGTCCAAAATCGAGAACGAA	3790 3781	Qy Db
3789 3780	ATCATTGTGCCTATCTTCGGCGAGAGCGAGGAGGACTACGATGACCTCGGCCAGGTGGTC	3730 3721	Оу
3729 3720	GGAGCCGAGTCCAATACAATTACCACATCTCAGAACGTCGACGATGAGGTCGATGACGTC	3670 3661	Oy Db
3669	GAATCTGGCTCCGACACACTGGAGCAGTCTCAACCTAAGAAGCCTGCATCTACTCATGTC	3610 3601	Oy Db
3609	GCACTGGAATCTTACAAGAAGTTCCTGCCTGAAGGAACAGATGTCGCCACTGTGGTGTCT	3550 3541	Qy Db
3549 3540	ATTAAGAACAAGAACTACACCGGCAATAGCCCAAGCGAGAATAATACAGACGTGAATAAC	3490 3481	Qy Db
3489 3480	AAGAAGCTCAGCTACCTCTCTAGCGGACTGCATCACCTGATCGCCGAGCTCAAGGAAGTC	3430 3421	Qу
3429 3420	AACTTCAAGGTCCTGTCTAAGCTCGAAGGCAAGCTGAAGGACAACCTGAACCTGGAGAAG	3370 3361	Qy Db
3369 3360	CCTCTGAAGACTCTCTCCGAGGAGAGCATCCAGACCGAGGATAACTACGCCAGCCTCGAG	3310 3301	Qy Db
3309	ACCAAGATTCTTCTCAAACACTACAAAGGCCTCGTCAAGTATTATAATGGCGAGTCTTCT	3250 3241	Qy
3249 3240	GTGTTCTTCAACAAGAAGAAGGAAGCCGAGATCGCCGAGACAGAGAACACTCTGGAGAAC 	3190 3181	Qy Db
3189 3180	CAGCTTGAAAGCAAACTCAACTCACTGAACAATCCGAAACAGTACTGCAGAACTTCTCA	3130 3121	Оу
12	AAAAAGAAAACAGTTGGTAAATATAAAAATGCAAATTAAAAAACTTACTT	3061	Db

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KEYWORDS
SOURCE
ORGANISM
                                                                                                              REFERENCE
AUTHORS
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A04562
                                                            FEATURES
                                                                                                                                                                           VERSION
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P.falciparum P.195 g
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                                                                    Cloning of DNA for protozoal antigens Patent: EP 0154454-A 2 11-SEP-1985; THE WELLCOME FOUNDATION LIMITED
                                                                                                                              Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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Holder, A.A., Sandhu, J.S.,
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                  /organism="Plasmodium
/db_xref="taxon:5833"
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FEKMMSK RY SY KVEKLTHPNITEASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKY
YKNLISK I ENEL ETLVENI KKDEZQLEEK HILEVEKTYPEKYELEVY
YKNLISK I ENEL ETLVENI KKDEZQLEEK HILEVEKYEDEK I LEVSDIVKVQVQKVLL
MNK I DELKKYQLIKNUELKHHHIVPNSYKOENKOEPYLIVLKKEIDKLKVYMEDY
YKNLISK I ENEL ETLVENI KKDEZQLEEK I TROENKEDEK I LEVSDIVKVQVQKVLL
MNK I DELKKYQLIKNUELKHHHIVPNSYKOENKOEPYLIVLKKEIDKLKVYMEDK
SLINEEKKNI KTQGQSDN SEPSTEGE I TGQATTK PGQQAGSALEGBSVQAQAQEQKQA
QPVPVPVPEKAKQVETPPAPVNNKTENVSKLDYLEVLYSTIVLKKEIDKLKVYMEKYE
SLINEEKKNI KTQGQSDN SEPSTEGE I TGQATTK PGQQASALEGBSVQAQAQEQKQA
QPVPVPVPEKAKQVPTPPAPVNNKTENVSKLDY LEVLXYGILVSY I CHKY I LVSHST
MNEKTLKQY KITKEEBSKLSSCDPLDLLFNIQNNI PVNYSMEDDSLNI VYHNYLMVYEK
EI GYVET I LLMEI YEKEMVCNLY KLKDDKI KNILLEEAKKVSTSVFTLSSSSMQPLSLT
PQDR PEVSANDDTSHSTNLNNSLKLEFENI LSLCKNK KNIY GELIGQK SERFYEKILKD
SDTYNESTT NEVKSKADDI NSLINDESK RKILEEDE I NNLKKTLQLESPILV KYKLKLE
RLEDKKT LLKYN KGLLVKY NGGESSPLKTLSLSESI OTENVASILENFKYLSKLEGKL
KDULNLEKKILLKYN KGLLVKY NGGESSPLKTLSLSENST I TTSQNVDDEVDDV I TVLL FGE
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LFQKEKMYLNEGTSGTAVTTSTPGSKGSVASGGSVASGGSVASGGSVASGGSVAS
GGSGNSRRTNPSDNSSDSDAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDN
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KLYFGYRKPLDNIKDAVGKMEDY IKKNKKIT IENINELIESKKKITDKNKNATKEEEKK
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Best Local Similarity Matches 3587; Conserv 216 ATGAAGATCATATTCTTTTTATGTTCATTTCTTTTTTTTATTATAAATACACAATGTGTA GAGCTGAAGTACCCACAGTTGTTCGACCTCACTAATCATATGCTGACACTGTGTGATAAC TCTGTGGCCTCTGGGGGTTCCGTCGCCTCCGGCGGCAGCCGTGGCATCAGGTGGCTCAGTG GATGCTAAATCTTACGCTGATTTAAAACACAGAGTACGAAATTACTTGTTAACTATCAAA GACGCCAAGTCCTACGCCGACCTCAAGCACCGAGTGAGAAACTATCTCCTCACTATCAAG GCTTCAGGTGGTTCAGGTAATTCAAGACGTACAAATCCTTCAGATAATTCAAGTGATTCA GCAAGCGGCGGTTCCGGGAACAGTCGAAGAACCAATCCATCTGACAACTCTAGCGATTCC TCAGTTGCTTCAGGTGGCTCAGTTGCTTCAGGTGGCTCAGTTGCTTCAGGTGGCTCAGTT GAACTCAAATATCCTCAACTCTTTGATTTAACTAATCATATGTTAACTTTGTGTGATAAT Conservative 54.88; 72.18; 0; Score 2706.2; Pred. No. 0; Mismatches 1343; DВ 9 Indels 45; Length Gaps 489 429 575 369 309 455 395 189 275 69 515 249

1629	1570 GTGGAGAAACTGACACACATAATACCTTTGCATCCTATGAGAATTCTAAGCATAATCTT	Qy
1569 1775	1510 AACAATAACATCGACCTGACCAACTTCGAGAAAATGATGGGAAAACGGTACTCTTACAAA 	Qу
1509 1715	1450 CTAAACGATATCACTAAAGAGTATGAAAAGCTGCTGAACGAGATCTATGATTCCAAATTC 	Qy Db
1449 1655	1390 AAAATTGAGAAGAAGAAAATTGAGAGTGACAAGAAAAGTTACGAAGACCGCAGCAAAAGT	Оу
1389 1595	1330 AAGAATATCTACACAGACAATGAGAGAAAGAAGTTTATCAACGAAATCAAGGAGAAGATC 	Оу
1329 1535	1270 AACGAGCTCAATAGCTTCGGTGACTTGATTAACCCCTTCGATTATACGAAAGAACCCTCT	Qy
1269 1475	1210 AATGAATATCCCAATGGTGTGACGTACCCTCTGTCTTATAACGATATCAACAACGCTCTC	Qу
1209 1415	CTCCGCCAAAGTCGAGACAAAGGAATCAACCGAACCT 	Оу
1149 1355	1090 ATTAAGTTCAACATAGATTCTCTCTTTACTGATCCCCTTGAGCTGGAGTACTACTTGAGA 	Qy Db
1089 1295	030 CTGGACAAGAACAAGAAGATAGAGGAGGGCACGAGAAAGAGATCAAAGAGATCGCCAA 	Qу
1029 1235	970 AAGATTAATGAAATTAAGAATCCTCCGCCAGCCAACTCTGGGAACACCCCCTAACACGCTG	Qу
969 1175	10 GTACTGGAGAAGCGCATAGACACCC 	Db
909 1115	GCCCAGTACGACCTGTCCATCT	Дb
849 1055	0 AAGACCATAGACAAAATAAGAATGCAACCAAGGAGGAAGAAAAAAAA	Оу Дъ
789 995	730 TATATTAAAAAGAATAAGAAGACCATCGAGAACATTAACGAGCTGATCGAAGAATCCAAA	Db Qy
729 935	70 GTCTTCGGATATCGCAAGCCTCTCGACAACATCAAGGACAATGTGGGAA 	DЬ
669 875	610 TGTCAAATTCCATTCAATTTGAAGATCAGAGCCAACGAGTTGGACGTATTGAAGAAGTTG	Db Qy
609 815	550 TTGAATTTCTACTTCGACTTGCTAAGGGCCAAACTGAATGACGTTTGCGCCAATGACTAT	Db Qy
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Дb	7	TTGAGAAACTTACACACCCTAATACTTTTGCATCCTATGAAAATTCTAAACATAATCTT 183
Qy	Ġ	œ
DЬ	1836	AAAAGTTAACAAAAGCTCTTAAATATATGGAAGATTATTCTTTAAGGAATATAC
Qy	1690	GAGAAAGAACTAAAGTATTACAAGAATCTCATAAGTAAGATCGAAAACGAGATCGAGACG 1749
Ъ	1896	AAAAAGAATTAAAATTATAAAAAATTTAATAAGCAAAATAGAAAATGAGATTG
Ωу	0	TTAAGAAGATGAAGAACAGTTGTTTGAGAAGAAGATTACAAAAC
망	1956	TTAGTTGAAAATATTAAAAAAGATGAAGAACAGCTTTTTGAAAAAAAA
Qy	1810	AAAATAAACCAGATGAGAAGATCCTGGAGGTCTCCGATATTGTTAAAGTCCAAC
рь	2016	AAGTTC
Qy	1870	AAGGTGCTCCTCATGAACAAGATTGATGAACTCAAGAAGACTCAACTCATTCTGAAGAAC 1929
Db	2076	AAAGTTTTATTAATGAACAAAATTGACGAATTAAAAAAGACTCAATTGATTTTAAAAAAAT 2135
Qy	1930	GTGGAGTTAAAACATAATATACATGTGCCGAATAGTTATAAGCAGGAGAATAAGCAGGAA 1989
Db	2136	GTAGAATTAAAACATAATATACATGTTCCCAATTCTTACAAACAA
Qy	1990	ACTACCTCATCGTACTCAAGAAAGAGATAGACAAACTGAAAGTGTT
рь	196	CCTTATTATTTAATTGTGTTGAAAAAAGAAATTGATAAAATTAAAAGTGTTCATGCCTAAG 2255
Оу	2050	GTCGAGAGCCTGATCAACGAAGAAGAAGAAGAACATTAAAACTGAAAGGACAGTCAGATAAC 2109
D.	2256	GTAGAATCATTGATAAATGAAGAAAAAAAAAAACATAAAAAACACAAGGTCAATCGGATAAT 2315
. Qy	2110	TCCGAGCCTTCCACAGAAGGAGAGATAACCGGACAGGCTACCACCAAGCCCGGACAACAG 2169
Db	2316	AAGCAACTACAAAACCTGGACAAC
Qy	2170	GCCGGTTCAGCTCTCGAAGGCGATAGCGTGCAAGCTCAAGCACAAGAGCAGAAGCAGGCA 2229
Db	2376	AAAAACAAGC
Qy	2230	CAGCCTCCAGTGCCAGTGCCCGTTCCAGAGGCTAAAGCTCAAGTGCCTACACCACCAGCT 2289
DЬ	2436	CAACCACCAGTACCAGTACCAGAAGCAAAAGCACAAGTCCCAACACCACCAGCA 2495
Qy	2290	CCTGTGAATAACAAGACCGAAGAATGTCAGCAAACTGGACTACCTTGAGAAGCTCTATGAG 2349
Db	2496	AGTAAATAAAAACTGAAAATGTTTCCAAATTAGATTATCTTGAAAAATTATATAT
Qy	C)	TTCCTGAATACATCCTACATCTGCCACAATATATCCTCGTCTCTCACAGCACTATGAAC 2409
DЪ	5	TTTTAAATACTTCATATATATGTCACAAATATATTTTGGTTTCACACTCAACTATG
Qy	2410	GAGAAGATTCTTAAACAGTACAAGATAACCAAGGAAGAGGAGGAGGTAAACTGTCCTCTTGT 2469
Db	2616	AAAAGATATTAAAACAATATAAAATTACAAAGGAGGAAAAAGCAAATTAAGTTCATG
Qy	47	GATCCACTGGACCTGCTGTTCAATATCCAGAACAACATTCCCGTTATGTATTCTATGTTC 2529
Db	2676	ATCCATTAGACTTATTGTTTAATATACAAAATAACATACCTGTAATGTATTCTAT
Qy	30	GATAGCCTCAACAATTCT 2547
Db	736	NTAGTTTATCACAACTATTTATGGGTTTATGAAAAAGAAATTGGTTA
Qy	2548	TCTCTCAACT
Db	2796	TTTATATTACTTATGGAAATTTATGAAAAAGGAAATGGTTTGTAATTTATATAAAC
Qy	2608	AAAGACAACGACAAGATTAAGAACCTTCTGGAGGAAGCTAAGAAGGTCTCCACCTCTGTT 2667
7	2856	AGGATAATGACAAAATTAAAAATTTATTAGAGGAAGCGAAAAAAGTATCCACATO

3995	3688 ATTACCACATCTCAGAACGTCGACGATGAGGTCGATGACGTCATCTTCTGCCTATCTTC	Оу
3687	3628 CTGGAGCAGTCTCAACCTAAGAAGCCTGCATCTACTCATGTCGGAGCCGAGTCCAATACA	Db 04
. 3627 . 3875	3568 AAGTTCCTGCCTGAAGGAACAGATGTCGCCACTGTGGTGTCTGAATCTGGCTCCGACACA	Db Qy
3567	3508 ACCGGCAATAGCCCAAGCGAGAATAATACAGACGTGAATAACGCACTGGAATCTTACAAGII	Db Q
3507	3448 TCTAGCGGACTGCATCACCTGATCGCCGAGCTCAAGGAAGTCATTAAGAACAAGAACTAC 	ДУ
3447	3388 AAGCTCGAAGGCAAGCTGAAGGACAACCTGGACCTGGAGAAGAAGAAGCTCAGCTACCTC	Оу
3387 3635	3328 GAGGAGCATCCAGACCGAGGATAACTACGCCAGCCTCGAGAACTTCAAGGTCCTGTCT	Db Qy
3327	3268 CACTACAAAGGCCTCGTCAAGTATTATAATGGCGAGTCTTCTCCCTCTGAAGACTCTCTCCC	Qy Db
3267	3208 AAGGAAGCCGAGATCGCCGAGACAGAGAACACTCTGGAGAACACCAAGATTCTTCTCAAA 	Qу
3207	3148 AACTCACTGAACAATCCGAAACACGTACTGCAGAACTTCTCAGTGTTCTTCAACAAGAAG	Оγ
3147	3088 AAGTATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAGCTTGAAAGCAAACTC	Оу
3087 3335	3028 CTGTACAACAAGTACAAACTGAAACTGGAGAGAGACTCTTCGACAAGAAGAAGAAGACAGTCGGC	Оy
3027 3275	2968 CGTAAGAAGCTGGAAGAGGGACATCAATAAGCTGAAGAAGACACTGCAACTGAGCTTCGAC	Ωy
2967 3215	2908 TICACTAACTICGTGAAATCIAAAGCCGATGATATCAACTCTCTAACGAIGAATCIAAA	Qу
2907 3155	2848 TCGTCCGAGAACTTCTACGAGAAGATACTGAAAGACAGCGACACATTCTATAACGAGAGC	ОУ
2847 3095	2788 GAGAACATCCTGTCTCTCCGCAAGAATAAGAACATCTACCAAGAACTTATTGGACAGAAAA	Дb
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WELLCOME FOUND LTD:THE
OS PLASMODIUM falciparum
PN JP 1986019490-A/1
PD 28-JAN-1986
PF 22-FEB-1984 GB 84 8404692, 26-SEP-1984 GB 84 8424340 PI
ANSONII AASAA HORUDAA, MAIKURU JIEEMUSU MORENO, PI KARERU
GERITSUTO ODEINKU
PC C12N15/00,A61K39/015,C07H21/04,C07K13/00,C12N1/20,C12P21/02,
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                                                   AACGAGCTCAATAGCTTCGGTGACTTGATTAACCCCTTCGATTATACGAAAGGAACCCTCT
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	2469	2410 GAGAAGATTCTTAAACAGTACAAGATAACCAAGGAAGAGGAGAGAGTAAACTGTCCTCTTGT	Qy
	2409	2350 TTCCTGAATACATCCTACATCTGCCACAAATATATCCTCGTCTCACAGCACTATGAAC	Дb
	55	496 CCAGTAAATAAAACTGAAAATGTTTCCAAATTAGATTATCTTGAAAAATTAT	Db
:	2349	CTGTGAATAACAAGACCGAGAATGTCAGCAAACTGGACTACCTTC	Qy
	49	436 CAACC	р 8
	<u>ر</u> و	230 САСССТСО ВСТСОСТВО ВСТСОССТВО ВСЕТВО ВСЕТВВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВО ВСЕТВВО ВСЕТВО	Q V
	2229	2170 GCCGGTTCAGCTCTCGAAGGCGATAGCGTGCAAGCTCAAGCACAAGAGCAGAAGCAGGCAG	Qy
	37	TCGGAACCATCAACCGAAGGAGAAATAACAGGACAAGCAACTACAAAAACCTG	B S
	9	110 TCCGAGCCTTCCACAGAAGGAGAGATAACCGGGACAGGCTACCACCAAGCCCGGACAAC	0γ
	2315	ZUSU GTCGAGGCCTGATCAACGAAGAAGAACAACAATAAAACTGAAGGACAGTCAGATAAC 	D 09
	25	196 CCTTATTATTTAATTGTGTTGAAAAAAGAAATTGATAAATTAAAAGTGTTCATGCCT	рь
	2049	100	Qy
	2195	AATTAAAACATAATATACATGTTCCCAATTCTTACAAACAA	Db
	1989	TGGAGTTAAAACATAATATACATGTGCCGAATAGTTATAAGCAGGAGAATAAGCAG	Qy
	13	076 AAAGTTTTATTAATGAACAAATTGACGAATTAAAAAAGACTCAATTGATTTAAAAA	Db .
	92	870 AAGGTGCTCCTCATGAACAAGATTGATGAACTCAAGAAGACTCAACTCATTCTGA	Qy
	07	016 GAAAATAAACCAGATGAAAAAATTTTAGAAGTATCTGACATTGTAAAAGTACAAGTTC	B 4
	8	810 GAAAATAAACCAGATGAGAAGATCCTGGAGGTCTCCGATATTGTTAAAGTCCAAGTGC	0γ
	2015	1/50 CTTGATGAACATTAAGAAGGATGAAGGACAGTTTTGAGAAGAAGATTACAAAGAGCTTTTTGAGAAGAAGATTACAAAGAGCATGAAGAACAGCTTTTTTGAAAAAAAA	B 4
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	1749 1955	1690 GAGAAAGAACTAAAGTATTACAAGAATCTCATAAGTAAGATCGAAAACGAGATCGAGACG	D Q
	1895	1836 GAAAAGTTAACAAAAGCTCTTAAATATATGGAAGATTATTCTTTAAGGAATATAGTAGTT	рb
	1689	AGAAGCTCACCAAAGCTCTTAAGTATATGGAGGACTATTCTCTGCGGAACATTGTT	Qy
	1629 1835	1570 GTGGAGAAACTGACACCATAATACCTTTGCATCCTATGAGAATTCTAAGCATAATCTT	Db Qy
	77	716 AATAATAATATAGATTTAACTAATTTCGAAAAAATGATGGGTAAAAGATATTCATATA	B
	56	510 AACAATAACATCGACCTGACCAACTTCGAGAAAATGATGGGAAAACGGTACTCTTACAA	Qy
	1509 1715	1450 CTAAACGATATCACTAAAGAGTATGAAAAGCTGCTGAACGAGATCTATGATTCCAAATTC 	Db Qy
	5	596 AAAATAGAAAAAAAAAATTGAATCTGATAAAAAATCTTACGAAGACAGATCTAAGT	В
	4 4	390 AAAATTGAGAAGAAGAAATTGAGAGTGACAAGAAAAGTTACGAAGACCGCAGCAAAAG	2 2
	1595		Db

3448 TCTAGCGGACTGCATCACCTGATCGCCGAGCTCAAGGAAGTCATTAAGAACAAGAACTAC 3507 	Qу
3388 AAGCTCGAAGGCAAGCTGAAGGACAACCTGAACCTGGAGAAGAAGAAGAAGCTCAGCTACCTC 3447 	ФФ
328 GAGGAGCATCCAG <i>I</i> 576 GAAGAATCAATTCAA <i>I</i>	Oy Oy
268 CACTACAAAGGCCTCGTCAAGTATTATAATGGCGAGTCTTCTCCTCTGA	Фр
3208 AAGGAAGCCGAGATCGCCGAGAGACAGAGAACACTCTGGAGAACACCCAAGATTCTTCTCAAA 3267 	Qy Db
148 AACTCACTGAACAATCCGAAACACGTACTGCAGAACTTCTCAGTGTTCT	Qу
3088 AAGTATAAGATGCAGATCAÁGAAGTTGACTCTGCTCAAGGAGCAGCTTGAAAGCAAACTC 3147	Qy
3028 CTGTACAACAAGTACAAACTGAAACTGGAGAGACTCTTCGACAAGAAGAAGAAGACAGTCGGC 3087	Qy Db
968 CGTAAGAAGCTGGAAGAGGACATCAATAAGCT 	Qу
2908 TTCACTAACTTCGTGAAATCTAAAGCCGATGATATCAACTCTCTTAACGATGAATCTAAA 2967	Qy
2848 TCGTCCGAGAACTTCTACGAGAAGATACTGAAAGACAGCGACACATTCTATAACGAGAGC 2907	Qy
AA 30	ДЬ
TTT 278	Qy Db
2668 AAAACTCTCTCTTCCAGCTCCATGCAACCACTGTCTCTCACACCTCAAGACAAGCCCGAA 2727 	pb .p
2608 AAAGACAACGACAAGATTAAGAACCTTCTGGAGGAAGCTAAGAAGGTCTCCACCTCTGTT 2667 	Оу
2548 CTCTCTCAACTGTTCATGGAGATATATGAGAAGGAGATGGTCTGCAACCTGTATAAACTC 2607	Qy Db
2530 GATAGCCTCAACA	Qу
SACCTGCTGTTC	Qy
616 GAAAAGATATTAAAACAAT ATAAAATTACAAAGGAGGAAGAAAGCAAATTAAGTTCATGT 26	Db

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Pan,W., Tolle,R. and Bujard,H.
A direct and rapid sequencing strategy
falciparum antigen gene gp190/MSA1
Mol. Biochem. Parasitol. 73 (1-2), 241-
                                                                                                                                                                                                                                                                                                                                                             Mackay, M., Goman, M., Bone, N., Hyde, J.E., Scaife, J., Certa, U., Stunnenberg, H. and Bujard, H. Polymorphism of the precursor for the major surface antigens plasmodium falciparum merozoites: studies at the genetic leve EMBO J. 4 (13B), 3823-3829 (1985)
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                                                                                /dev_stage="blood
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GAACTCAAATATCCTCAACTCTTTGATTTAACTAATCATATGTTAACTTTGTGTGATAAT
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                                                                                                                                                                                                            GACGCCAAGTCCTACGCCGACCTCAAGCACCGAGTGAGAAACTATCTCCTCACTATCAAG
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NEIETIVENITKHDEBOLFEKKITKDENKEDEKILEVSDIVKVOVOKVLLANKIDEKIK

NEIETIVENITKHDEBOLFEKKITKDENKEDEKILEVSDIVKVOVOKVLLANKIDELKK

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EYPNGVTYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKEK
IKIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKRY
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SIYNKQLEEAHNLI SVLEKRI DTLKKNEN I KELLDKI NEI KNPPPANSGNTPNTLLDK
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 AATAATAATATAGATTTAACTAATTTCGAAAAAATGATGGGTAAAAGATATTCATATAAA
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                                          TTAAATGATATAACAAAAGAATATGAAAAATTACTTAATGAAATTTATGATAGCAAATTC
                                                    CTAAACGATATCACTAAAGAGTATGAAAAGCTGCTGAACGAGATCTATGATTCCAAATTC
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2709	2650 AAGGTCTCCACCTCTGTTAAAACTCTCTCTTCCAGCTCCATGCAACCACTGTCTCTCACA	οy
2684	2625 TGTAATTTATATAAACTTAAGGATAATGACAAAATTAAAAATTTATTAGAGGAAGCGAAA	Db
2649	AAGCTAAG	Qy
2624	2565 GATAGCTTAAACAATAGTTTATCACAACTATTTATGGAAATTTTATGAAAAAGAAATGGTT	DЬ
2589		Qy
2529 2564	2470 GATCCACTGGACCTGCTGTTCAATATCCAGAACAACATTCCCGTTATGTATTCTATGTTC:	Db Qy
	445 GAAAAGATATTAAAACAATATAAAATTACAAAGGAAGAAAGCAAATTAAGTTCATGT	5
4	410 GAGAAGATTCTTAAACAGTACAAGATAACCAAGGAAGAGGAGGAGTAAACTGTCCTCTTGT	y Oy
2444		Db
2409	2350 TTCCTGAATACATCCTACATCTGCCACAAATATATCCTCGTCTCTCACAGCACTATGAAC	Qy
2349 2384	2290 CCTGTGAATAACAAGACCGAGAATGTCAGCAAACTGGACTACCTTGAGAAGCTCTATGAG :	pb 64
2324	265 CAACCACCAGTACCAGTACCAGTACCAGAAGCAAAAGCACAAGTCCCAACACCACCAGCA	В
2289	230 CAGCCTCCAGTGCCAGTGCCCGTTCCAGAGGCTAAAGCTCAAGTGCCTACACCCACC	Qy
2264	O GCCGGTTCAGCTCTCGAAGGCGATAGCGTGCAAGCTCAAGCACAAGAGCAGAAGCAGGCA	물 성
2 0	143 ICUGARACCAICAACUGAGAGAAATAACAGGACAAGCAACTACAAAACCTIGGACAACAA	2
2169	2110 TCCGAGCCTTCCACAGAAGGAGAAGATAACCGGACAGGCTACCACCACCAGCCCGGACAACAG	P 09
2144		당 .
2109		Qy
2049 2084	1990 CCATACCTCATCGTACTCAAGAAAGAGATAGACAAACTGAAAGTGTTCATGCCCAAA :	Ф
2024	965 GTAGAATTAAAACATAATATACATGTTCCCAATTCTTACAAACAA	Db
1989	1930 GTGGAGTTAAAACATAATATACATGTGCCGAATAGTTATAAGCAGGAGAATAAGCAGGAA	Qy
96		Db
٥	870 AAGGTGCTCCTCATGAACAAGATTGATGAACTCAAGAAGACTCAACTCATTCTGAAGAAC	ΟV
1869 1904	1810 GAAAATAAACCAGATGAGAGAGCTCTGGAGGTCTCCGATATTGTTAAAGTCCAAGTGCAG	ру
84	785 TTAGTTGAAAATATTAAAAAAGATGAAGAACAGCTTTTTGAAAAAAAA	ď
1809	750 CTTGTTGAGAACATTAAGAAGGATGAAGAACAGTTGTTTGAGAAGAAGATTACAAAAGAC	Оу
1784	1725 GAAAAAGAATTAAAAATATTATAAAAAATTTAATAAGCAAAATAGAAAATGAGATTGAAACA	DЬ
1749	G	Qy
1689 1724	1630 GAGAAGCTCACAAAGCTCTTAAGTATATGGAGGACTATTCTCTGCGGAACATTGTTGTG :	Db Qy
1664	605 GTTGAGAAACTTACACACCATAATACTTTTGCATCCTATGAAAATTCTAAACATAATCTT	Db
1629	1570 GTGGAGAAACTGACACACCATAATACCTTTGCATCCTATGAGAATTCTAAGCATAATCTT	Qy

3789	ATCATTGTGCCTATCTTCGGCGAGAGGGGGGGGGGGGGG	3730	Qy
3729 A 3764	GGAGCCGAGTCCAATACAATTACCACATCTCAGAACGTCGACGATGAGGTCGATGACGTC	3670 3705	Фу
3669 3704	GAATCTGGCTCCGACACACTGGAGCAGTCTCAACCTAAGAAGCCTGCATCTACTCATGTC	3610 3645	Ωy
r 3609 r 3644	GCACTGGAATCTTACAAGAAGTTCCTGCCTGAAGGAACAGATGTCGCCACTGTGGTGTCT	3550 3585	Qy Db
F 3584	- ATTAGAACAAGAACTACACCGGCAATAGCCCAAGCGAGATTAATACAGACGTGAATAAC 	3525	ДУ
 		. 4	Db Qy
		3405	Db Qy
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T 3309	ACCAAGATTCTTCTCAAACACTACAAAGGCCTCGTCAAGTATTATAATGGCGAGTCTTCT	3250 3285	Qy db
3249		3190 3225	Qу Дъ
A 3189 F 3224	CAGCTTGAAAGCAAACTCAACTGACTGAACAATCCGAAACACGTACTGCAGAACTTCTCA	3130 3165	Qy Db
3 3129 A 3164	AAGAAGAAGACAGTCGGCAAGTATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAG 	3070 3105	Оу
C 3069	CTGCAACTGAGCTTCGACCTGTACAACAAGTACAAACTGGAAACTGGAGAGACTCTTCGAC 	3010 3045	Qy Db
A 3009	CTTAACGATGAATCTAAACGTAAGAAGCTGGAAGAAGACATCAATAAGCTGAAGAAGAACACA CTTAACGATGAATCAATAAGCTAAGAAGAAGACA	2950 2985	Qу
r 2949 A 2984	ACATTCTATAACGAGAGCTTCACTAACTTCGTGAAATCTAAAGCCGATGATATCAACTCT	2890 2925	ОУ
C 2889 F 2924	GAACTTATTGGACAGAAATCGTCCGAGAACTTCTACGAGAGATACTGAAAGACAGCGAC 	2830 2865	Qy Db
A 2829 I A 2864	AACTCACTGAAACTGTTTGAGAACATCCTGTCTCTCGGCAAGAATAAGAACATCTACCAA	2770 2805	Qу
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TGTGAATGTACTAAACCTGATTCTTATCCACTTTTCGATGGTATTTTCTGCAGTTCCTCT
                                                                         CAAGAAGGAGATAAGTGCGTGGAGAACCCAAACCCTACCTGCAATGAAAACAATGGCGGG
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                              TGCGAGTGTACTAAGCCCGACTCCTATCCACTCTTCGACGGGATTTTTTTGCTCCAGCTCT
                                                                                                                                                                              TCTGGATGTTTCAGACATTTAGATGAAAGAGAAGAATGTAAATGTTTATTAAATTACAAA
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971 042	.911	851 922	1791 1865	.731	.671 .745	.611	.625	1491 1565	1431 1505	1371 1445	1311 1385	1260 1325	1200 1265	1149 1205	1089 1145	1029 1085	969 1025	965

2958 3119	2899 AACGAGAGCTTCACTAACTTCGTGAAATCTAAAGCCGATGATATCAACTCTCTTTAACGAT	Оy
2898 3062	2839 GGACAGAAATCGTCCGAGAACTTCTACGAGAGATACTGAAAGACAGCGACACATTCTAT 	ОУ
2838 3002	2782 CTGTTTGAGAACATCCTGTCTCTCGGCAAGAATAAGAACATCTACCAAGAACTTATT	ОУ
2781 2942	2722 CCCGAAGTGAGCGCTAACGACGACGACCTCCACTCGACCAACCTTAATAACTCACTGAAA	gb Qy
2721 2882	2688 CATGCAACCACTGTCTCACACCTCAAGACAAG	ОУ
2687 2822	2658CACCTCTGTTAAAACTCTCTCTTCCAGCTC	DP QA
2657 2762	ACCTTCTG	Db Qy
2616 2702	2557 CTGTTCATGGAGATATATGAGAAGGAGATGGTCTGCAACCTGTATAAACTCAAAGACAC 	ОУ
2556 2642	2497 CAGAACAACATTCCCGTTATGTATTCTATGTTCGATAGCCTCAACAATTCTCTCTC	Db Qy
2496 2582	2437 ACCAAGGAAGAGGAGAGTAAACTGTCCTTTGTGATCCACTGGACCTGCTGTTCAATATC	Оy
2436 2522	2377 AAATATATCCTCGTCTCTCACAGCACTATGAACGAGAAGATTCTTAAACAGTACAAGATA	Дy
2376 2462	2317 AGCAAACTGGACTACCTTGAGAAAGCTCTATGAGTTCCTGAATACATCCTACATCTGCCAC	D 24
2316 2402	2257 GAGGCTAAAGCTCAAGTGCCTACACCACCAGCTCCTGTGAATAACAAGACCGAGAATGTC	Дb
2256 2342	2206 CAAGCACAAGAGCAGAAGCAGGCACAGCCTCCAGTGCCAGTGCCCGTTCCA	Db Qy
2205 2282	2146 GCTACCACCAAGCCCGGACAACAGGCCGGTTCAGCTCTCGAAGGCGATAGCGTGCAAGCT	ОУ
2145 2222	2092 GAAGGACAGTCAGATAACTCCGAGCCTTCCACAGAAGGAGAGATAACCGGACAG	Дy
2091 2162	2032 AAAGTGTTCATGCCCAAAGTCGAGAGGCCTGATCAACGAAGAAGAAGAACATTAAAACT	Фр
2031 2102	1972 CAGGAGAATAAGCAGGAACCATACTACCTCATCGTACTCAAGAAAGA	Db Qy

δÃ Вp δÃ B Qγ DЪ δÃ Ъ νQ Ър Q B Qy Db ρ 밁 δÃ B Qy 밁 Q В Ωy В Qy Ъ Ωy ₽ Qy В ,Q Вb Q DЬ Qy Вþ ğ 4017 3648 3480 3319 3360 3840 3597 3660 3600 3540 3079 3019 GAATCTAAACGTAAGAAGCTGGAAGAGAGACATCAATAAGCTGAAGAAGAAGACACTGCAACTG AGCGACTTGATTCCCTATAAAGACCTGACCTCCTCTAACTACGTTGTCAAGGACCCATAC GTGAAGGACATTCTGAACAGCCGCTTTAATAAGAGAGAAAATTTCAAGAACGTCTTGGAG GGAGTATATAGAAGCTTAAAAAAAACAAATTGAAAAAAACATTATTACATTTAATTTAAAT GGCGTCTATAGGTCTCTCAAGAAACAGCTGGAGAATAACGTGATGACCTTCAATGTCAAC GAGGACTACGATGACCTCGGCCAGGTGGTCACCGGTGAGGCTGTCACTCCTTCCGTGATT CAAAATTATGACGAAGAAGATGATTCCTTAGTTGTATTACCCATTTTTGGAGAATCCGAA CAGAACGTCGACGATGAGGTCGATGACGTCATTGTGCCTATCTTCGGCGAGAGCGAG GAAACACAAATACCAACTTCAGGCTCTTTATTAACAGAATTACAACAAGTAGTACAATCA GATGTAACTCCATCTCCATTATCTGTAAGGGTAAGTGGTAGTTCAGGATCCACAAAAGAA TCTTACAAGAAGTTCCTGCCTGAAGGAACAGATGTCGC------AAGAACTACACCGGCAATAGCCCAAGCGAGAATAATACAGACGTGAATAACGCACTGGAA GTCCTGTCTAAGCTCGAAGGCAAGCTGAAGCAGACCTGGAGAAGAAGAAGAAGCTC CTTCTCAAACACTACAAAGGCCTCGTCAAGTATTATAATGGCGAGTCTTCTCCTCTGAAG AACAAGAAGAAGGAAGCCGAGATCGCCGAGACAGAGAACACTCTGGAGAACACCCAAGATT GAACTTGGCCAAGACAAA,TGCAAATTAAAAAACTTACTTTATTAAAAGAACAATTAGAA TTGAACGATATCTTAAATTCACGTCTTAAGAAACGAAAATATTTCTTAGATGTATTAGAA GATAATGACGAATATTTAGATCAAGTAGTAACTGGAGAAGCAATATCTGTCACAATG--------CACTGTGGTGTCTGAATCTGGCTCCGACACACTGGAGCAGTCTCAACCTAA TCTTACGAAAATTTTCTCCCAGAAGCAAAAGTTACAACAGTTGTAACTCCACCTCAACCA AGCTACCTCTAGCGGACTGCATCACCTGATCGCCGAGCTCAAGGAAGTCATTAAGAAC TCAAAATTGAATTCACTTAATAACCCACATAATGTATTACAAAACTTTTCTGTTTTCTTT AGCAAACTCAACTCACTGAACAATCCGAAACACGTACTGCAGAACTTCTCAGTGTTCTTC ACAGTCGGCAAGTATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAGCTTGAA AAAAATTATACAGGTAATTCTCCCAAGTGAAAATAATAAGAAAGTTAACGAAGCTTTAAAA TCTTTCTTATCAAGTGGATTACATCATTTAATTACTGAATTAAAAGAAGTAATAAAAAAT AACAAAAAAAAAGAAGCTGAAATAGCAGAAACTGAAAACACATTAGAAAAACACAAAAAATA ---GCCTGCATCTACTCATGTCGGAGCCGAGTCCAATACAATTACCACATCT 4059 4196 3539 3239 4076 4016 3819 3959 3899 3839 3647 3779 3558 3659 3498 3599 3378 3479 3419 3359 3299 3138 3179 3879 3699 3596 3198 3078 3018 3438

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LIDGYEEINELLYKLMFYYDLLRAKLMDACANSYCO.FFNLKTARNELDVLKKIVFGY
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KSVQIPKVPYPNGIVYPLPLTDIHNSLAADNDKNSYGDLAMVPDTKEKINEKIITDNKE
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/chromosome="9"
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/strain="HN1"
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CH-4002, Switzerland
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of Plasmodium falciparum
                    DB 3;
                    Length 5243;
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LOCUS DEFINITION

AF062348 5243 bp DNA Plasmodium falciparum strain HN1 merozoite precursor (msp1) gene, complete cds.

surface linear

protein

INV 09-FEB-2001

Query Match 26. Best Local Similarity 56. Matches 2919; Conservative

0;

Mismatches

1978;

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17;

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CACGAAGAAAAAATAAAAGAAATTGCC 11	8 CTCCCTGAGAATAAGAAAAAAAGAAGTCGAGGGACACGAA	06
CACGAGAAAGAGATCAAAGAGATCGCC 10	CTGCTGGACAAGAACAAGAAGATAGAGGAGCACGAC	Ñ
AGCCAACTCTGGGAACACCCCTAACACG 1026 	0 AAGATTAATGAAATTAAGAATCCTCCGCCAGCCAAC 	0 7
TGAAAATATCAA <i>I</i> TGAAAACATAAAC	0 GTACTGGAGAAGCGCATAGACACCCTCAAGAAGAATGA 	<u> </u>
GCTTGAAGAAGCCCATAACCTCATCAGC 909 	0 GCCCAGTACGACCTGTCCATCTATAACAACAGCTTG	88
GGAGGAAGAAAGAAGATTGTACCAG 849 	0 AAGACCATAGACAAAAATAAGAATGCAACCAAGGAGGAG 	79 82
CATTAACGAGCTGATCGAAGAATCCAAA 789 	0 TATATTAAAAAGAATAAGAAGACCATCGAGAACATTAAC 	73 76
CAAGGACAATGTGGGAAAGATGGAAGAT 729 	0 GTCTTCGGATATCGCAAGCCTCTCGACAACATCAAGGAC 	0
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GAAGAGATCAATGAACTCCTGT 	0 ATTCATGGCTTCAAATATCTGATTGACGGTTACGAAGAG 	49 52
IAATCATATGCTGACACTGTGTGATAAC 4 A	0 GAGCTGAAGTACCCACAGTTGTTCGACCTCACTAATCAT 	σ ω
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C		AAAACTGAAGGAC	GAAAG AAAAG	ACCAC	GCAGG	TCAAC	ALIGIAN	TTGTTA	AAAAA	GAAGA	CGAAG	CGAAA	TTTAA	TCTGC	TAATT	GAATT	TGCAA	AAAAC	ATTTT	GATCT	TAAAA	AGTTACGAAG	TAACA	CGAAA	GATACTAAAG	TTATA	ATTCATAATTC	CAA	AAATACC	AACCG	AGAAA	AGAGA	TATTA
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AGGCCGG	TTGCA	rccgA	GTCGA	CCATA	CATA	GTGGA	nang i	AAGGT	ACACA	GAAAA'	TTAAC.	CTTGT	GAAAA	GAGAA.	CAAAA	ATAATCTTGAGAAGCTC	STTGA	GTGGA	AATAA	AACAA	TATGA	CTAAA	GATTTAG	AAAT	AAAAT	AAGAA	AATGA	AACGA	CCAAA	CCCAA	GATGT	ACATO	AGTTT.
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CTCTC	CGAAA	CACA	IGATC	TAATT	TCATC	AACAT 	18811	TCATG	CAAAT	CAGAT	AAATA	ACATT	TTAAT	TAAAG	AAAAG	CCAAA	AAAGATATAATAAT	rgaca	TTGAC.	rcgac	CAAAAAAGG	CACT.	AAAAAAAC	AGAAG	CAGAT	ACACA	ATTCA	ATAGC	TTGTA	rgacg	TAAA	CAAA	TGAT
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CGATA	GAAGA	AGAGATAACCGG	AGAGA AAAGA	AAAAA	CAAGA	ACATG CATG		GATTG	TTCCT	GATCC	TAGTG	GGATG	TTATA	CAAGA	TTCAT	TAAGT	TAATA	TAATA	TGTCG	CAACT	ATTATGAAGAATTAC	GTATG	ATTAATCAC	TGAGA	GGAAA	TGAGA	TGATT	TGACT	TTTAC	TCTGT	AGATC		TGAAT
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Qy Qy 밁 Qy 밁 Qy Ъ Qγ Ъ QΥ Ъ δÃ Вþ Qy Dр δÃ B Qγ DЪ Qy Ъ Qy В Qy Ъ δÃ В Ωy В οy дδ 밁 δÃ Вþ DЪ Qy 4116 4056 3939 3819 3759 3519 3459 3399 3996 3829 3769 3597 3699 3568 3639 3579 3448 3879 3508 3208 AAGTCTGACCTTGACTCTATTAAAAAGTATATCAACGATAAG------ATTCTGAACAGCCGCTTTAATAAGAGAGAAAATTTCAAGAACGTCTTGGAGAGCGACTTG 4008 CTGTCCAAAATCGAGAACGAATACGAAGTGCTCTATCTGAAACCTCTGGCAGGCGTCTAT GACGAAGAAGATGATTCCTTAGTTGTATTACCCATTTTTGGAGAATCCGAAGATAATGAC --GCCTGCATCTACTCATGTCGGAGCCGAGTCCAATACAATTACCACATCTCAGAACGTC TCAAGTGGATTACATCATTTAATTACTGAATTAAAAGTAATAAAAAATTAAT TCTAGCGGACTGCATCACCTGATCGCCGAGCTCAAGGAAGTATTAAGAACAAGAACTAC CATTATAAAGGACTTGTTAAATATTATAATGGTGAATCATCTCCATTAAAAAACTTTAAGT CACTACAAAGGCCTCGTCAAGTATTATAATGGCGAGTCTTCTCCCTCTGAAGACTCTCTCCC AAGGATGATTTAGAATCAATTAAAAAAGTTATCAAAGAAGAAAAGGAGTTCCCATCATCA AATGATATTAAATTTGCACAGGAAGGTATAAGTTATTATGAAAAGGTTTTAGCGAAATAT ACCGATATCAATTTCGCTAATGATGTGCTGGGGTATTACAAGATCCTGAGCGAAAAATAC ATTCCCTATAAAGACCTGACCTCCTAACTACGTTGTCAAGGACCCATACAAGTTCCTC CTCTCAGGATTTGAAAATGAATATGATGTTATATATTTAAAAACCTTTAGCTGGAGTATAT GAATATTTAGATCAAGTAACTGGAGAAGC---AATATCTGTCACAATGGATAATATC GACGATGAGGTCGATGACGTCATCATTGTGCCTATCTTCGGCGAGGAGCGAGGAGGACTAC ATACCAACTTCAGGCTCTTTATTAACAGAATTACAACAAGTAGTACAATCACAAAATTAT CCATCTCCATTATCTGTAAGGGTAAGTGGTAGTTCAGGATCCACAAAAGAAGAAACACAA CACTGTGGTGTCTGAATCTGGCTCCGACACACTGGAGCAGTCTCAACCTAAGAA-----AATTTTCTCCCAGAAGCAAAAGTTACAACAGTTGTAACTCCACCTCAACCAGATGTAACT AAGCTCGAAGGCAAGCTGAAGGACAACCTGAACCTGGAGAAGAAGAAGCTCAGCTACCTC 4128 4068 4175 4115 3948 4055 3888 3995 3828 3938 3768 3878 3818 3650 3758 3698 3567 3638 3507 3578 3518 4415

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Shan, Z.X., Yu, X.B., Li, X.R., Ma, C.L. and Fang, J.M.
Molecular cloning and sequence analysis of major merozoite;
Molecular cloning and sequence analysis of major merozoite;
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Dp QA

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TCTGTGGCCTCTGGGGGTTCCGTCGCCTCCGGCGGCAGCGTGGCATCAGGTGGCTCAGTG

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GCTGTTACAACTAGTACACCTGGTTCAGGTGGTTCAGTTACTTCAGGTGGTTCAGGTGGT
                              GCCGTTACAACCAGCACACCCGGTTCTAAAGGGTCTGTGGCTAGCGGTGGCTCCGGTGGG
                                                                                                          ACAGGTTATAGTTTATTTCAAAAAGGAAAAAATGGTATTAAATGAAGGAACAAGTGGAACA
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                                                                                                                                                            University of Medical Sciences,
Guangdong 510089, P.R.China
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YNLFIY NKOLOEAHNLI SYLEKRIDTILKKNENI KELLEDIDK IKTDAEKLTTGSKRNP
LPENKKEVEGHEEK I KEIAKTIK FNIDSLETDPLELETYLEKKKEVDYTPKSODPT
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KSOLIKYPYPKOJ TVY PLPLDDI HNSLAADNDKNSYGDLMNPDTYEKI IREKI ITONKE
RKI FINNÍKKJEDLEKNINHTKEONKKLLEDYEKSKNDYEELLEKYYEMKFUNNEDK
DVYDKI FSARYTYNVEKOKY NNKFSSSNNSYNOKOKALSYLEDYSLEKGI SEKDF
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LIKKIEDLEKI ELLKNAQLKDS I HVPNI J KPONKPEPYL I VLKKEVDKLKEFI PKV
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EALKSYENFLDEAKVTTYVTPPQDDVTPSPLSVRVSGSSGSTEEDTQIPTSGSLLTEL
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NEYIIEDSFKLLNSEQKNTLLKSYKYIKESVENDIKFAQEGISYYEKVLAKYKDDLES
IKKVIKEEKEFPSSPPTTPPSPAKTDEQKKESKFLPFLTNIETLYNNLVNKIDDYLIN
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LIDGYEE_NELLYKLNFYYDLLRAKLNDACANSYCQIPFNLKIRANELDVLKKIVFGY
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/isolate="FCC1/HN"
/db_xref="taxon:5833"
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1365 1362	TTCGATTATACGAAAGAACCCTCTAAGAATATCTACACAGACAATGAGAGAAAGAA	30 30	_ ~
1305 1302	CGCTCTCAACGAGCTCAATAGCTTCGGTGACTTGATTAACCCC	1255	~
1254 1242	GAACCTAATGAATATCCCAATGGTGTGACGTACCCTCTGTCTTATAACGAT	19 18	~ ~
1194 1182	ACAAAG AAATCT	14 12	_ ~
1143 1122	TTCTCTCTTTACTGATCCCCTTGAGCTGGGTACTAC	1084	~
1083 1062	AAGAACAAGAAGATAGAGGAGGACACGAGAAAGAGATCAAAGAGATCGCC	1027	_ ~
1026 1002	AAGATTAATGAAATTAAGAATCCTCCGCCAGCCAACTCTGGGAACACCCCTAACACG	970	~
969 942	GAAAATATCAAAGAACTGCTCGAC GAAAACATAAAGAAATTACTTGAA	910	
909 882	AACAAACAGCTTGAAGAAGCCCATAACCTCATCAGC	850	
849 822	AAGAAGTTGTACCAG AAAAAATTATACCAA	790	
789 762	ATCGAAGAATCCAAA TGAAGGAAGTAAG	730	-
729 702	AGATGGAAGAT AATGGAAGAT	670	~
669 642	TGTCAAATTCCATTCAATTTGAAGATCAGAGCCAACGAGTTGGACGTATTGAAGAAGTTG	583	~
609 582	AATGACTAT ATAGTTAT	550	~
549 522	CCTGTACAAG ATTATATAAA	463	~
489 462	CCACAGTTGTTCGACCTCACTAATCATATGCTGACACTGTGTGTG	430	~
429 402	GACGCCAAGTCCTACGCCGACCTCAAGCACCGAGTGAGAAACTATCTCCTCACTATCAAG	370	
369 342	GCAAGCGGCGGTTCCGGGAACAGTCGAAGAACCAATCCATCTGACAACTCTAGCGATTCC	310 283	

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NAMARIGANITAANATCATGTGATCCAGTTAGATITATTATTATATTCCATCCAACTGTCAACTGTTCATIC

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4650	4591 AACACTAACGACTTCGAAGCAATTAAAAAATTGATAAATGATGATGATAACGAAAAAAGATATG	Db
4491	AGACCTGTCTACCGATTATAACCACAACAATCTC	Qy
4590		뮹
43	372 GTTAAAATCAAGGAGCTGAACTACCTCAAAACAATCCAAGACAAGCTGGCAGATTTCAAG	0 5
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4470		Db
4311	4252 CTGCCCTTCCTGAATAACATCGAACCCTGTACAAGACAGTGAACGACAAAATCGACCTC	Qy
4410	4351 CCACCAACAACACCTCCGTCACCAGCAAAAACAGACGAACAAAAGAAGGAAAGTAAGT	ДЪ
4251	GGCGAGAATGAAAAATAT	Qy
4350	4291 AAGGATGATTTAGAATCAATTAAAAAAGTTATCAAAGAAGAAAAGGAGTTCCCATCATCA	DЬ
4230	ACCTTGACTCTATTAAAAAGTATATCAACGATAAG	Qy
4290	4231 AATGATATTAAATTTGCACAGGAAGGTATAAGTTATTATGAAAAGGTTTTAGCGAAATAT	망
4188		Qy
4230	4171 AATTCAGAACAAAAAAAACACACTTTTAAAAAAGTTACAAATATATAAAAAGAATCAGTAGAA	Db
4128		Qy
4170	ATTTAAATTATTG	Db
4068	TTCCCTATAAAGACCTGACCTCCTCTAACTACGTTGTCAAGGACCCATACAAGTTCCTC	Qy
4110	4051 ATCTTAAATTCACGTCTTAGAGAAACGAAAATATTTCTTAGATGTATTAGAATCTGATTTA	DЪ
4008		Qy
4050	3991 AGAAGCTTAAAAAAACAAATTGAAAAAAACATTATTACATTTAAATTTGAACGAT	Db
3948	CTTCAATGTCAACGTGAAGGAC	Qy
3990	3931 CTCTCAGGATTTGAAAATGAATATGATGTTATATATATTTAAAACCTTTAGCTGGAGTATAT	Db
3888	TGTCCAAAATCGAGAACGAATACGAAGTGCTCTATCTGAAACCTCTGGCAGGCGTCTAT	Qy
3930	3874 GAATATTTAGATCAAGTAGTAACTGGAGAAGCAATATCTGTCACAATGGATAATATC	Db
3828	TTGATAACATT	Qy
3873	3814 GACGAAGAAGATGATTCCTTAGTTGTATTACCCATTTTTGGAGAATCCGAAGATAATGAC	Db
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3813	3754 ATACCAACTICAGGCTCTTATTAACAGAATTACAACAAGTAGTACAATCACAAAATTAT	Дb
3708	TCAGAACGTC	Qy
3753	CATCTCCATTATCTGTAAGGGTAAGTGGTAGTTCAGGATCCACAAAAGAAGAAGAAACACAA	В
3650	3597 CACTGTGGTGTCTGAATCTGGCTCCGACACACTGGAGCAGTCTCAACCTAAGAA	Qγ
3693	3634 AATTTTCTCCCAGAAGCAAAAGTTACAACAGTTGTAACTCCACCTCAACCAGATGTAACT	Db
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                                                                                                                                                                                                                                                               Submitted (21 JAN-1999) K. Tanabe, Osaka
Biology, 5-16-1 Ohmiya, Asahi-ku, Osaka,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antigen; glycoprotein; p190 gene; signal malaria parasite P. falciparum.
                                                                                                                                                                                                                                                    Sequence revised by author
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    /note="p190 precursor"
                                                                                                                                                           /db_xref="taxon:5833"
                                                                                                                                                                            /strain="MAD20"
LIDGYEEINELLYKLNFYYDLLRAKLNDACANSYCQIPFNLKIRANELDVLKKIVFGY
                                                                                                                                             /clone_lib="(lambda)NM1149
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LVSNSSMOCKLLEYNLTPEEERELKSCOPLDILFNIONNIPAMYSLYDSMNODOHL
FFELYCKEMITYLHKLKEENHIKKLLEEOKOJTGTSSTSSPGNTTVNTAQSATHSNSO
NQOSNASSTNTONGVAVSGPAVVEESHDELTYLS ISNDLKGTVELLNLGNKTKYVPNP
LTI STTEMEKTYENLIKNNDTYENDDIKQFVKSNSKVITGLTETQKNALNDEIKKLKD
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FKHISSNEYIIEDSFKLLNSEOKNTLLKSYKNIKGSVENDIKFAOEGISYVEKVLAKY
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LIKKIEDLRKIELFLKNAQLKDSIHVPNIYKPQNKPEPYYLIVLKKEVDKLKEFIVKV
KDMLKKEQAVLSSITQPLVAASETTEDGGHSTHTLSQSGETEVTEETEVTEETVGHTT
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YNLF I YNKQLQEAHNL I SYLEKRIDTLKKNEN IKKLLED I DK I KTDA ENPTTGSKPNP
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                                                                                  DVVDKIFSARYTYNVEKQRYNNKFSSSNNSVYNVQKLKKALSYLEDYSLRKGISEKDF
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                                         DSYPLFDGIFCSSSNFLGISFLLILMLILYSFI"
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193. .5238
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3028. .3030
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ATGAAGATCATATTCTTTTATGTTCATTTCTTTTTTTTTATTATAAATACACAATGTGTA 195 Matches Query Match Best Local

Local Sinhes 2904; 10

Similarity

26.1%; llarity 56.4%; Conservative

Score 1290.4; DB 3; Pred. No. 1.1e-272; D; Mismatches 1996;

Indels

Gaps

17;

Length 5392; 246;

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1194	HATI AAATITTAACATTGATAGTTTATTTACTGATCCACTTGAATTAGAATTATTAT AGAGAAGAATAAGAATATAGACATCTCCGCCAAAGTCGAGACAAGA	1144	
14	ATTAAGTTCAACATAGATTCTCTCTTTACTGATCCCCTTGAGCTGGAGTACTAC	80	
1083 1197	CTGCTGGACAAGAACAAGAAGATAGAGGGAGGACACGAGAAAGAGATCAAAGAGATCGCC	1027 1138	
1026 1137	AAGATTAATGAAATTAAGAATCCTCCGCCAGCCAACTCTGGGAACACCCCTAACACG	970 1078	•
969 1077	GTACTGGAGAAGGGCATAGACACCCTCAAGAAGAATGAAAATATCAAAGAACTGCTCGAC	910 1018	•
909 1017	GCCCAGTACGACCTGTCCATCTATAACAAACAGCTTGAAGAAGCCCATAACCTCATCAGC	958 958	
849 957	AAGACCATAGACAAAATAAGAATGCAACCAAGGAGGAAGAAAAGAAGTTGTACCAG 	790 898	
789 897	TATATTAAAAAGAATAAGAAGACCATCGAGAACATTAACGAGCTGATCGAAGAATCCAAA	730 838	•
729 837	GTCTTCGGATATCGCAAGCCTCTCGACAACATCAAGGACAATGTGGGAAAGATGGGAAGAT 	670 778	
669 777	TGTCAAATTCCATTCAAGTTGAAGATCAGAGCCAACGAGTGGACGTATTGAAGAAGTTG	610 718	
609 717	TTGAAITTCIACTTCGACTIGCTAAGGGCCAAACTGAATGACGTTTGCGCCAATGACTAT	550 658	-
549 657	ATTCATGGCTTCAAATATCTGATTGACGGTTACGAAGAGATCAATGAACTCCTGTACAAG	490 598	
489 597	GAGCTGAAGTACCCACAGTTGTTCGACCTCACTAATCATATGCTGAGACACTGTGTGAGAAAC	430 538	•
429 537	GACGCCAAGTCCTACGCCGACCTCAAGCACCGAGTGAGAAACTATCTCCTCACTATCAAG	370 478	
369 477	GCAAGCGGCGGTTCCCGGGAACAGTCGAAGAACCAATCCATCTGACAACTCTAGCGATTCC	310 418	•
309 417	CGTGGCATCAGGTGGCTCAGTG 	250 376	•
249 375	GCCGTTACAACCAGCACACCCGGTTCTAAAGGGTCTGTGGCTAGCGGTGGCTCCGGTGGG 	190 316	
189 315	ACCGGATACAGCCTGTTCCAGAAGGAGGAGAAGATGGTGCTGAATGAA	130 256	-
129 255	ACCCACGAATCCTATCAGGAGCTGGTTAAGAAACTGGAAGCTTTGGAAGATGCCGTCCTT	70 196	

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2255	CAAGCTCAAGCACAAGAGCAGAAGCAGGCACAGGCTCCAGTGCCAGTGCCCGTTCC	2200	Qy
2334	ACACACATTATCCCAATCAGGAGAAACAGAAGTAACAGAAGAAACAGAAGTAACAGAA	2275	ДЪ
2199	GGACAGGCTACCACCCAAGCCCGGACAACAGGCCGGTTCAGCTCTCGAAGGCGATAGCGTG	2140	Qy
2274	TTAGT	2215	Db X
2139	TOAKETEGAGGGGAGAGAGAGAGGGGGGGGGGGGGGGGGGGG	9	O _V
2214	AAATTAAAAGAATTTATACCAAAAGTAAAAGAAGCTTAAAAGAAAG	15	₽ 5
0 1	AAACTGAAACTGTTCATGCCCAAAGTCGAGAGCCTGATCAACGAAGAGAGAAGAAGATT	0.0	Q !
2025 2154	TATAAGCAGGAGATAAGCAGGAACCATACTACCTCATCGTACTCAAGAAAGA	1966 2095	Dh Qy
2094	GATAGTATTCATGTACCA	2035	Db
1965		1906	Qy
2034	GATATTGTAAAATTACAAGTACAAAAAGTTTTATTAATTA	1975	DЬ
1905		1846	Оу
1974	CTAGAAAAAATTTTAAAAGGACTAACACATTCAGCAAATGCTTCCTTAGAAGTATCT	1918	Db
1845	TTTGAGAAGAAGATTACAAAAGACGAAAATAAACCAGATGAGAAGATCCTGGAGGTCTCC	1786	Qy
1917	GGCCTCGAAGCTGATATAAAAAAATTAACAGAAGAAATAAAGAGTAGTGAAAACAAAATT	1858	Db
1785	AAGATCGAAAACGAGATCGAGACGCTTGTTGAGAACATTAAGAAGGATGAAGAACAGTTG	1726	Qy
1857		1798	ф
1725		1666	Оу
1797	TCTAATAATTCTGTATATAATGTTCAAAAATTAAAAAAGGCTCTTTCATATCTTGAAGAT	1738	Db
1665	TA	1606	Оу
1737	TTCAGTGCAAGATATACATATAATGTTGAAAAACAAAGATATAATAATAAATTTTTCATCC	1678	Db
1605	CTGACACACCATAATACC	1546	Qy
1677	GAAAAATTTTATGAAATGAAATTTAATAATAATTTTGACAAAGATGTCGTAGATAAAATA	1618	Db
1545		1486	Qy
1617	CAAAATAAAAATTACTTGAAGATTATGAAAAGTCAAAAAAGGATTATGAAGAATTACTT	1558	Db
1485		1426	Qy
1557	ATTAATAACATTAAAAAAACAAATTGATTTAGAAGAAAAAAACATTAATCACACAAAAGAA	1498	Db
1425		1366	Qy
1497	GATACTAAAGAAAAATTAATGAAAAAATTATTACAGATAATAAGGAAAAGAAAAAATATTC	1438	Дb
1365	TTCGATTATACGAAAGAACCCTCTAAGAATATCTACACAGACAATGAG	1306	Qy
1437	ATTCATAATTCATTAGCTGCAGATAATGATAAAAATTCATATGGTGATTTAATGAATCCT	1378	Db
1305	ATCAACAACGCTCTCAACGAGCTCAATAGCTTCGGTGACTTGATTAACCCC	1255	Qy
1377		1318	οф
1254		1195	Qy
1317		1258	Db

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4548		4489	Db
4233	CAA	4231	Qy
4230	CTGAGCGAAAAATACAAGTCTGACCTTGACCTCTATTAAAAAGTATATCAACGATAAG	4174	Qy
4488		4429	Db
4173	AAGGACTCCATCGACACCGATATCAATTTCGCTAATGATGTGCTGGGGTATTACAAGATC	4114	Qy
4428		4369	Db
4113	CCATACAAGTTCCTCAATAAAGAGAAGAGGGGATAAATTTCTGTCTAGTTACAACTATATC	4054	Qy
4368		4309	Db
4053 4308	TTGGAGAGCGACTTGATTCCCTATAAAGACCTGACCTCCTCTAACTACGTTGTCAAGGAC	3994 4249	Оу
3993	GTCAACGTGAAGGACATTCTGAACAGCCGCTTTAATAAGAGAGAAAATTTCAAGAACGTC	3934	Qy
4248		4189	Db
3933	CTGGCAGGCGTCTATAGGTCTCTCAAGAAACAGCTGGAGAATAACGTGATGACCTTCAAT	3874	Qy
4188		4129	Db
3873	GTGATTGATAACATTCTGTCCAAAATCGAGAACGAATACGAAGTGCTCTATCTGAAACCT	3814	Оу
4128		4069	
3813 4068	AGCGAGGAGGACTACGATGACCTCGGCCAGGTGGTCACCGGTGAGGCTGTCACTCCTTCC	3754 4012	Оy
3753	ACATCTCAGAACGTCGACGATGAGGTCGATGACGTCATTGTGGCCTATCTTCGGCGAG	3694	Qy
4011		3952	Db
3693	ACCTAAGAAGCCTGCATCTACTCATGTCGGAGCCGAGTCCAATACAATTACC	3642	Qy
3951		3892	· · · Db
3641	CACTGTGGTGTCTGAATCTGGCTCCGACACACTGGAGCAGTCTCA	3597	Qy
3891		3832	Db
3596	CTGGAATCTTACAAGAAGTTCCTGCCTGAAGGAACAGATGTCGC	3553	Qy
3831		3772	Db
3552 3771	ACGTGAATAACGCA AAGTTAACGAAGCT	3493 3712	Qy Db
3492	AAGCTCAGCTACCTCTCTAGCGGACTGCATCACCTGATCGCCGAGCTCAAGGAAGTCATT	3433	Qy
3711		3652	Db
3432	TTCAAGGTCCTGTCTAAGCTCGAAGGCAAGCTGAAGGACAACCTGAACCTGGAGAAGAAGII	3373	Qy
3651		3592	Db
3372	CTGAAGACTCTCTCCGAGGAGAGAGCATCCAGACGAGGATAACTACGCCAGCCTCGAGAAC	3313	Qy
3591		3532	Db
3531	AGATTCTTCTCAAACACTACAAAGGCCTCGTCAAGTATTATAATGGCGAGTCTTCTCCT	3472	Оy

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                                                                                                    antigen; glycoprotein.

p.falciparum (isolate FC27 from Papua New Guinea), cDNA to mRNA,
clone Ag75, gl.1, gl26, pEPG3.3.

plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

l (bases 1 to 5754)

Peterson, M.G., Coppel, R.L., McIntyre, P., Langford, C.J., Woodrow, G.,

Parown, G.V., Anders, R.F. and Kemp, D.J.

Variation in the precursor to the major merozoite surface antigens
of plasmodium falciparum

Mol. Biochem. Parasitol. 27 (2-3), 291-301 (1988)
                                                                                                                                                                                                                                                                                                                         P.falciparum major merozoite cds, isolate FC27.
                                                                                                                                                                                                                                                                                                                   cds, i
M19143
                                                                                                                                                                                                                                                                                                 M19143.1 GI:160412
                                     Location/Qualifiers
1. .5754
/organism="Plasmodium falciparum"
/isolate="FC27 (Papua, New Guinea)"
                                                                                                                                                                                                                                                                                                                                                bp mRNA linear INV 14
surface antigen (PMMSA) mRNA,
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Matches 2904; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                            ACACATGAAAGTTATCAAGAACTTGTCAAAAAACTAGAAGCTTTAGAAGATGCAGTATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGAAGATCATATTCTTTTATGTTCATTTCTTTTTTTTATAAATACACAATGTGTA 180
TCAGTTGCTTCAGTTGCTTC--
                              TCTGTGGCCTCTGGGGGTTCCGTCGCCTCCGGCGGCAGCGTGGCATCAGGTGGCTCAGTG
                                                                                                                          GCTGTTACAACTAGTACACCTGGTTCAAGTGGTTCAGTTACTTCAGGTGGTTCAGTTGCT
                                                                                                                                                               GCCGTTACAACCAGCACACCCGGTTCTAAAGGGTCTGTGGCTAGCGGTGGCTCCGGTGGG
                                                                                                                                                                                                                                                               ACAGGTTATAGTTTATTTCAAAAGGAAAAAATGGTATTAAATGAAGGAACAAGTGGAACA
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DVVDKIFSARTTYNVEKQRYNNKFSSSNNSVYNVOKLKKALSYLEDYSLRKGISEKDF
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TVTITLPPKEESAPKEVVVENSIEERELKSCOPLDLLFNIQNNIPAMYSLYDSMNIDLQHL
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NQQSNASSTNTQNGVAVSSGPAVVEESHPPLTVLSISNDLKGIVSLLNGLNKTKVPNP
LTISTTEMEKRYENILKNNDTYFNDDIKQFVKSNSKVITGLTETQKNALNDELKKLKD
TLQLSSDLYNKKKLKLDRLFNKKKELGQDKMQIKKLTLLKEQLESKLNSLNNHNVLQ
NFYFENKKEABEIAFTENTLENKKILLKHYKGLVKYYKGSSSPLKTLSEVSIQTEDN
NESVFENKKEABEIAFTENTLENKKILLKHYKGLVKYYKGSSSPLKTLSEVSIQTEDN
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upstream
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709 c 708 g 1798
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178. .5223
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NNKKVNEALKSYENFLPEAKVTTVVTPPQPDVTPSPLSVRVSGSSGSTKEETQIPTSG
SLLTELQQVVQLQNYDEEDDSLVVLPIFGESEDNDEYLDQVVTGEAISVTMDNILSGF
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LPENKKKEVEGHEEKIKEIAKTIKFNIDSLFTDPLELEYYLREKNKVDVTPKSQDPT
KSVQIPKVPYPNGIYYPLFLTDIHNSLAADNDKNSYGDLMNPDTKEKINEKIITDNKE
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LFQKEKMVLNEGTSGTAVTTSTPGSSGSVTSGGSVASVASGASVASGGSGSVASGGSGNS
RRTNPSDNSSDSNTKTYADLKHRVQNYLFTIKELKYPELFDLTNHMLTLSKNVDGFKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSYPLEDGIFCSSSNFLGISFLLILMLILYSFI"
121. .17/7
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EREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADATCTEEDSGSSRKKITCECTKP
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IDDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNTNDFEAIKKLINDD
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ENEYDVIYLKPLAGVYRSLKKQIEKNILKSYKYIKESVENDIKFAQEGISYYEKVLAKY
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RKPLDNIKDNVGKMEDYIKKNKTTIANINELIEGSKKTIDQNKNADNEEGKKKLYQAQ
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/note="precursor"
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121. .5226
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1. .5754
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/db_xref="GI:160413"
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1365 1482	1306 TTCGATTATACGAAAGAACCCTCTAAGAATATCTACACAGACAATGAGAGAAAGAA	Оy
1305 1422	1255 ATCAACAACGCTCTCAACGAGCTCAATAGCTTCGGTGACTTGATTAACCCC	ОУ
1254 1362	1195 GAATCAACCGAACCTAATGAATATCCCAATGGTGTGACGTACCCTCTGTCTTATAACGAT	Db Qy
1194 1302	144 TTGAGAGAGAAGAATAAGAATATAGACATCTCCGCCAAAGTCGAGACAAAG	D 04
1143 1242	084 AAAACCATTAAGTTCAACATAGATTCTCTCTTTACTGATCCCCTTGAGCTGGAGTACTAC	Db Qy
1083 1182	1027 CTGCTGGACAAGAACAAGAAGATAGAGGAGCACGAGAAAGAGATCAAAGAGATCGCC	Db Qy
1026 1122	970 AAGATTAATGAAATTAAGA ATCCTCCGCCAGCCAACTCTGGGAACACCCCTAACACG	Дb
969 1062	910 GTACTGGAGAAGCGCATAGAACACCCTCAAGAAGAATGAAAATATCAAAGAACTGCTCGAC	Db Qy
909	50 GCCCAGTACGACCTGTCCATCTATAACAAACAGCTTGAAGAAGCCCATAACCTCATCAGC	Db Qy
849 942	790 AAGACCATAGACAAAAATAAGAATGCAACCAAGGAGGAAGAAAAAAAA	D Q
789 882	730 TATATTAAAAAGAATAAGAAGACCATCGAGAACATTAACGAGCTGATCGAAGAATCCAAA	Db Qy
729 822	670 GTCTTCGGATATCGCAAGCCTCTCGACAACATCAAGGACAATGTGGGAAAGATGGAAGAT	Оy
669 762	610 TGTCAAATTCCATTCAATTTGAAGATCAGAGCCAACGAGTTGGACGTATTGAAGAAGTTG 	B 04
609 702	550 TTGAATTTCTACTTCGACTTGCCTAAGGGCCAAACTGAATGACGTTTGCGCCAATGACTAT	Db 09
549 642	490 ATTCATGGCTTCAAATATCTGATTGACGGTTACGAAGAGATCAATGAACTCCTGTACAAG 	D
489 582	430 GAGCTGAAGTACCCACAGTTGTTCGACCTCACTAATCATATGCTGAGCACTGTGTGAGATAAC	Db Qy
429 522	370 GACGCCAAGTCCTACGCCGACCTCAAGCACCGAGTGAGAAACTATCTCCTCACTATCAAG	Оу
369 462	310 GCAAGCGGCGGTTCCGGGAACAGTCGAAGAACCAATCCCATCTGACAACTCTAGCGATTTCC	ОУ

2311 ANIGICANCANACINONCIACATRICANANCINCIACIACATRICATRICATRICATACIACATRICATRICA	Db 2/	
2256AGAGGCTAAAGCTCCAAGTGCCTACACCACCAGCTCCTGTGAATAACAAGACCGAG	0у 2:	
2320 GAAACAGTAGGACACACAACAACGGTAACAATAACATTACCACCAAAAGAAGAAGCA	Db 2:	
2200 CAAGCTCAAGCAAGAAGCAGAAGCAGCACAGCCTCCAGTGCCAGTGCCCGTTCC	Qy 2:	
2260 ACACACATTATCCCAATCAGGAGAAACAGAAGTAACAGAAGAAACAGAAGTAACAGAA	Db 2:	
2140 GGACAGGCTACCACCAAGCCCGGGACAACAGGCCGGTTCAGCTCTCGAAGGCGGATAGCGTG 2199	Ωу 2:	
2200 TCAAGTATTACACAACCTTTAGTTGCAGCAAGCGAAACAACTGAAGATGGGGGTCACTCC	Db 2:	
2086 AAAACTGAAGGACAGTCAGATAACTCCGAGCCTTCCCACAGAAGGAGAGATAACC	Qy 2(
2140 AAATTAAAAGAATTTATACCAAAAGTAAAAGACATGTTAAAGAAAG	Db 2:	
2026 AAACTGAAAGTCTTCATGCCCCAAAGTCGAGGCCTGATCAACGAAGAGAAGAAGAAGAACATT 2085	Ωу 2	
2080 TATAAACCACAAAATAAACCAGAACCATATTATTTAATTGTATTAAAAAAAA	Db 20	
1966 TATAAGCAGGAGAATAAGCAGGAACCATACCTCATCGTACTCGAAGAAGAGAGATAGAC 2025	0у 1	
2020 AAGATAGAATTATTTTAAAAAAATGCACAACTAAAAGATAGTATTCATGTACCAAATATT	Db 20	
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1903 CTAGAAAAAATTTTAAAGGACTAACACATTCAGCAAATGCTTCCTTAGAAGTATCT 1959	Db 1:	
CAAAAGACGAAAATAAACCAG	0у 1:	
1843 GGCCTCGAAGCTGATATAAAAAAATTAACAGAAGAAATAAAGAGTAGTGAAAACAAAATT 1902	Db 16	
CGAGACGCTTGTTGAGAACATTAAGAAGGA	0у 1	
1783 TATTCTTTAAGAAAAGGAATTTCTGAAAAAGAFTTTAATCATTATATCATTTGAAAACT 1842	Db 1.	
CTGCGGAACATTGTTGTGGAGAAAGAACTAAAGT	Qу 1	
1723 TCTAATAATTCTGTATATAATGTTCAAAAATTAAAAAAGGCTCTTTCATATCTTGAAGAT 1782	Db 1:	
1606 TATGAGAATTCTAAGCATAATCTTGAGAAGCTCACCAAAGCTCTTAAGTATATGGAGGAC 1665	Оу 1	
1663 TTCAGTGCAAGATATACATATAATGTTGAAAAACAAAGATATAATAATAATTTTCATCC 1722	Db 10	
CAAAGTGGAGAAACTGACACACATAATACCTTTG	Оу 1:	
.603 GAAAAATTTTATGAAATGAAATTTTAATAATAATTATTGACAAAGATGTCGTAGATAAAAAA 1662	Db 10	•
486 AACGAGATCTATGATTCCAAATTCAACAATAACATCGACCTGACCAACTTCGAGAAAATG 1545	0у 1.	
1543 CAAAATAAAAAATTACTTGAAGATTATGAAAAGTCAAAAAAGGATTATGAAGAATTACTT 1602	Db 1:	
Ω	0у 1.	
1483 ATTAATAACATTAAAAAACAAATTGATTTAGAAGAAAAAAACATTAATCACACAAAAGAA	Db 1,	

TCATT 3492	AAGCTCAGCTACCTCTAGCGGACTGCATCACCTGATCGCCGAGCTCAAGGAAGTCATT	- U.A.	Qy
 AAA 363	TTTAGAGCATTAAGTAAAATAGATGGAAAACTCAATGATAATTTAG	57	Db
AGAAG 3432	TTCAAGGTCCTGTCTAAGCTCGAAGGCAAGCTG	3373	Qy
TCGAGAAC 3372 TAGAAAAA 3576	CTGAAGACTCTCTCCGAGGAGAGGACCAGACCGAGGACTAACTA	3313 3517	Db Qy
351	AAAATAT	4-5	Db
CTCCT 3312	AAGATTCTTCTCAAACACTACAAAGGCCTCGTCAAGTATTAT	3253	Qy
11 ACA 345		39	Db
ACACC 3252		3193	Qy
 CTGTT 3396		333	Db
CAGTG 3192	CTTGAAAG	3133	Q
AA 333		3277	라
AGCAG 3132	AAGAAGACAGTCGGCAAGTATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGG	3073	Qy
TAAG 3276	CAGTTATCATTTGATTATATAATAAATATAAATTAAAATTAGATAGA	3217	Db
ACAAG 3072	CAACTGAGCTTCGACCTGTACAACAAGTACAAACTGAAACTGGAGAGACTCTTCGACAAG	3013	γQ
ij	_	3160	Db
CACTG 3012	AACGATGAATCTAAACGTAAGAAGCTGGAAGAGGACATCAATAAGCTG	2953	Qy
		3100	B
CTCTT 2952	TTCTATAACGAGAGCTTCACTAACTTCGTGAAATCTAAAG	2893	Qy
 ATACC 3099	ACCATTTCTACAACAGATGGAAAAATTTTATGAGAATATTTTAAAAAATAATG	3040	망
. ≫	CTTATTGGACAGAAATCGTCCGAGAACTTCTACGAGAAGA	2833	Qy
CATTA 3039	TTGAAAGGTATTGTTAGTCTCTTAAATCTTGGA	2980	DЬ
AAGAA 2832	CTGAAACTGTTTGAGAACATCCTGTCTCTCGGCAAGAATAAGAACATCTACCAAG	2776	Qy
11 ACGAT 2979	GGTCC	2920	В
ACTCA 2775	GCCCGAAGTGAGCGCTAACGACGACACCTCTCACTCGACCAACCTTAATAAC	272	Qy
CATCT 2919	CAAAACCAACAATCAAA	2860	В
2720		2682	Qy
TC	ACATCCAGTCCTGGAAATACAACCGTAAATACTGCTCAAT	2800	Db
ICTTC 2681	AAGCTAAGAAGGTCTCCACCTCTGTTAAAACTCTCT	2642	Qy
CATCT 2799	GAGGAAAAT	2740	Вb
2641		2611	Qy
 AAAA 27	CAACATCTCTTTTTGAATTATATCAAAAGGAAATGA	2680	Db
CAAA 2610	TCTCAACTGTTCATGGAGATATATGAGAAGGAGATGGTCTGCAACCTGTATAAACT	2551	Qγ
 TTTA 267		62	망 :
TCTC 255	AATATCCAGAACAACATTCCCGTTATGTATTCTATGTTCGATAGCCTCAACA	49	ογ
 ATTT 2619	ATCTTACTCCAGAAGAAGAAATGAATTAAAATCATGTGATCATTAGATTATT	2560	DЬ

4 AAGCTGGCAGAATTTCAAGAAAATAACAATTTCGTCGGAATTGCAGACCTGTCTACCGAT 447	Qy 441 Db 471	
4 GAGAAGAGCAATGTGGAAG [†] TTAAAATCAAGGAGCTGAACTACCTCAAAACAATCCAAGAC 4	Qy 435 Db 465	
4 AACGACAAAATCGACCTCTTCGTAATTCACCTGGAGGCCAAGGTCCTCAACTATACTTAC 43	Qy 429 Db 459	
4 AAGAAGGAAAGTTACTTCCATTTTTAACAAACATTGAGACCTTATACAATAACTTA 4	Db 453	
4	Qу 423	
GAGAAGTTCCCATCATCACCACCAACAACACCTCCGTCACCAGCAAAAACAGACGAACAA 4	Db 447	
4 GTTTTAGCGAAATATAAGGATGATTTAGAATCAATTAAAAAAGTTATCAAAGAAGAA	4.	
CTGAGCGAAAAATACAAGTCTGACCTTGACTCTATTAAAAAGTATATCAACGATAAG 4	. 41	
4 AAAGAATCAGTAGAAAATTAAATTTGCACAGGAAGGTATAAGTTATTATGAAA	Db 435	
.14 AAGGACTCCATCGACACCGATATCAATTTCGCTAATGATGTGCTGGGGTATTACAAGATC 417	Qy 41:	
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4	Qу 405	
194 TIGGAGAGCGACTIGATICCCTATAAAGACCTGACCTCCTCTAACTACGTTGTCAAGGAC 405 	Qy 399 Db 423	
4 TTAAATTTGAACGATATCTTAAATTCACGTCTTAAGAAACGAAAATATTTCTTAGATGTA 4	Db 417	
4 GTCAACGTGAAGAGACATTCTGAACAGCCGCTTTAATAAGAGAGAAAATTTCAAGAACGTC 39	Qу 393	
4 TTAGCTGGAGTATATAGAAGCTTAAAAAAACAAATTGAAAAAAAA	Db 411	
4 CTGGCAGGCGTCTATAGGTCTCTCAAGAAACAGCTGGAGAATAACGTGATGACCTTC	Qу 387	
4 ACAATGGATAATATCCTCTCAGGATTTGAAAATGAATATGATGTTATATATTTT	Db 405	
4 GTGATTGATAACATTCTGTCC	Qу 381	
4 AUCHARGENORALTRUGATIANUL LUGEUN KARGITOSI UN UN SANGRULIGI UN LUCU SEL 1	Db 399	
/ CAATTACAAAATTAIGACGAAGAAGATGATTCCTTAGTIGTATTACCCCATTTTTGGAGAAA	, (L	
4 ACATCTCAGAACGTCGACGATGAGGTCGATGACGTCATTGTGCCTATCTTCGGCGAG 3	3 G	
	Db 3877	
2 ACCTAAGAAGCCTGCATCTACTCATGTCGGAGCCGAGTCCAATACAATTACC 36	Qу 364	
TAACTCCATCTCCATTATCTGTAAGGGTAAGTGGTAGTTCAGGATCCAC	Db 381	
7	Qу 359	
7 TTAAAATCTTACGAAAATTTTCTCCCAGAAGCAAAAGTTACAACAGTTGTAACTCCACCT 38	Db 375	
ω	Qу 355	
97 AAAATAAAAATTATACAGGTAATTCTCCAAGTGAAAATAATAAGAAAGTTAACGAAGCT 37	Db 369	
ω	Оу 349	
37 AAATTATCTTTCTTATCAAGTGGATTACATCATTTAATTACTGAATTAAAAGAAGTAATA 36	Db 363	

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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGGAAGACAGCGGCTCTAACGGAAAGAAATCACATGCGAGTGTACTAAGCCCGACTCC
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                                                                     Submitted (18-JUL-1994) Ralf Tolle, Abt. Prof. H. fur Molekulare Biologie (ZMBH), Univ. Heidelberg, Feld 282, 69120 Heidelberg, Germany On Aug 5, 1995 this sequence version replaced gi:
                                                                                                                                                                                                            Exp. Para
95354793
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                                                                                                                                                                                                                         merozoite surface antigen-1
Exp. Parasitol. 81 (1), 47-
                                                                                                                                                                                                                                                     Tolle,R., Bujard,H. and Cooper,J.A. Plasmodium falciparum: variations within
                                                                                                                                                                                                                                                                                                                   Mol. Biochem.
96123395
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                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Alveolata; Apicomplexa;
1 (bases 1 to 5312)
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/db_xref="taxon:5833"
/chromosome="9"
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GGTTCCGTCGCCTCCGGCGGCAGCGTGGCATCAGGTGGCTCAGTGGCAAGCGGCGGTTCC
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                                                                      GCAAGTGCTCAAAGTGGTGCAAGTGCTCAAAGTGGTGCCAAGTGCTCAAAGTGGTACAAGT
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ETEVTEETEETEETVGHTTTVTITLPFTQRSPPKEVKTVENSIEHKSNIDNSQALTKTV
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NIPAMYSLYDSMNNDLOHLFFELYQKEMIYYLHKLKEENHIKKLLEEQKQITGTSSTS
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RVSGSSGSTKETSTUNNLLSGFENSYDVIYLKPLAGVYRSLKKQIEKNIFTFTNLNLNDILN
QVYTGEAISVTMNLLSGFENSYDVIYLKPLAGVYRSLKKQIEKNIFTFTNLNLNDILN
SRLKKRKYFLDVLESDLMQFKHISSNBYIEDSSFKLMSGEDNETDLSVXTYKYKYKSENSTENST
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KFLPFLTNIETLYNNILVNKIDDYLINILKAKINDCNUEKDEAPVRIFKLSDLKAIDKI
KFLPFLTNIETLYNNILVNKIDDYLKINLKKINCONUEKDEAPVRIFKLSDLKAIDKI
QLFKNPYDFEAIKKLINDDTKKDMLGKLLSTGLYQNFPNTIISKLIEGKEQDMLAISQ
HQCVKKQCPENSGCFRHILDEREBCKCLLNYKQEGDKCVENPNPTCNENNGGCDADATC
TEEDSGSSRKKITCECTKPDSYPLFDGIFCSSSNFLGISFLLILMLILYSFI"
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TIDONKADNEEGKKKLYQAQYDLS IYNKQLEEAHNLISYLEKRIDTLKKENIKLLY
DKINEIKNPPBANSGNTPNYILDKNKKIEEHBEKIKEIAKTIKRNIDSLFTDDFLEEKY
YLREKNKKYDYTPKSQDPTKSYQIPKYPYPNGIYYPLPLTDIHNSLAADNDKNSYGDL
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ANGSLEVSDIVKLQVQKVLLIKKIEDLRKIELFLKNAQLKDSIHVPNIYKPQNKPEPY
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/dev_stage="blood
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pred. No. 1.1e-268;
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CAATAGCTTCGGTGACTTGATTAACCCCTTCGATTATACGAAAGAACCC 132 	-CAACGAGCTCAATA(ATAATGATAAAAATT(42
TEGTGACGTACCCTCTGTCTTATAACGATATCAACAACGCTCT	ATCCCAATG	36
CGCCAAAGTCGAGACAAAGGAATCAACCGAACCTAATGA 	ATAGACATCTCCGCCAAAGT	1165 1309
ACTGATCCCCTTGAGCTG 	GATTCTCTCTTTACTGATCCC	1105 1249
AGCACGAGAAAGAGATCAAAGAGATCGCCAAAACCATTAAGTTCAACATA 1104 	AAGATAGAGGAGCACGAGAA!	1045 1189
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ACACCCTCAAGAAGAATGAAAATATCAAAGAACTGCTCGACAAGATTAATGAAATT 984 	ATAGACACCCTCAAGAAGAAI 	925 1069
ACAAACAGCTTGAAGAAGCCCATAACCTCATCAGCGTACTGGAGAAGCGC 924 	TCCATCTATAACAAACAGCTI 	865 1009
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TCGAGAACATTAACGAGCTGATCGAAGAATCCAAAAAGACCATAGACAAA 804 	AGAACAI CAAATAI	745 889
ACAACATCAAGGACAATGTGGGAAAGATGGAAGATTATATAAAAAAAA	ATC	685 829
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AGCACCGAGTGAGAAACTATCTCCTCACTATCAAGGAGCTGAAGTACCCA 444 	CGAGT AGAGT	385 529
GAAGAACCAATCCATCTGACAACTCTAGCGATTCCGACGCCAAGTCCTAC 384 	GGGAACAGTCGAAGAACCAATCC	325 469
GTCCAAGTGGTACAAGTCCATCATCTCGTTCAAACACTTTACCTCGTTCA 468	GGTCCAAGTGGTCCAAGTGGTAC	409

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3 2451 A 2625	2392 TCTCACAGGACTATGAACGÁGAAGATTCTTAAACAGTACAAGATAACCAAGGAAGAAGAGGAG 	dd VQ
C 2391 A 2565	2332 CTTGAGAAGCTCTATGAGTTCCTGAATACATCCTACATCTGCCACAAATATATCCTCGTC	dq Qy
C 2331 T 2505	2272 GTGCCTACACCACCAGCTCCTGTGAATAACAAGACCGAGAATGTCAGCAAACTGGACTAC 	Qγ
A 2271 F 2445	2221 AAGCAGGCACAGCCTCCAGTGCCAGTGCCCGTTCCAGAGGCTAAAGCTCAA	Фр
3 2220 A 2385	ର – ର	дь Qy
C 2160 A 2325	2103AGATAACTCCGAGCCTTCCACAGAAGGAGAGATAACCGGACAGGCTACCAAGCCCA 	ФФ
- 2102 A 2265	2047 AAAGTCGAGAGCCTGATCAACGAAGAAGAAGAACATTAAAACTGAAGGACAGTC	ДУ
2046 A 2205	1987 GAACCATACTACCTCATCGTACTCAAGAAAGAGATAGACAAACTGAAAGTGTTCATGCCC 	Qy db
1986 1 2145	1927 AACGTGGAGTTAAAACATAATATACATGTGCCGAATAGTTATAAGCAGGAGAATAAGCAG 	Db Db
1926	1867 CAGAAGGTGCTCCTCATGAACAAGATTGATGAACTCAAGAAGACTCAACTCATTCTGAAG 	Db Qy
1866 A 2025	1807 GACGAAAATAAACCAGATGAGAAGATCCTGGAGGTCTCCGATATTGTTAAAGTCCAAGTG	DP Pp
1 1806 1 1968	1747 ACGCTTGTTGAGAACATTAAGAAGGATGAAGAACAGTTGTTTGAGAAGAAGATTACAAAA 	Db Qy
1746 1908	1687 GTGGAGAAAGAACTAAAGTÄTTACAAGAATCTCATAAGTAAGATCGAAAACGAGATCGAG 	рь
1686 1 1848	1627 CITGAGAAGCTCACAAGCTCTTAAGTATATGGAGGACTATTCTCTGCGGAACATTGTT 	Дy
1626 1788	1567 AAAGTGGAGAAACTGACACACCATAATACCTTTGCATCCTATGAGAATTCTAAGCATAAT 	Qy Db
1566	1507 TTCAACAATAACATCGACCTGACCAACTTCGAGAAAATGATGGGAAAACGGTACTCTTAC	: Qy
1506 1668	1447 AGTCTAAACGATATCACTAAAGAGTATGAAAAGCTGCTGAACGAGATCTATGATTCCAAA 	Оy
1446	1387 ATCAAAATTGAGAAGAAGAAAATTGAGAGTGACAAGAAAAGTTACGAAGACCGCAGCAAA 	Qу

3513	454 GGACTGCATCACCTGATCGCCGAGCTCAAGGAAGTCATTAAGAACAAGAACTACACCGGC	Qy
3702	3643 GATGGAAAACTCAATGATAATTTACATTTAGGAAAGAAAAATTATCTTTCTT	망
3453	AAGGCAAGCTGAAGGACAACCTGAACCTGGAGAAGAAGAAGCTCAGCTACCTCTAGC	Qy
3642	3583 TCAATTCAAACAGAAGATAATTATGCCAATTTAGAAAAATTTAGAGTATTAAGTAAAATA	DЬ
3393		Qy .
3333 3582	3274 AAAGGCCTCGTCAAGTATTATAATGGCGAGTCTTCTCCCTCTGAAGACTCTCTCCGAGGAG	ОУ
3522	463 GCTGAAATAGCAGAAACTGAAAACACATTAGAAAACACAAAAATATTATTGAAACATTAT	Db
3273	3214 GCCGAGATCGCCGAGACAGAGAACACTCTGGAGAACACCCAAGATTCTTCTCAAACACTAC	Qy
3462		Db d
3213	154 CTGAACAATCCGAAACACGTACTGCAGAACTTCTCAGTGTTTCTTCAACAAGAAGAAGGAA	φ.
3153	3094 AAGATGCAGGTCAAGAAGTTGACTCTGCTCAAGGAGCAGCTTGAAAGCAAACTCAACTCA 31	B 6
3342		Db
3093	3034 AACAAGTACAAACTGAAACTGGAGAGAGACTCTTCGACAAGAAGAAGAAGACGCGCAAGTAT	Qy
3282	GCATTAAATGATGAAATTAAAAATTAAAAGATACTTTACAGTTATCATTTGATTTATAT	pb .
2022	4 AAGCTGGAAGAGGACATCAATAAGCTGAAGAGACACACTCCAACTTGAGCTTTCGACTTAC	0
2973 3222	2914 ARCTTCGTGAAATCTAAAGCCGATGATATCAACTCTCTTAACGATGAATCTAAACGTAAG	gb Qy
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2853	CTGTCTCTCGGCAAGAATAAGAACATCTACCAAGAACTTATTGGACAGAAATCGTCC	Qy
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	UNIQUEDIT FOUT OF TABLE TO TRACE TO SERVICE	2 5
2736	2703 TCTCACACCTCAAGACAA	P Oy
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2865	2806 TTATTAGAGGAGCAAAAACAAATAACTGGAACATCATCTACATCCAGTCCTGGAAATACA	Ф
2657		Qy
2805		DЬ
2631		Qy
2571 2745	2512 GTTATGTATGTTCGATAGCCTCAACAATTCTCTCTCTCAACTGTTCATGGAGATA	Qу Db
2685	2626 AATGAATTAAAATCATGTGATCCATTAGATTTATTTAATATTTCAAAATAACATACCT	Ф
2511		Qy

4494	AATAACAATTTCGTCGGAATTGCAGACCTGTCTACCGATTATAACCACAACAATCTCCTG	4435	Qy	
4779	AAAATAACTAAACTTAGTGATTTAAAAGCAATTGATGACAAAATAGATCTTTTTAAAAAC	4720	Db	
4434		4375	Qy	
4719	TTAATTAACTTAAAGGCAAAGATTAACGATTGTAATGTTGAAAAAGATGAAGCACATGTT	4660	В	
4374		4315	Оу	
4659	CCATTTTTAACAAACATTGAGACCTTATACAATAACTTAGTTAATAAAATTGACGATTAC	4600	Ф	
4314		4255	Qy	
4599	CCAACAACACCTCCGTCACCAGCAAAAACAGACGAACAAAGAAGGAAAGTAAGT	4540	Db	
4254	CTG	4231	Оу	
4539	GATTTAGAATCAATTAAAAAAGTTATCAAAGAAGAAGAAGGAGAAGTTCCCATCATCACCA	4480	рь	
4230		4195	Qy	
4479	ATTAAATTTGCACAGGAAGGTATAAGTTATTATGAAAAGGTTTTAGCGAAATATAAGGAT	4420	Db	
4194		4135	Qy	
4419	GAACAAAAAAACACACTTTTAAAAAGTTACAAATATATAAAAGAATCAGTAGAAAATGAT	4360	ф	
4134		4075	Qy	
4359		4300	рь	
4074		4015	Qy	
4299	AATTCACGTCTTAAGAAACGAAAATATTTCTTAGATGTATTAGAATCTGATTTAATGCAA	4240	Вρ	
4014		3955	Qy	
4239	TTAAAAAAACAATTGAAAAAAACATTTTACATTTAATTTTGAACGATATCTTA	4180	Db	
3954		3895	Qy	
4179	GATTTGAAAATGATATATATATATATATATAAAACCTTTAGCTGGAGTATATAGAAGC	4120	Ф	
3894	GTCT	3835	Qy	
4119	TTAGATCAAGTAGTAACTGGAGAAGCAATATCTGTCACAATGGATAATATCCTCTCA	4063	ДЬ	
3834		3775	Qy	
4062	GAAGATGATTCCTTAGTTGTATTACCCATTTTTGGAGAATCCGAAGATAATGACGAATAT	4003	Db	
3774		3715	Qy	
4002		3943	рь	
3714	AT.	3655	Qy	
3942		3883	Db	
3654		3603	Qy	
3882	CTCCCAGAAGCAAAAGTTACAACAGTTGTAACTCCACCTCAACCAGATGTAACTCCATCT	3823	Db	
3602	CACTGT	3574	Qy	
3822	ATTCTCCAAGTGAAAATAATAAGAAAGTTAACGAAGCTTTAAAATCTTACGAAAATTTT	3763	Db	
3573		3514	Qy	
3762		3703	Db	

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KEYWORDS
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PFAGP195
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                                                                                                                                                                                                                                                                                                                                  Exp. Para
89005525
                                                                                                                                                                                                                                                                                                                                                                                                                                                          major merozoite surface antigen.
P.falciparum (strain Uganda-Palo Alto) DNA.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida;
1 (bases 1 to 5276)
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M37213
M37213.1 GI:160315
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                                                                                                                                                                                                                                                                                                                                                                                        major merozoite
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falciparum major merozoite surface antigen (gp195) gene,
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DSLFTDPLELEYYLREKNKKVDVTPKSQDPTKSVQIPKVPYPNGIVYPLPLTDIHNSI
                TLKKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEEKIKEIAKTIKFNI
                                   LNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMEDYIKKNKTTI
ANINELIEGSKKTIDQNKNADNEEGKKKLYQAQYDLSIYNKQLEEAHNLISVLEKKID
                                                                       /protein_id="AAA29611.1"
/db_xref="GI:160316"
                                                                                                                                                                                                                                       /organism="Plasmodium
/db_xref="taxon:5833"
                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                    /codon_start=
                                                                                                                                                                                                   /note="major merozoite surface
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e antigen (gp195) of the Uganda-Palo Alto
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> LSINDLKGIVSLLILIGNKTKVPNPLTISTTEMEKFYENILKNNDTYFNDDIKOFVKS
> NSKVITGLTETOKNALNDEIKKLKDTLOLSFDLYNKYLKKDLEGOKMQI
> KKLTLLKEQLESSKLUSLUMPHAVLQNESVEFAKKKEKLEGOKMQI
> KKLTLLKEQLESSKLUSLUMPHAVLQNESVEFAKKKEKELGOKMQI
> KKLTLLKEQLESSKLUSLUMPHAVLQNESVEFAKKKEKELGOKMQI
> KKLTLLKEQLESSKLUSLOQUESVEFAKKKEKELGOKMQI
> LVKYYNGESSPLKTLSEVSIQTEDNYANLEKFRVLSKIDGKLNDNLHLGKKKLSFLSS
> GLHQLLTELKEVIKNKYTGNSSSENNKKVNBALKSYENEFFERSKVTTVVTPPQPDVT
> PSPLSYRVSGSGSTKEEDQLFTSGSLLTELQOVVQLQNYDEEDDSLVVLFFEGESED
> NDEYLDQVTTGEAISVTMDNILSGFENEYDVIYLKPLAGVYRSLKKQIEKNIFTFNLN
> UNDILNSRLKKRXFLDVLESDLMQFKHISSNEYIEBSSFKTLNSGKWYLLKSYKYI
> KESVENDIKFAQGEISVTKKVLKEKEKFPSSPPTTPBSPAKTO
> LNDILNSRLKKRXFLDVLESDLMQFKHISSNEYIEBSSFKTLPBSPAKTO
> KESVENDIKFAQGEISVTKKVLKLDDYLINLKAKINDCNVEKDEAHVKITKLSDLK
> EQKKESKFLPFLTNIETLYNNLVNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLK KLLEDYEKŚKDYEELLEKFYEMKFNNNFDKDVVDKIFSARTTNVEKQRYNNKESSS
> NNSVYNVQKLKRALSYLEDYSLEKGISEKDFNHYTILKTGLEADIKKLTEEIKSSENK
> ILEKNEKGLTHBANASLEVDTVKLOVQKVLLIKKIEDLRKIELFLKNAQLKDSIHVP
> NIYKPQNKPEPYYLIVLKKEVDKLKEFIPKVKDMLKKEQAVLSSITQPLVAASETTED
> GGHSTHTLSQSGETEVTEETEETEETVEHTTTVTITLEPKEVKVVENSIEHKSNDNSQ
> ALTKTVYLKKLDEFLTKSYICHKYILVSNSSMDQKLLEVYNLTPEEENELKSCDPLDL
> LENIQNNIFAMYSLYDSMNNDLOHLEFELYQKEMIYYLHKLKEENHIKKLLEEGKOT
> GTSSTSSPGNTTVNTAQSATHSNSQNQQSNASSTNTQNGVAVSSGPAVVEESHDPLTV DADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSSNFLGISFLLILMLILYSFI " AIDDKIDLFKNHNDFDAIKKLINDDTKKDMLGKLLSTGLVQNFPNTIISKLIEGKFQD MLNISQHQCVKKQCPENSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGC

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ATTAATGAATTATTATATAAATTAAAACTTTTATTTTGATTTATTAAGAGCAAAATTAAAT
                         ATCAATGAACTCCTGTACAAGTTGAATTTCTACTTCGACTTGCTAAGGGCCCAAACTGAAT 588
                                                                     ATGCTGACACTGTGTGATAACATTCATGGCTTCAAATATCTGATGACGGTTACGAAGAG
                                                                                                             AATTACTTGTTCACTATTAAAGAACTCAAATATCCCGAACTCTTTGATTTAACCAATCAT
                                                                                                                            AACTATCTCCTCACTATCAAGGAGCTGAAGTACCCACAGTTGTTCGACCTCACTAATCAT
                                                                                                                                                                     CCAGCTGATGCAAGCGATTCAGATGCTAAATCTTACGCTGATTTAAAAACACAGAGTACGA
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                                                        ATGTTAACTTTGTGATAATATTCATGGTTTCAAATATTTAATTGATGGATATGAAGAA
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1710	AAGTATATGGAGGACTATTCTCTGCGGAACATTGTTGTGGAGAAAGAA	1651	Qy
1740	AATAAATTTTCATCCTCTAATAATTCTGTATATAATGTTCAAAAATTAAAAAAAGGCTCTT	1681	Db
1650	AATACCTTTGCATCCTATGAGAATTCTAAGCATAATCTTGAGAAGCTCACAAAGCTCTT	1591	Qy
6	GTCGTAGATAAATATTCAGTGCAAGATATACATATAATGTTGAAAAACAAAGATATAAT	O)	Db '
1590		1531	Ŷ
σ	GAT	LTI	망
1530	TGACC	1471	γQ
1560	AATCACACAAAAGAACAAAATAAAAAATTACTTGAAGATTATGAAAAAGTCAAAAAAGGAT	1501	B
1470		1411	Qy
1500	GAAAGAAAATATTCATTAATAACATTAAAAAACAATTGATTTAGAAGAAAAAAAA	1441	Ъ
1410	AGAGAAAGAAGTTTATCAACGAAATCAAGGAGAAGATCAAAATTGAGAAGAAGAAAATT	1351	δÔ
1440	ര —	1381	рb
1350	CAGAC	1291	Qy
1380		1321	Db
1290	CTGTCTTATAACGATATCAACAA	1240	Qy
1320		1261	Db
1239		1188	Qy
1260	GAATTAGAATATTATTAAGAGAAAAAAATAAAAAAGTTGATGTAACACCTAAATCACAA	1201	Db
1187	GAGCTGGAGTACTACTTGAGAGAGAGAATAAGAATATAGACATCTCCGCCAAA	1129	Qy
1200	ATAAAAGAAATTGCCAAAACTATTAAATTTAACATTGATAGTTTATTTA	1141	Db
1128		1069	Qy
1140	GGAAATACACCAAATACTCTCCTTGATAAGAACAAAAAAATCGAGGAACACGAAGAAAAA	1081	DЬ
1068	GGGAAC	1009	γO
1080	AACATTAAGGAATTACTTGATAAGATAAATGAAATTAAAAATCCCCCACCGGCCAATTCT	1021	Db
1008	_	949	Qy
1020		961	Db
948	_	889	Qy
960	GGAAAAAAAATTATACCAAGCTCAATATGATCTTTCTATTTACAATAAACAATTAGAA	901	В
888	- ດ	829	Оу
900	GAATTAATTGAAGGAAGTAAGAAAACAATTGATCAAAATAAGAATGCAGATAATGAAGAA	841	рь
828	- a	769	Qy
840	ATGTAGGAAAATGGAAGATTACATTAAAAAAATAAAACAACCATAGCAAATATAAAT	781	В
768	AATGTGGGAAAGATGGAAGATTATATTAAAAAGAATAAGAAG	709	Qy
	TAGACGTACTTAAAAAACTTGTGTTCGGATATAGAAAACCATTAGACAATATTAAAGAT	N) 4	B 5
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N		661	Db
648	G	589	Qy

2720	2682 CAGCTCCATGCAACCACTGTCTCACACCTCAAGACAA	Qy
2814	2755 ACATCCAGTCCTGGAAATACAACCGTAAATACTGCTCAATCCGCAACTCACAGTAATTCC	Db
2681	TGTTAAAACTCTCTCTTC	Оу
2754	2695 GAGGAAAATCACATCAAAAAAATTATTAGAGGAGCAAAAAAAA	Db
2657	ACAACGACAAGATTAAGAACCTTCTGGAGGAAGCTAAGAAGGTCTCACAACGACGACGAAGGAAGCTAAGAAGGTCTC	Ωу
2610 2694	2551 TCTCAACTGTTCATGGAGATATATGAGAAGGAGATGGTCTGCAACCTGTATAAACTCAAA	Db Qy
2634	575 AATATTCAAAATAACATACCTGCTATGTATTCATTATATGATAGTATGAACAATGATTTA	DЪ
2550		Qy
2574		Db
2490		Qy
2514		Db
2430	371 TGCCACAAATATATCCTCGTCTCTCACAGCACTATGAACGAGAAGATTCTTAAACAGTAC	Ωy
2454	395 GCCTTGACAAAACAGTTTATCTAAAGAAATTAGATGAATTTTTAACTAAATCATATATA	B X
w	311 AATGTCAGGCAAACTGGGACTAGCTTGGAGAAGCTTGTATGAGTTGCTGGAATACATCGTAGGAGT	0 5
7304		₹ .
2310	2251 GTTCCAGAGGCTAAAGCTCAAGTGCCTACACCACCAGCTCCTGTGAATAACAAGACCGAG	O _V
2334	2191 PATATOCA DELAPOCA CARDENCA PARA POR CARDEN POR CAR	Db 43
22/4	ANGAT - GGGGGTCACTCCACACACACTATCCCCAATCAGGAGAAAACAGAAGTAACAGAA	} E
2190	131 GAGATAACCGGACAGGCTACCACCAAGCCCGGACAAGGCCGGTTCAGCTCTCGAAGGC	, Qy
2215	2156 AAGAACAAGCTGTCTTATCAAGTATTACACAACCTTTAGTTGCAGCAAGCGAAACAACTG	Db .
2130		Qy
2155	2098 AAAAAAGTAGATAAATTAAAAGAATTTATACCAAAAGTAAAAGACATGTTAAAGA	DЬ
2070	CGAA	Qy
2097	2038 CATGTACCAAATATTTATAAACCACAAAATAAACCAGAACCATATTATTTAATTGTATTA	Db
2010	ATGTGCCGAATAGTTATAAGCAGGAGAATAAGCAGGAACCATACTACCTCATCGTACTC	Qγ
2037	1978 ATAGAAGACTTAAGAAAGATAGAATTATTTTTAAAAAATGCACAACTAAAAGATAGTATT	Db
1950		Qy
1977	1918 TCCTTAGAAGTATATGATATTGTAAAATTACAAGTACAAAAAGTTTTATTAATTA	ΩЬ
1890	AACAAG	Qy
1917	1861 AGTGAAAACAAATTCTAGAAAAAAATTTTAAAGGACTAACACATTCAGCAAATGCT	Db
1830	AGAAG	Qy
98	801	рь ×
7 (11 БАСЗАПСТСАПА АСТВАССВОВА В СОВСЕТСО СОПТОТОТОВ В В ВСОВОТОСТВОВ В ВСОВОТОТОТОВ В В ВСОВОТОТОВ В В В ВСОВОТОТОВ В В В ВСОВОТОТОВ В В В В В В В В В В В В В В В В	2 5
1800	1741 TCATATCTTGAAGATTATTCTTTAAGAAAAGGATTTCTGAAAAAGATTTTAATCATTAT	Db

3753 3951	ACATCTCAGAACGTCGACGATGAGGTCGATGACGTCATTGTGCCTATCTTCGGCGAG	3694 3892
9 9	AGAAGCCTGCATCTACTCATGTCGGA 	8 6
3641 3831	AACT	3597 3772
3596 3771	GGAATCT AAAATCT	3553 3712
3552 3711	7 - 7	3493 3652
3492 3651	AAGCTCAGCTACCTCTCAGCGGACTGCATCACCTGATCGCCGAGCTCAAGGAAGTCATT	3433 3592
3432 3591	TTCAAGGTCCTGTCTAAGCTCGAAGGCAAGCTGAAGGACAACCTGAACCTGGAGAAGAAG	3373 3532
3372 3531	CTGAAGACTCTCTCCGAGGAGAGCATCCAGACCGAGGATAACTACGCCAGCCTCGAGAAC	3313 3472
3312 3471	AAGATTCTTCTCAAACACTACAAAGGCCTCGTCAAGTATTATAATGGCGAGTCTTCTCCT	3253 3412
3252 3411	TTCTTCAACAAGAAGAAGGAAGCCGAGATCGCCGAGACAGAGAACACTCTGGAGAACACCC	3193 3352
3192 3351	CTTGAAAGCAAACTCAACTGAACAATCCGAAACACGTACTGCAGAACTTCTCAGTG	3133 3292
3132 3291	AAGAAGACAGTCGGCAAGTATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAG	3073 3232
3072 3231	CAACTGAGCTTCGACCTGTACAACAAGTACAAACTGAAACTGGAGAGAGA	3013 3172
3012 3171	AACGATGAATCTAAACGTAAGAAGCTGGAAGAGGGACATCAATAAGCTGAAGAAGACACTG 	2953 3115
2952 3114	TTCTATAACGAGAGCTTCACTAACTTCGTGAAATCTAAAGCCGATGATATCAACTCTCTT	2893 3055
2892 3054	CTTATTGGACAGAAATCGTCGAGAACTTCTACGAGAAGATACTGAAAGACAGCGACACA	2833 2995
2832 2994	CTGAAACTGTTTGAGAACATCCTGTCTCTCGGCAAGAATAAGAACATCTACCAAGAA	2776 2935
2775 2934	GCCCGAAGTGAGGGCTAACGACGACACCTCTCACTCGACCAACCTTAATAACTCA	2721 2875
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906 GAAAGAGAAGAATGTTATTAAATTACAAACAAGAAGGTGATAAATGTGTTGAA 4	р
4654 GAGCGCGAAGAGTGCCAAGTGTCTCCTGAACTACAAACAA	Qy
4594 CAGCACCAATGCGTGAAGAAAACAGTGCCCCCAGAATAGCGGCTGTTTCAGGCATCTGGAC 4653	оду Оу
4534 GCCAAAACAGTGCTGAGCAATCTGCTCGACGGCAACCTGCAGGGCATGCTGAACATCTCC 4593	D 04
	Db
474 TATAACCACAACAATCTCCTGACCAAGTTTCTGTCCACTGGCATGGTGTTCGAAAACCTC 45	Qy
4414 AAGCTGGCAGATTTCAAGAAAATAACAATTTCGTCGGAATTGCAGACCTGTCTACCGAT 4473 	Qу
4354 GAGAAGACCAATGTGGAAGTTAAAATCAAGGAGCTGAACTACCTCAAAACAATCCAAGAC 4413 	рь о _ў
549 GTTAATAAAATTGACGATTACTTAACTTAAAGGCAAAGATTAACGATTGTAATGTT 46	DP 43
4489 AAGAAGGAAAGTAAGTTCCTTCCATTTTTAACAAACATTGAGACCTTATACAATAACTTA 4548	da da
TCGAAACCCTGTA	Qy
4231	Qy Db
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4309 AAAGAATCAGTAGAAAATGATATTAAATTTGCACAGGAAGGTATAAGTTATTATGAAAAG 4368 4174 CTGAGCGAAAAATACAAGTCTGAGCTTGACTCTATTAAAAAGTTATATCAACGATAAG 4230	Ov Db
AAGGACTCCATCGACACCGATATCAATTTCGCTAATGATGTGCTGGGGTATTACAAGATC 41	Qy
4054 CCATACAAGTTCCTCAATAAAGAGAAGAAGAATAAATTTCTGTCTAGTTACAACTATATC 4113 	Qy
189 TTAGAATCTGATTTAATGCAATTTAAACATATATCCTCAAATGAATACATTATTGAAGAT 42	Db 4
4129 TTAAATTTGAACGATATCTTAAATTCACGTCTTAAGAAAACGAAAATATTTCTTAGATGTA 4188	<u> </u>
934 GTCAACGTGAAGACATTCTGAACAGCCGCTTTAATAAGAGAGAAAATTTCAAGAACGTC 3	VΩ
3874 CTGGCAGGCGTCTATAGGTCTCTCAAGAAACAGCTGGAGAATAACGTGATGATCATTTAGT 3933	Оу
3814 GTGATTGATAACATTCTGTCCAAAATCGAGAACGAATACGAAGTGCTCTATCTGAAACCT 3873 	Qy Db
754 AGCGAGGAGGACTACGATGACCTCGGCCAGGTGGTCACCGGTGAGGCTGTCACTCCTTCC 3	Qy Db

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3 (bases 3594 to 5541)
Weber,J.L., Sim,B.K., Lyon,J.A. and Wolff,R. Merozoite surface protein sequence from the human malaria parasite Plasmodium falciparum Nucleic Acids Res. 16 (3), 1206 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Variation in the gene encoding a major merozoite surface antigen of
the human malaria parasite Plasmodium falciparum
Nucleic Acids Res. 14 (8), 3311-3323 (1986)
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 3593)
Weber, J.L., Leininger, W.M. and Lyon, J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glycoprotein; surface antigen; tandem repeat
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SGTSAQGGTSGTSGTSGTSGTSAQSGTSGTSAQSGT
SGTSAQGGTSGTSGTSGTSGTSAQSGTSGTSAQSGT
SGTSAQGGTSGTSGTSGTSGTSGTSGTSGTSAQSGTSGTSAQSGT
SGTSAQGGTSGTSGTSGTSPSSRS WILPRS WISGASPADASDSDAKSYADLKHRVK
NUPTRIKELFT I KELKYPELFDLTNHMLTLCDNIHGFKYLIDGTEINELLYKLNFYFDLLRAK
KUNDVCANDYCQIFFNLKIRANELDVLKKLVFGYRKPLDNIKONYGKMEDYIKKNKTTI
ANINELIEGSKKTIDQNKNADNEEGKKKLYQAQYDLSIYNKQLEEAHNLISYLEKRID
TLKKNENIKELLDKINELKNPPPANGGWTPNTLDKNKKIEBHEEKIKEINKTIKFNI
SSLFTDPLELEXYLREKNKKUDYTPKSQDFTKSVQIFKYPYBYGIYYPLPLTDIHNSL
AADNDKNSYGDLMPDTKEKINEKIITDNKERKIFINNTLDEKKINDLEEKKINHTKEQNK
KLLEDYEKSKKOYEELLEKFYEMKFNNNFDKDVVDKIFSARYTYNVEKGYNNKFSSS
NSYYNYQKIKKALSYLEDYSLRKGISEKDFNHYYTLKTGLEADIKKLTEEIKSSENK
LFNIQNNIPAMYSLYDSMNNDLQHLFFELYQKEMIYYLHKLKEENHIKKLLEEQKQIT
GTSSTSSPGNTTVNTAQSATHSNSQNQQSNASSTNTQNGVAVSSGPAVVEESHDPLTV
LSISNDLKGIVSLLNLGNKTKVPNPLTISTTEMEKFYENILKNNDTYFNDDIKQFVKS
                                                                      ILEKNEKGLTHSANASLEVYDIVKLQVQKVLLIKKIEDLRKIELFLKNAQLKDSIHVP
NIYKRQNKPEFYYLIYUKKEVDKLKEFIPKYKDKJKKEQAVLSSITQPLVAASETTED
GGHSTHTLSQSGETEVTEETBETEETGHTTTVTITLPKEVKVVENSIEHKSNDVSQ
ALTKTVYLKKLDEFLTKSYICHKYILVSNSSMDQKLLEVYNLTPEEENELKSCDPLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="CAMP (Malaysia)"
/db_xref="taxon:5833"
283 .5463
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="SWISS-PROT:P04934"
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/db_xref="GI:9895"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="pot. major merozoite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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TTGGACGTATTGAAGAAGTTGGTCTTCGGATATCGCAAGCCTCTCGACAACATCAAGGAC
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                                                                     GACGTTTGCGCCAATGACTATTGTCAAATTCCATTCAAGTTTGAAGATCAGAGCCAACGAG 648
                                                                                                                                    ATCAATGAACTCCTGTACAAGTTGAATTTCTACTTCGACTTGCTAAGGGCCAAACTGAAT 588
                                                                                                                                                                                                    ATGCTGACACTGTGTGATAACATTCATGGCTTCAAATATCTGATTGACGGTTACGAAGAG
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                                                                                                                   ATTAATGAATTATTATAAATTAAACTTTATTTGATTTATTAAGAGCAAAATTAAAT
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/note="19 imp. tandem repeats 1"

2542. .2586

/note="5 imp. tandem repeats 2"
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LNDILMSRLKRKYFLDVLESDLMGFKIISSNEYIIEDSEKFENESSPDYRTLKSYKYI
KESVENDIKFAQOEGISYYEKVLAKYKDDLESIKKVIKBEKEKPSSPDYRTPDSPBAKD
EQKKESKFLPFLTNIETLYNNLVNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLK
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LVKYYKGESSPLKTLSEVSIQTEDNYANLEKFRYLSK LDGKLNUCHLGKKKLSFLSS
GLHHLITELKEVIKNKNYTGNSPSENNKKVNEALKSYENFLPEAKVTTVYLPPOPDYD
PSPLSVRVSGSSGSTKEETQIPTSGSLLTELQOVVOLONYDEEDDSLVVLPIFGESED
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MLNISQHQCVKKQCPENSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGC
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	1770 2142	1 AAGAATGTCATAAGTAAGATCGAAAACGAGATCGAGACGCTTGTTGAGAACATTAAGAAG 	1711 2083
	1710 2082		1651 2023
	1650 2022	1 AATACCTTTGCATCCTATGAGAATTCTAAGCATAATCTTGAGAAGCTCACCAAGCTCTT	1591 1963
	1590 1962	L AACTTCGAGAAAATGATGGGAAAACGGTACTCTTACAAAGTGGAGAAACTGACACACCAT 	1531 1903
	1530 1902	TATGAAAAGCTGCTGAACGAGATCTATGATTCCAAATTCAACAATAACATCGACCTGACC	1471 1843
	1470 1842	L GAGAGTGACAAGAAAAGTTACGAAGACCGCAGCAAAAGTCTAAACGATATCACTAAAGAG 	1411 1783
	1410 1782	GAGAGAAAGAAGTTTATCAACGAAA 	1351 1723
	1350 1722	1 GACTTGATTAACCCCTTCGATTATACGAAAGAACCCTCTAAGAATATCTACACAGACAAT	1291 1663
	1290 1662	CTGTCTTATAACGATATCAACAACGCT	1240 1603
•	1239 1602	GATCCTACGAAATCTGTTCA	1188 1543
	1187 1542	GAGCTG	1129 1483
	1128 1482	ATCAAAGAGATCGCCAAAACCATTAAGTTCAACATAGATTCTCTCTTTACTGATCCCCT	1069 1423
	1068 1422	GGGAACACCCCTAACACGCTGCTGGACAAGAACAAGAAGATAGAGGAGGAGCACGAGAAAGAG 	1009
	1008 1362	AATATCAAAGAACTGCTCGACAAGATTAATGAAATTAAGAATCCTCCGCCAGCCA	949 1303
	948 1302	GAAGCCCATAACCTCATCAGCGTACTGGAGAAGCGCATAGACACCCTCAAGAA	889 1243
	888 1242	3 GAAAAGAAGATTGTACCAGGCCCAGTACGACCTGTCCATCTATAACAACAGCTTGAA 	829 1183
	828 1182	GAGCTGATCGAAGAATCCAAAAAGACCATAGACAAAAATAAGAATGCAACCAA	769 1123
	768 1122	9 AATGTGGGAAAGATGGAAGATTATATTAAAAAGAATAAGAAG	709 1063
	1062	3 TTAGACGTACTTAAAAAACTTGTGTTCGGATATAGAAAACCATTAGACAATATTAAAGAT	100:

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2721GCCCGAAGTGAGGGCTAACGACGACACCTCTCACTCGACCAACCTTAATAACTCA 2775	Qy
3097 CAAAACCAACAATCAAATCCATCCTCTACCAATACCCAAAAATGGTGTAGCTGTATCATCT 3156	Db
2682 CAGCTCCATGCACCTGTCTCTCACACCTCAAGACAA 2720	Qy
3037 ACATCCAGTCCTGGAAATACAACCGTAAATACTGCTCAATCCGCAACTCACAGTAATTCC 3096	рь
2658CACCTCTGTTAAAACTCTCTCTTC 2681	Qy
2977 GAGGAAAATCACATCAAAAAATTATTAGAGGAGCAAAAAAAA	Db
2611 GACAACGACAAGATTAAGAACCTTCTGGAGGAAGCTAAGAAGGTCTC 2657	Qy
2917 CAACATCTCTTTTTGAATTATCAAAAAGGAAATGATTATTATTTACATAAACTAAAA 2976	Db
2551 TCTCAACTGTTCATGGAGATATATGAGAAGGAGATGGTCTGCAACCTGTATAAACTCAAA 2610	Qу
2857 AATATTCAAAATAACATACCTGCTATGTATTCATTATATGATAGTATGAACAATGATTTA 2916	Db
TATGTTCGATAGCCTC	Qy
2797 AATCTTACTCCAGAAGAAGAAATGAATTAAAATCATGTGATCCATTAGATTTATTATTT 2856	Db
2431 AAGATAACCAAGGAAGAAGGAGAAGTAAACTGTCCTCTTTGTGATCCACTGGACCTGCTGTTC 2490	Qy
2737 TGTCATAAATATATTTTAGTATCAAACTCTAGTATGGACCAAAAATTATTAGAGGTATAT 2796	DЬ
2371 TGCCACAAATATATCCTCGTCTCTCACAGCACTATGAACGAGAAGATTCTTAAACAGTAC 2430	Qy
2677 GCCTTGACAAAAACAGTTTATCTAAAAGAAATTAGATGAATTTTTAACTAAATCATATATA 2736	Db
2311 AATGTCAGCAAACTGGACTACCTTGAGAAGCTCTATGAGTTCCTGAATACATCCTACATC 2370	Qy
2617 CCAAAAGAAGTTAAAAGTTGAAAAATTCAATAGAACATAAGAGTAATGACAATTCACAA 2676	Db
	Qy
2557 GAAACAGAAGAAACAGAAGAACAGTAGGACACAACAACGACAACAACAATAACATTACCA 2616	Db
2191 GATAGCGTGCAAGCTCAAGCACAAGAGCAGAAGCAGGCACAGCCTCCAGTGCCAGTGCCC 2250	Qy
2498 AAGAT-GGGGGTCACTCCACACACACATTATCCCAATCAGGAGAAACAGAACTAACAGAA 2556	DЬ
2131 GAGATAACCGGACAGGCTACCACCAAGCCCGGACAACAGGCCGGTTCAGCTCTCGAAGGC. 2190	Qy
2438 AAGAACAAGCTGTCTTATÇAAGTATTACACAACCTTTAGTTGCAGCAAGCGAAACAACTG 2497	рь
2071 GAGAAGAACATTAAAACTGAAGGACAGTCAGATAACTCCGAGCCTTCCACAGAAGGA 2130	Qy
2380 AAAAAAGAAGTAGATAAATTAAAAGAATTTATACCAAAAGTAAAAGACATGTTAAAGA 2437	Db
2011 AAGAAAGAGATAGACAAACTGAAAGTGTTCATGCCCAAAGTCGAGAGCCTGATCAACGAA 2070	Qy
2320 CATGTACCAAATATTTATĄAACCACAAAATAAACCAGAACCATATTATTTAATTGTATTA 2379	Db
1951 CATGTGCCGAATAGTTATĀAGCAGGAGAATAAGCAGGAACCATACTACCTCCATCGTACTC 2010	Оy
2260 ATAGAAGACTTAAGAAGĀTAGAATTATTTTTAAAAAATGCACAACTAAAAGATAGTATT 2319	Db
1891 ATTGATGAACTCAAGAAGACTCAACTCATTCTGAAGAACGTGGAGTTAAAACATAATATA 1950	Qy
2200 TCCTTAGAAGTATATGATATTGTAAAATTACAAGTACAAAAAGTTTTATTAATTA	Db ·
1831 ATCCTGGAGGTCTCCGATATTGTTAAAGTCCAAGTGCAGAAGGTGCTCCTCATGAACAAG 1890	Qy
2143 AGTGAAAACAAAATTCTAGAAAAAAATTTTAAAGGACTAACACATTCAGCAAATGCT 2199	Db
1771 GATGAAGAACAGTTGTTTGAGAAGAAGAATAACAAAGACGAAAATAAACCAGATGAGAAG 1830	VΩ

3873	3814 GTGATTGATAACATTCTGTCCAAAATCGAGAACGAATACGAAGTGCTCTATCTGAAACCT	Qy
4290	4234 TCCGAAGATAATGACGAATATTTAGATCAAGTAACTGGAGAAGCAATATCTGT	Db
3813	3754 AGCGAGGAGGACTACGATGACCTCGGCCAGGTGGTCACCGGTGAGGCTGTCACTCCTTCC	Qy
23	41	B .
75	3694	Q V
3693 4173	3642 ACCTAAGAAGCCTGCATCTACTCATGTCGGAGCCGAGTCCAATACAATTACC	ρ Q
4113	4054	В
3641	3597CACTGTGGTGTGTCTGAATCTGGCTCCGACACTCTGGAGCAGTCTCA	Qy
20	3994	Db -
59	3553 CTGGAATCTTACAAGAAGTTCCTGCCTGAAGGAACAGATGTCGC	Qy
3993	3433 ANAMAKANGANCITACANCGGANTAGUCUCANGGANGHATINATKUGACGIGAATTAACGGA 1	B &
93	3874 AAATTATCTTTCTTATCAAGTGGATTACATCATTTAATTACTGAATTAAAAGAAG	D D
3492	343	Qy
3873	3814 TTTAGAGTATAAGTAAAATAGATGGAAAACTCAATGATAATTTACATTTAGGAAAGAAA	рь
3432	3373	Qy
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$\frac{3}{2}$	3253 AAGATTCTTCTCAAACACTACAAAGGCCTCGTCAAGTATTATAATGGCGAGTCTTCTCC	Qy
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ν ⊢	3133 CTTGAAAGCAAACTCAACTGAACATCCGAAACGTACTGCAGAACTTCTCAGTG	3 8
3573	_	Db
3132	3073 AAGAAGACAGTCGGCAAGTATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGC	Qy
51		Ър
3072	3013 CAACTGAGCTTCGACCTGTACAACAAGTACAAACTGAAACTGGAGAGACTCTTCGAC	Qy
3453	2933 ARCUATUCHATUTHAACUTHAGARCCTIGGARGAGGACTICAATRAGCTIGAAGAAGACACTIC 1	B 5
	333/ INIIIIAAIGHIGHIHICAAACANIICGIAAAAICTAATTCAAAAGTAATTACAGGT	2
95	2893 TTCTATAACGAGAGCTTCACTAACTTCGTGAAATCTAAAGCCGATGATATCAACTCTC	ş 8
ω		р ;
2892	2833 CTTATTGGACAGAAATCGTCCGAGAACTTCTACGAGAAGATACTGAAAGACAGCGACAC	Q V
2832 3276	2776 CTGAAACTGTTTGAGAACATCCTGTCTCTGGCAAGAATAAGAACATCTACCAAGAA	Qy Db

4893	TATCCACTCTTCGACGGGATTTTTTGCTCCAGCTCTAATTTCCTGGGCATCTCCTTCCT	4834	Qy
5367	TCAGGTAGCAACGGAAAGAAATCACATGTGAATGTACTAAACCTGATT	5308	рь
4833	AGG	4774	Qy
4773 5307	AACCCAAACCCTACCTGCAATGAAAACAATGGCGGGTGTGACGCCGATGCTAAATGCACC	4714 5248	Qy Дъ
4713 5247	GAGATAAGTGCGTC	4654 5188	Оу
4653 5187	CAGCACCAATGCGTGAAGAAACAGTGCCCCCAGAATAGCGGCTGTTTCAGGCATCTGGAC	4594 5128	Оу
4593 5127	GCCAAAACAGTGCTGAGCAATCTGCTCGACGGCAACCTGCAGGGCATGCTGAACATCTCC	4534 5068	Qу
4533 5067	TATAACCACAACAATCTCCTGACCAAGTTTCTGTCCACTGGCATGGTGTTCGAAAACCTC	4474 5011	ОУ
4473 5010	AAGCTGGCAGATTTCAAGAAAAATAACAATTTCGTCGGAATTGCAGACCTGTCTACCGAT	4414 4951	Qy
4413 4950	GAGAAGAGCAATGTGGAAGTTAAAATCAAGGAGCTGAACTACCTCAAAACAATCCAAGAC	4354 4891	Оy
4353 4890	AACGACAAAATCGACCTCTTCGTAATTCACCTGGAGGCCAAGGTCCTCAACTATACTTAC	4294 4831	Qу
4293 4830	GGCGAGAATGAAAATATCTGCCCTTCCTGAATAACATCGAAACCCTGTACAAGACAGTG	4234 4771	Оу
4233	GAGAAGTTCCCCATCACCACCCACCAACAACACCTCCGTCACCAGCAAAAACAGACGAACAA	4231 4711	Db
, μ ω	TGAGCGAAAAATACAAGTCTGACCTTGACTCTATTAAAAAGTATATCAACGATAAG-		Оу
4173 4650	> ->		Qy Db
4113 4590	CCATACAAGTTCCTCAATAAAGAGAAGAGGGATAAATTTCTGTCTAGTTACAACTATATC	4054 4531	Оy
4053 4530	TTGGAGAGCGACTTGATTCCCTATAAAGACCTGACCTCCTCTAACTACGTTGTCAAGGAC		Qy Db
3993 4470	GTCAACGTGAAGGACATTCTGAACAGCCGCTTTAATAAGAGAGAAAATTTCAAGAACGTC	3934 4411	Qy
3933 4410	CTGGCAGGCGTCTATAGGTCTCTCAAGAAACAGCTGGAGAATAACGTGATGACCTTCAAT	3874 4351	Оy
4350		4291	Db

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KEYWORDS
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                                                                              GTGACCCACGAATCCTATCAGGAGCTGGTTAAGAAACTGGAAGCTTTGGAAGATGCCGTC
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ACAGCTGTTACAACTACTACACCTGGTTCAAAGGGTTCAGTTGCTTCAGGTGGTTCAGGT
                                        ACGGCCGTTACAACCAGCACACCCGGTTCTAAAAGGGTCTGTGGCTAGCGGTGGCTCCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 1968)
Li,X.R., Liu,S.C., Chishti,A.H. and Oh,S.S.
Direct Submission
Submitted (04-FEB-2002) Section of Hematology/Oncology Research,
St. Elizabeth's Medical Center, Tuft's University School of
Medicine, 736 Cambridge Street, Boston, MA 02135, USA
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L1, X.R., Liu, S.C., Chishti, A.H. and Oh, S.S.
83 kba subfragment of MSP-1 gene of Plasmodium
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D13357
D13357.1
Jongwutiwes, S.
Direct Submission
Submitted (05-OCT-1992) Somchai Jongwutiwes, Institute of Tropi
Medicine, Nagasaki Univ., Dept. of Protozoology; 12-4
Sakamoto-machi, Nagasaki 852, Japan (Tel:0958-47-2111(ex.3747),
                                                                                                                                 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium 1 (bases 1 to 1636)
Jongwutiwes, S., Tanabe, K. and Kanbara, H.
Sequence conservation in the C-terminal part of the precurso
                                                                                                                                                                                       EGF-like domains; major merozoite surface protein Plasmodium falciparum (isolate 806) merozoite, DN2 Plasmodium falciparum
                                                                                  the major merozoite surface proteins (MSP1) of Plasmodium falciparum from field isolates Mol. Biochem. Parasitol. 59 (1), 95-100 (1993) 93295445
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12-4 Sakamoto-machi
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Institute of Tropical Medicine
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/translation="PLKTLSEESIQTEDNYASLENFKYLSKLEGKLKDNLNLEKKKLS
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EGF-like domains;
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Mol. Biochem. Parasital
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Phone:
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Department of Protozoology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (05-OCT-1992) Somchai Jongwutiwes, Institute of Tropical Medicine, Nagasaki Univ., Dept. of Protozoology; 12-4 Sakamoto-machi, Nagasaki 852, Japan (Tel:0958-47-2111(ex.3747), Fax:0958-47-6607)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum (isolate 808) merozoite, DNA.
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Direct Submission
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12-4 Sakamoto-machi
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JOURNAL MEDLINE REFERENCE KEYWORDS SOURCE ORGANISM RESULT 20 PFAMSP828 COMMENT REFERENCE VERSION ACCESSION DEFINITION AUTHORS TITLE AUTHORS TITLE JOURNAI Jongwutiwes, S.
Direct Submission
Submitted (05-CCT-1992) Somehai Jongwutiwes, Institute of Tropical Submitted (05-CCT-1992) Somehai Jongwutiwes, Institute of Tropical Medicine, Nagasaki Univ., Dept. of Protozoology; 12-4
Sakamoto-machi, Nagasaki 852, Japan (Tel:0958-47-2111(ex.3747), Jongwutiwes, S., Tanabe, K. and Kanbara, H. Sequence conservation in the C-terminal part of the the major merozoite surface proteins (MSP1) of Plasm falciparum from field isolates
Mol. Biochem. Parasitol. 59 (1), 95-100 (1993) PFAMSP828

P. falciparum DNA for the precursor to the major merozoite proteins, C-terminal.

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13360.1 GI:391798

EGF-11ke domains; major merozoite surface protein precursor plasmodium falciparum (isolate 828) merozoite, DNA.

Plasmodium falciparum Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium (isolate 828) Fax:0958-47-6607) Submitted (05-OCT-1992) Somchai Jongwutiwes Department of Protozoology (bases 1 to ţ DDBJ by: Plasmodium precursor INV 29-MAY-2002

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Nagasaki University 12-4 Sakamoto-machi Institute of Tropical

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EECKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDS
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Mol. Blochem. Parasitol. 59 (1), 95-100 (1993)
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D13362
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EGF-like domains; major merozoite surface protein
Plasmodium falciparum (isolate 837) merozoite, DNA
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Submitted (05-OCT-1992) to DDBJ by:
Somchai Jongwutiwes
Department of Protozoology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jongwutiwes, S.
Direct Submission
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                                                                                                                                                                                                                                                                                 Mol.
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                                                                                                                    Somchai Jongwutiwes
Department of Protozoology
Institute of Tropical Medicine
                                                                                                                                                                                 Submitted (05-OCT-1992) Somchai Jongwutiwes, Institute of Tropical Medicine, Nagasaki Univ., Dept. of Protozoology; 12-4 Sakamoto-machi, Nagasaki 852, Japan (Tel:0958-47-2111(ex.3747),
                                                                                                                                                                                                                                                                                   the major merozoite surface proteins (MSPI) of Plasmodium falciparum from field isolates
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Jongwutiwes, S., Tanabe, K. and Kanbara, H.
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                                                                                                                                                          Submitted (05-OCT-1992) to DDBJ by:
                                                                                                                                                                         Fax:0958-47-6607
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                                                                                                       Nagasaki University
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ATAAGAGAGAAATTTCAAGAACGTCTTGGAGAGCGACTTGATTCCCTATAAAGACCTGA
                                               TAGAAAATAACGTTATGACATTTAATGTTAAGGATATTTTAAATTCACGATTTA
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NLITKELSTGKVFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQNSGCFRHLDER
EECKCLLNYKOLGDKCVENPNFTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDS
YPLFDGIFCSSSNFLGISFLLILMLILYSFI"
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/tsrclhhllaelkeyiknknytgnspsynnyddynnalesykkflpectdvaptyvses
gsdtleqsqpkkpasthygaesttittsqnvddevddvi ivpifgeseedyddlgvy
tgeavtpsyidnilskieneyevlylkplagvyrslkkqlennymtenynvkdilnsr
fnkremfknylesdllpykdlyssnyvvkdpykflnkekrdkflssynyikdsldtd
nfandvlgyykilsekyksdldsikkyindkqgenekylpflnnietlyktyndkidl
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/protein_id="BAA02617.1"
/db_xref="GI:391825"
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/chromosome="9"
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Direct Submission
Submitted (05-0CT-1992) Somchai Jongwutiwes, Institute of Tropical Medicine, Nagasaki Univ., Dept. of Protozoology; 12-4
Medicine, Nagasaki 852, Japan (Tel:0958-47-2111(ex.3747),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D13361
D13361.1 GI:391800
D13361.1 GI:391800
EGF-like domains; major merozoite surface protein precursor.
Plasmodium falciparum (isolate 834) merozoite, DNA.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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NFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDL
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/tlsSGLHLIAELKEVIKNKNYTGNSPSUNDDEVDDVIJVFTGESEEDDDDLGVV
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TGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSR
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/protein_id="BAA02622.1"
/db_xref="GI:391801"
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/db_xref="taxon:5833"
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                                                 CCACTGGCATGGTGTTCGAAAAACCTCGCCAAAAACAGTGCTGAGCAATCTGCTCGACGGCA
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EGF-like domains; major merozoite surface protein precursor.
Plasmodium falciparum (isolate 844) merozoite, DNA.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 1636)
Jongwutiwes, S., Tanaba, K. and Kanbara, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P. falciparum DNA for the precursor to the
                                                                                                                                                                                                                                                                                                                                                           Submitted (05-OCT-1992) Somchai Jongwutiwes, Institute of Tropical Medicine, Nagasaki Univ., Dept. of Protozoology; 12-4
Sakamoto-machi, Nagasaki 852, Japan (Tel:0958-47-2111(ex.3747),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence conservation in the C-terminal part of the the major merozoite surface proteins (MSPI) of Plasm falciparum from field isolates
MOI. Biochem. Parasitol. 59 (1), 95-100 (1993)
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12-4 Sakamoto-machi
                                                                                                                                                                                                                                                                                           Department of Protozoology
                                                                                                                                                                                                                                                                                                             Somchai Jongwutiwes
                                                                                                                                                                                                                                                                                                                             Fax:0958-47-6607)
Submitted (05-OCT-1992) to DDBJ
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               /gene="MSP1"
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                                                                                   /organism="Plasmodium
/db_xref="taxon:5833"
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ACCESSION VERSION KEYWORDS SOURCE RESULT 25 PFAMSP8222 LOCUS DEFINITION

REFERENCE

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ORGANISM proteins, C-terminal.

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13359.1 GI:391796
EGF-like domains; major m
Plasmodium falciparum (is
Plasmodium falciparum
Eukaryota; Alveolata; Api
1 (bases 1 to 1636) PFAMSP8222 P. falciparum DNA for the or merozoite surface (isolate 822/2 and 8 1636 bp precursor DNA r to the e protein 827) merc linear major m merozoite, r INV 29-MAY-2002 merozoite surface

Apicomplexa;

Haemosporida;

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Submitted (05-0CT-1992) Somehai Jongwutiwes, Institute of Tropical Medicine, Nagasaki Univ., Dept. of Protozoology; 12-4
Sakamoto-machi, Nagasaki 852, Japan (Tel:0958-47-2111(ex.3747),
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12-4 Sakamoto-machi
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Department of Protozoology
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Submitted (05-OCT-1992)
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FNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSKYNYIKDSIDTDI
NFANDVLGYYKILSEKYKSDLDSIKKYINDBKQGENEKYIPFLNNIETLYKTVNDKIDL
EVIHLEAKVLNYTYEKSNYEVKIKELNYLKTIQDKLADFKNNNETGLADLSTDYNNN
NLLTKFISTGMYFENLAKTVLSNLLDGNLQGMLNISGHGCVKKQCPQNSGCFHILDER
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/codon_start=3
/product="major merozoite surface
/protein_id="BAA02620.1"
/db_xref="GI:391797"
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Olafsson,P., Matile,H. and Certa,U. Plasmodium falciparum: the repetitive MSA-1 surface protein RO-71 isolate is recognized by mouse antibody against the nonrepetitive repeat block of RO-33 Exp. Parasitol. 74 (4), 381-389 (1992)
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                                                                                                                                                          Certa, U., Rotmann, D., Matile, H. and Reber-Liske, R. A naturally occurring gene encoding the major surf precursor p190 of Plasmodium falciparum lacks trip EMBO J. 6 (13), 4137-4142 (1987)
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p190 gene; variable surface antigen.
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/isolate="RO-33 Ghana"
/db_xref="taxon:5833"
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                               GCAAGCGGCGGTTCCGGGAACAGTCGAAGAACCAATCCATCTGACAACTCTAGCGATTCC
                                                                                                  TCTGTGGCCTCTGGGGGTTCCGTCGCCTCCGGCGGCAGCGTGGCATCAGGTGGCTCAGTG
                                                                                                                                    GTTGTTGCAAAGCCTGCAGATGCTGTAAGTACTCAAAGTGCTAAAAATCCTCCAGGTGCT
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                                                                   ACAGTACCTTCAGGTACTGCAAGTACTAAAGGTGCTATAAGATCTCCAGGTGCTGCA - - -
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PYPRGIVYPLPLTDIHUSLAADUDKUSYGDLANDHTKEKIVEKIITDUKERKIFINNI
KKOIDLEEKNINHTKEONKKLLEDYEKSKKDYEELLEKY EMKENINHINDVYDKIFINNI
KKOIDLEEKNINHTKEONKKLLEDYEKSKKDYEELLEKY EMKENINHINDVYDKIFS
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GLEADIKKLTEEIKSSENKILEKNFKGLTHSANASLEVSDIVKLOVOKVLLIKKIEDL
RKIELFLKNAOLKDSIHVPNIYKPONKPEPYVLIVLKKEVDKLKEFIPKVKDMLKKEO
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SGPAVVEESHDPLTVLSISNDLKGIVSLULGNKTKVENPDLTISTTEMEKFYENILKI
MIPIFNDDIKOFVKSNSKVITGLTETOKNALNDEIKKLKDTLOLSFDLYNKYKLKLDR
LFNKKELGODKMOIKKLTTLLKEQLESKLNS"
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3247. 3270
/note="results in a single point frame to KI; frameshift mutation a 430 c 437 g 1081 t
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337. .>351
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LFQKEKWULKGGANTQVVAKPADAVSTGSAKNPPSGTASTKGAIRSFGANPS
DDSSDSDAKSYADLKREVQNYLFTIKELKYPELFDLTNHMLTLCDNIHGFKYLIDFYE
EINELLYKLNFYFDLLRAKLNIVCANDYCQIFFNLKIRANELDYLKKLVFGYRKFLDF
EINELLYKLNFYFDLLRAKLNIVCANDYCQIFFNLKIRANELDYLKKLVGAYDLFIY
IKDNVGKMEDYIKKNKTTIANINELLEGSKKTIDQNKNADNEEGKKKLYQAYDLFIY
IKDNVGKMEDYIKKNKTTIANINELLEGSKKTIDQNKNADNEEGKKKLYQAYDLFIY
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/note="MAD20 mRNA"
266. >3518
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203. .>3518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="This frameshift results in 11 new amino acids present in MAD-20 or K1; frameshift mutation FS-1"
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               ATAACATTAAAAAACAAATTGATTTAGAAGAAAAAAACATTAATCACACAAAAGAACAAA 1738
                                                                                  ATAATTCATTAGCTGCAGATAATGATAAAAAATTCATATGGTGATTTAATGAATCCTCATA 1618
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AGAGTAAACTGTCCTCTTGTGATCCACTGGACCTGCTGTTCAATATCCAGAACAACATTC
                                                                                                                         TATCAAACTCTAGTATGGACCAAAAATTATTAGAGGTATATAATCTTAC---TCCAGAAG
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                                         AAAATGAATTAAAATCATGTGATCGATTAGATTTATTATTTAATATTCAAAATAACATAC
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ORGANISM
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DEFINITION
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PFP190G
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TITLE
Query Match
Best Local Similarity 56.1
Matches 1511; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (09-NOV-1987) Ulrich 2FE, Grenzacher Str. 124, 4002 (bases 1 to 3518)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A naturally occuring gene enc
precursor P190 of plasmodium
EMBO J. 6 (1987) In press
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                                                                                                                                                                                                                    /translation="MKI IFFICSFLFF | INTQCVTHESYQELVKKLEALEDAVLTGYS
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DSSDSDÁKSYADLKHRVONYLFT I KELKY PELFEDLTNHMLTLCDNI HGFKYLLOGYE
EINELLYKLNEY FDLLKAKLNDYCANDYCQI PFNIKI RANELDULKKLVFGY RKPLDF
IKDNYGKMEDY IK KNRTT I ANINELI EGSKKTI LOOKNANDEEGKKKLVQAOYDLFIY
NKQLQEAḤNILI SVLEKRIDTILKK NENIKKLLEDIDK IK IDAEK PTTGVNQI LS LRLEK
ESRHEEK İKEJAKT I KENIDRLETDPLELEYYLREKNKKVDYTEKSQDPTKSQQIPKV
PYPNGI VYPLPLTDI HNSLAADNDKNSYGDLANPHTKEKI NEK I ITDNKERK I FINNI
KKQI DLEEKNINHTKEONKKLLEDY EKSKKVEELLEK YE EMKFNINHNKOVDKIFS
ARTYYLVKEÇQAY NIKTESSANUSYYNVQKLKALISYLEDY SLIKGI SEKDENHYYTLKT
GLEADIKKLTEEI KSSENK I LEKNFKGLTHSANASLEVSDIVKLQVQKVLLIKK IEDL
RKI ELFLKNAOLKDSIHVPNIYKPONKPEPYYLLVKKEVDKLKEFI PKVVDMLKKEQ
AVLSSITOPLVAASETTEDGGHSTHTLSQSGETEVETSETEETVGHTTTVTITITLDRKEV
KVVENSI EHKSNDNSQALTKTVVLKKLDEFLTKSY I CHKY I LVSNSSMDQKLLEVYNL
TPEENBELKSCORLDLLENIQNIN PAMYSCLYDSNNNDLOHLFFELYQKEMIYYLHKKE
PROTECTOR GEGENTOWNEN OF THE NOOLOGEN SCENNTONIONE
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/clone="RO-33/1"
337. .>3518
                                                                                                                                   MIPIFNDÐIKOFVKSNSKVITGLTETOKNALNDEIKKLKDTLQLSFDLYNKYKLKLDR
LFNKKKELGQDKMQIKKLTLLKEQLESKLNS"
                                                                                                                                                                                  ENHIKKLLEEPKQITGTSSTSSPGNTTVNTAQSATHSNSQNQOSNASSTNTQNGVAVS
SGPAVVEËSHDPLTVLSISNDLKGIVSLLNLGNKTKVPNPLTISTTEMEKFYENILKI
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/db_xref="SWISS-PROT:P19598"
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in codon)"
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/strain="Ro-33"
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Score 711.8;
Pred. No. 1.6e
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8; DB 3;
1.6e-145;
hes 1072;
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parum lacks tripeptide
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1147 1438	1088 CCATTAAGTTCAACATAGATTCTCTCTTTACTGATCCCCTTGAGCTGGAGTACTACTTGA.	Db Qy
1087 1378	1028 TGCTGGACAAGAACAAGAAGATAGAGGAGCACGAGAAAGAGATCAAAGAGATCGCCAAAA	Qy
1027 1320	970 AAGATTAATGAAATTAAGAATCCTCCGCCAGCCAACTCTGGGAACACCCCTAACACGC	Оу
969 1260	910 GTACTGGAGAAGCGCATAGACACCCTCAAGAAGAATGAAAAATATCAAAGAACTGCTCGAC	Db Qy
909 1200	50 GCCCAGTACGACCTGTCCATCTATAACAAACAGCTTGAAGAAGCCCATAACCTCATCAGC	рь
849 1140	90 AAGACCATAGACAAAATAAGAATGCAACCAAGGAGGAAGAAAAGAAGAAGTTGTACCAG 	B 8
789 1080	730 TATATTAAAAAGAATAAGAAGACCATCGAGAACATTAACGAGCTGATCGAAGAATCCAAA	Оy
729 1020	670 GTCTTCGGATATCGCAAGCCTCTCGACAACATCAAGGACAATGTGGGAAAGATGGAAGAT	Фр
960	610 TGTCAAATTCCATTCAATTTGAAGATCAGAGCCAACGAGTTGGACGTATTGAAGAAGTTG	Оy
900	550 TTGAATTTCTACTTCGACTTGCGAAGGGCCAAACTGAATGACGTTTGCGCCAATGACTAT	B 6
549 840	490 ATTCATGGCTTCAAATATCTGATTGACGGTTACGAAGAGTCAATGAACTCCTGTACAAG	рb
489 780	AAC H AAT	ρ Q
429 720	0 GACGCCAAGTCCTACGCCGACCTCAAGCACCGAGTGAGAAACTATCTCCTCACTATCAAG 	Db Qy
369 660	10 GCAAGCGGCGGTTCCGGGAACAGTCGAAGCAATCCATCTGACAACTCTAGCGATTCC 	B 6
ū c	TO INTERPOLET TO BOOK TICK OF THE CONTROL OF THE CO	B 5
249 576	U GCCGTTACAACCAGCACCAGCTCTAAAAGGGTCTGTGGCTAACGGTGCTCCGGTGGG	B 6
₽ 8	30 ACCGGATACAGCCTGTTCCAGAAGGAGAAGATGGTGCTGAATGAA	Db Oy
129 456	70 ACCCACGAATCCTATCAGGAGCTGGTTAAGAAACTTGGAAGCTTTGGAAGATGCCGTCCTT	оу В
396	7 ATGAAGATCATATTCTTTTTATGTTCATTTCTTTTTTTTT	DЪ

150 CCACCAAGCCCGACAACAGGCCGGTTCAGCTCTCGAAGCGATIAGCGTCCAAGCTCCAAG 10		Qy Db
	1 (
990 CTGAAGGACAGTCAGATAACTCCGAGCCTTCCACAGAAGGAGAGAGA	2090	70 VG
)30 TGAAAGTGTTCATGCCCAAAGTCGAGAGAGACCATGATCAACGAAGAAGAAGAAGAACATTAAAA 2089 	2030 2336	Qy Db
970 AGCAGGAGAATAAGCAGGAACCATACTACCTCATCGTACTCAAGAAAGA	1970 2271	Qy Db
	1910 2216	Db Qy
0 TTGTTAAAGTCCAAGTGCAGAAGGTGCTCCTCATGAACAAGATTGATGAAGCACAGAGAGA 19 	1850 2156	ДУ
AGAAGAAGATTAAAAAAAGACGAAAATAAACCAGATGAGAAGATCCTGGAGGTCTCCGATA 1 1 1 1 1 1 1 1 1 1	1790 2099	Qy db
TCGAAAACGAGATCGAGACGCTTGTTGAGAACATTAAGAAGGATGAAGAACAGTTGTTTG 1	1730 2039	ду Оу
70 CTCTGCGGAACATTGTTGTGAAGAAGAACTAAAGTATTACAAGAATCTCATAAGTAAG	7	dd Vo
AGAATTCTAAGCATAATCTTGAGAAGCTCACCAAAGCTCTTAAGTATATGGAGGACTATT 16	1610 1919	Db Qy
350 GAAAACGGTACTCTTACAAAGTGGAGAAACTGACACACAC	185	Qy Db
AGATCTATGATTCCAAATTCAACAATAACATCGACCTGACCACCTTCGAGAAAATGATGG 15	99	Qy Db
ACGAAGACCGCAGCAAAAGTCTAAACGATATCACTAAAGAGTATGAAAAGCTGCTGAACG 14	1430 1739	Qy da
	1370 1679	Qy Db
ATTATACGAAAGAACCCTCTAAGAATATCTACACAGACAATGAGAGAAAGAA	1310 1619	Qy Db
	1259 1559	Qy Db
199 CAACCGAACCTAATGAATATCCCAATGGTGTGACGTACCCTCTGTCTTATAACGATATCA 1258 	1199 1499	Qy Db
148 GAGAAAGAATAAGAATATKAGCATCTCCGCCAAAGTCGAGACAAAGAAT 1198 	1439	рь

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REFERENCE
AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                  Blackman,M.J., Ling,I.T., Nicholls,S.C. and Holder,A.A. Proteolytic processing of the Plasmodium falciparum merozoite surface protein-1 produces a membrane-bound fragment containing epidermal growth! factor-like domains
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Plasmodium falciparum
Bukaryota; Alveolata; Apicomplexa; Haemosporida;
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 MLILYSFI"
1. .72
                                                                                    /product="merozoite surface protein 1"
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                                                                                                                                                                                                                                /gene="MSP1"
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/db_xref="taxon:5833"
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Best Local Similarity
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42 kDa s
isolate
                                                                                                                                                                                                                                                             Submitted (04-DEC-2000) Section St. Elizabeth's Medical Center, Medicine, 736 Cambridge Street,
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Plasmodium
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AF325919
AF325919.1 GI:1275139
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Direct Submission
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         /product="merozoite surface protein 1"
/protein_id="AAK07641.1"
/protein_id="AAK07641.1"
/db_xref=="Gi:12751399"
/translation="AVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTF
/translation="AVTPSVIDNILSKIENEYEVLYSKYVKDPYKFLNKEKROKENLSSY
NVIKDSIDTDINFANDVLGYVKILSEKYKSDLDSIKKYIDDKOGENEKYLPFLNNIET
LYKTVNDKIDLEVIHLEAKVLMYTYEKSNVEVKIKELMYLKTIODKLADFKKNNNEVG
IADLSTDYNHNNILTTKELSTGMYFENLAKTTLSNILDGNLQGMLNISQHQCVKKQCPQ
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                                                                                                                   /gene="MSP-1"
/codon_start=1
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/isolate="FCB-1"
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Tuft's University School
Boston, MA 02135, USA
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                                                                          CTGTACAAGACAGTGAACGACAAAATCGACCTCTTCGTAATTCACCTGGAGGCCAAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                           GATGCTARATGCACCGAGGAAGACAGCGGCTCTAACGGAAAGAAATCACATGCGAGTGT 4818
                                                                                                                   ATGCTGAACATCTCCCCAGCACCAATGCGTGAAGAAACAGTGCCCCCCAGAATAGCGGCTGT
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                     GATAAATGTGTTGAAAATCCAAATCCTACTTGTAACGAAAATAATGGTGGATGTGATGCA
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                                                                                                                            AGTTATAATTATAAGGATTCAATAGATACGGATATAAATTTTGCAAATGATGTTCTT
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Plasmodium falciparum (strain Vietnam Oak Knoll)

Plasmodium falciparum

Eukaryota; Alveolata; Apicomplexa; Haemosporida;

1 (bases 1 to 1065)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Louis-Wileman, V., Shi, Y., Collins, W. and Lal, A. Primary amino acid sequence of the carboxyl-terminal region of the merozoite surface protein (MSP-1) of plasmodium falciparum Vetnam Coak knoll (PVO) strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFASURFPRO 1065 bp DNA linear INV 26-JI Plasmodium falciparum merozoite surface protein (MSP-1) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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Similarity 74.2%;
88; Conservative
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/db_xref="taxon:5833"
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                                                                                                                                                                                          Plasmodium falciparum
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; F
1 (bases 1 to 999)
1 (bases 1 to 999)
Jongwutiwes, S., Tanabe, K., Nakazawa, S., Yanagi, T.
Sequence variation in the tripeptide repeats and opigo (MSA-1) of Plasmodium falciparum from field minchem, Parasitol. 51 (1), 81-89 (1992)
                                                                                                                                                                                                                                                                                                                                                       999 bp
Plasmodium falciparum clone 808
(p190) gene, partial cds.
M77715
                                                                                                                                                                                                                                                                                                                                                    (p190) gene,
M77715
                                                                                    University, Ramad, Pathumwan, on May 21, 2002 this sequence
                                                                                                                                                                                                                                                                                                         T-cell epitope; major merozoite Plasmodium falciparum.
                                                                                                               Submitted (21-MAY-2002)
                                                                                                                                Direct Submission
                                                                                                                                              2 (bases 1 to 999)
Jongwutiwes,S.
                                                                                                                                                                                                                                                                                                                                       M77715.2 GI:2104|0168
                                                                                                                                                                            1373473
/organism="Plasmodium f
/db_xref="taxon:5833"
/map="9"
/clone="808"
                                                                          Location/Qualifiers
                                                             .999
                                                                                      Faculty of Medicine, Chulalongkorn
umwan, Bangkok 10330, Thailand
quence version replaced gi:309698.
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             GAGCTGATCGAAGAATCCAAAAAAGACCATAGACAAAAAATAAGAATGCAACCAAGGAGGAA
                                                                                                                             GATGTATGTGCTAATGATTATTGTCAAATACCTTTCAATCTTAAAATTCGTGCAAATGAA
                                                                                                                                                                                                                                           GACGTTTGCGCCAATGACTATTGTCAAATTCCATTCAATTTGAAGATCAGAGCCAACGAG
                                                                                                                                                                                                                                                                                        ATCAATGAACTCCTGTACAAGTTGAATTTCTACTTCGACTTGCTAAGGGCCCAAACTGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                         AACTATCTCCTCACTATCAAGGAGCTGAAGTACCCACAGTTGTTCGACCTCACTAATCAT
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GAAAAAAAAATTATACCAAGCTCAATATGATCTTTCTATTTACAATAAACAATTAGAA
                                                       GAATTAATTGAAGAAAGTAAGAAAACAATTGATAAAAATAAGAATGCAACTAAAGAAGAA
                                                                                                                 ATGTTAACTTTGTGTGATAATATTCATGGTTTCAAATATTTAATTGATGGATATGAAGAA
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/product="major merozoite surface antigen"
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/db_xref="GI:21040169"
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LLTIKELKYPOLFDLYNMLTLCDN1HGFKYLLDGYEEINELLYKLMFYFDLLRAKLN
DVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMEDYIKKNKTIEN
INELLESSKKTIDKNKNATKEBEKKKLYGAVULSINKQLEBAHNLISVATKHRNITI"
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1 127 c 159 g 295 t
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<1. .>999
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 99)
Jongwutiwes, S., Tanabe, K., Nakazawa, S., Yanagi, T. and Kanbara, H. Sequence variation in the tripeptide repeats and T cell epitopes pl90 (MSA-1) of Plasmodium falciparum from field isolates MGL. Biochem. Parasitol. 51 (1), 81-89 (1992)
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Plasmodium falciparum clone 827
(p190) gene, partial cds.
M77719
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On May 21, 2002 this sequence version replaced
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KKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNID"
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University, Rama4, Pathumwan, Ba
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodiu
1 (bases 1 to 999)
Jongwutiwes, S., Tanabe, K., Nakazawa, S., Yanagi, T. and Kanl
Sequence variation in the tripeptide repeats and T cell ep
190 (MSA-1) of plasmodium falciparum from field isolates
plachem. Parasitol. 51 (1), 81-89 (1992)
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Direct Submission
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T-cell epitope; major
Plasmodium falciparum.
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/db_xref="taxon:5833"
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Bangkok 10330, Thailand
version replaced gi:309716.
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                                                  University, Rama4, Pathumwan, Sequence update by submitter On May 21, 2002 this sequence
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Plasmodium falciparum
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa;
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M77713
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Plasmodium falciparum clone
                                                                    Submitted (21-MAY-2002) Faculty of Medicine, University, Rama4, Pathumwan, Bangkok 10330,
                                                                                           Jongwutiwes, S.
Direct Submission
                                                                                                                                             Jongwutiwes, S., Tanabe, K., Nakazawa, S., Yanagi, T. Sequence variation in the tripeptide repeats and Sequence variation that tripeptide repeats and 1919 (MSA-1) of Plasmodium falciparum from field Mol. Biochem. Parasitol. 51 (1), 81-89 (1992)
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/db_xref="taxon:5833"
/map="9"
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SGGSVASGGSVASGGSVASGGSVASGGSGNSRFTNFSDNSSDSDAKSVADLKHAVNNY
LLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLLDGYEEINELLYKLNFYFDLLRAKNI
DVCANDYCQIPRNLKIANELDVLKKLVFGYRKPLDNIKDNVCKMEDYIKKNKKTIEN
INELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTL
KKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNID"
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/protein_id="AAA29660.2"
/db_xref="GI:21040165"
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Pramsodium falciparum clone 822B me
(p190) gene, partial cds.
M77718
M77718.2 GI:21040174
T-cell epitope; major merozoite sur
Plasmodium falciparum.
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Submitted (21-MAY-2002) Faculty of Medicine, Chulalongkorn
University, Rama4, Pathumwan, Bangkok 10330, Thailand
On May 21, 2002 this sequence version replaced g1:309703.
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                              Conservative
                                                                                                                                            /codon_start=1
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<1. .>999
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<1. .>999
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/db_xref="taxon:5833"
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                                                11.5%;
73.1%;
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                         Score 568.6; DB 3;
Pred. No. 4.3e-114;
0; Mismatches 269;
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TCTGTGGCCTCTGGGGGGTTCCGTCGCCTCCGGCGGCAGCGTGGCATCAGGTGGCTCAGTG
                                                                          GCCGTTACAACCAGCACACCCGGTTCTAAAGGGTCTGTGGCTAGCGGTGGCTCCGGTGGG
                                                                                                                      ACACATGAAAGTTATCAAGAACTTGTCAAAAAAACTAGAAGCTTTAGAAGATGCAGTATTG
                                                                                                                                                                                  ACCCACGAATCCTATCAGGAGCTGGTTAAGAAACTGGAAGCTTTGGAAGATGCCGTCCTT 129
                                             GCTGTTACAACTAGTACACCTGGTTCAAAGGGTTCAGGTGGCTCAGTTGCTTCAGGTGGT
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Direct Submission
Submitted (22-APR-1998) Molecular Immunology,
Submitted Socinstrasse 57, Basel 4002, Switze
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence diversity of the merozoite surface protein 1 of Plasmodium falciparum in clinical isolates from the Kilombero District,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="mspl"
/note="p190; surface
activity"
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66. .1133
/gene="msp1"
/product="merozoite surface
66. .>1133
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/protein_id="Aac69742.1"
/db_xref="GI:3821979"
/translation="MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYS
/translation="MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYS
LFQKEKMYLNEGTSGTAVTTSTPGSKGSGGSVASGGSGGSGGSVASVASGGSVASVAS
GGSGNSRTINFDUSSSSDAKSYADLKHRVQNYLFTIKELKYPELFDLTNHMLTICDN
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KIVFGYRKPLDNIKDNVGKMEDYIKKNKTTIANINELIEGSKKTIDQNKNADNEEGKK
KLYQAQYNLFIYNKQLQEAHNLISVLEKRIDTLKKNENIKKLLDKINEIKNPPPANSG
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                                                                                                                                                                                                                                                                                                                                                                                    NTPNTLLDKNKKIEEHEEKIKE"
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                                                    AAGATAAATGAAATTAAAAATCCCCCCACCGGCCAATTCTGGAAATACACCAAATACTCTC
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                                                                                                                                                          GCTCAATATAATCTTTTTATTTACAATAAACAATTACAAGAAGCACATAATTTAATAAGC
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RESULT 38 AF286876 LOCUS REFERENCE AUTHORS TITLE SOURCE ORGANISM REFERENCE KEYWORDS VERSION ACCESSION DEFINITION AUTHORS JOURNAL 2 (bases 1 to 1080)
Goel, V.K., Liu, S.-C., falciparum Unpublished Plasmodium Plasmodium (msp-1) mRNA, AF286876 AF286876 Plasmodium 38 Eukaryota; AF286876.1 Eukaryota; Alveolata; falciparum clone NA, partial cds. falciparum falciparum GI:9438194 Chisthi, A.H. MSP-1 gene of Chisthi, A.H. Apicomplexa; 1080 6 bp gene of merozoite and Oh,S. f FCB-1 st and Haemosporida; mRNA Oh, S. strain linear surface of. Plasmodium. Plasmodium protein INV 25-JUL-2000

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/protein_id="AAF87595.1"
/protein_id="AAF87595.1"
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/db_xref="taxon:5833"
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                                                                                                                                                                                                                                  Direct Submission Submitted (18-JUL-1994) Ralf Tolle, Abt. Prof. H. E Submitted (18-JUL-1994), Ralf Tolle, Abt. Prof. H. E fur Molekulare Biologie, (ZMBH), Univ. Heidelberg, Feld 282, Heidelberg, 69120, Germany
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/organism="Plasmodium
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                                            GCAGTCTCAACCTAAGAA------GCCTGCATCTACTCATGTCGGAGCCGAGTCCAAT 3684
                                                                                                                                                                          GAGAAGAAGAAGCTCAGCTACCTCTCTAGCGGACTGCATCACCTGATCGCCGAGCTCAAG 3483
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                                                                                        ACTCCACCTCAACCAGATGTAACTCCATCTCCATTATCTGTAAGGGTAAGTGGTAGTTCA 600
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sneyliedsfklunsgkntllksykyiikesvedlkkaggegisyyekylakkykbdls
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/codon_start=1
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/db_xref="SPTREMBL:Q25924"
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/dev_stage="blood stage"
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Submitted (21-MAY-2002) Faculty of Medicine, Chulalongkorn
University, Rama4, Pathumwan, Bangkok 10330, Thailand
On May 21, 2002 this sequence version replaced gi:309707.
Location/Qualifiers
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T-cell epitope; major merozoite surface antigen; plasmodium falciparum

Plasmodium falciparum

Plasmodium falciparum

Eukaryota; Alveolata; Apicomplexa; Haemosporida;
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Jongwutiwes, S.
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                                                                                                                                            /product="major merozoite surface antigen"
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1 125 c 150 g 303 t
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71.78;
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GAAGCCCATAACCTCATCAGCGTACTGGAGAAGCGCATAGACACCCTCAAGAAGAATGAA
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                                                                                                             TCTTCTCCTCTGAAGACTCTCTCCGAGGAGGAGCATCCAGACCGAGGATAACTACGCCAGC 3363
                                                                                                                                                         GAAAACACAAAAATATTATTGAAACATTATAAAGGACTTGTTAAATATTATAATGGTGAA
                                                                                                                                                                                                                                                TTTTCTGTTTTCTTTAACAAAAAAAAAAGAAGCTGAAATAGCAGAAACTGAAAACACATTA 180
                                                                   TCATCTCCATTAAAAACTTTAAGTGAAGTATCAATTCAAACAGAAGATAATTATGCCAAT 300
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Direct Submission
Submitted (18-JUL-1994) Ralf Tolle, Abt. Prof. H. Bujard, Zentrum für Molekulare Biologie, (ZMBH), Univ. Heidelberg, Im Neuenheimer Feld 282, Heidelberg, 59120, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  merozoite surface antigen-1
Exp. Parasitol. 81 (1), 47-54 (1995)
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 1956)
Tolle,R., Bujard,H. and Cooper,J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 1956)
Tolle,R.
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LQQVVQLQNYDEEDDSLVVLPIFGESEDNDEYLDQVVTGEAISVTMONILSGFENEYD

VIYLKPLAGGY RSLKKQIEKNLTETFINLHUNDILNSRLKKRXYFLDVLESDLMGFKHTS

SNEYIIEDSFKLLNSEQKNTLLKSYKYIKESVENDIKFAQEGISYYEKVLAKYKDDLE

SIKKVIKEEKSFPSSPFTTPSSPAKTDEQKKESKFLPFLINIETLYNNLVNKIDDYLI

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GKLLSTGLVQNFPNTIISKLIEGKFQDMLNISQHQCVKKQCPQNSGCFRHLDEREECK

CLLAYKQEGDKCVENPNFTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLF
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/protein_id="CAA84555.1"
/db_xref="GI:535248"
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/chromosome="9"
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/isolate="RO-33"
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57.7%;
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1437	ACTIACGAGAACGCAATGTGGAAGTTAAAATCAAGAGCTGAGATTAAAAGCACTAAAAACAATG	1378	Db Q9
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4347 1377	A CAGTGAACGACAAANTCGACCTTCGTAATTCACCTGGAGCCAAGGTCCTCAACTAT	4288 1318	Дy
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4287	CAAGGCGAGAATGAAAAATATCTGCCCTTCCTGAATAACATCGAAACCCTGTACAAG	4231	Qy
1257	GAAGAAAAGGAGTTCCCATCATCACCACCAACAACACCTCCGTCACCAGCAAAAACAGAC	1198	Db
4230	GATAAG	4225	Qy
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4224		4165	Qy
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4164		4105	Qy
1077	ATTGAAGATTCATTTAAATTATTGAATTCAGAACAAAAAAAA	1018	Db
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1017	TTAGATGTATTAGAATCTGATTTAATGCAATTTAAACATATATCCTCAAATGAATACATT	958	DЬ
4044	-	3985	Qy
957	ACATTTAATTTAAATTTGAACGATATCTTAAATTCACGTCTTAAGAAACGAAAATATTTC	898	Db
3984	ACCTTCAATGTCAACGTGAAGGACATTCTGAACAGCCGCTTTAATAAGAGAGAAAATTTC	3925	Qy
897	TTAAAACCTTTAGCTGGAGTATATAGAAGCTTAAAAAAACAAATTGAAAAAAACATTTTT	838	Db
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837	TCTGTCACAATGGATAATATCCTCTCAGGATTTGAAAAATGAATATGATGTTATATAT	781	Db
3864	ACTCCTTCCGTGATTGATAACATTCTGTCCAAAATCGAGAACGAATACGAAGTGCTCTAT	3805	Qy
780	TTTGGAGAATCCGAAGATAATGACGAATATTTAGATCAAGTAGTAACTGGAGAAGCAATA	721	Db
3804	TTCGGCGAGAGCGAGGAGGACTACGATGACCTCGGCCAGGTGGTCACCGGTGAGGCTGTC	3745	Qy
720	CAAGTACAATTACAAAATTATGACGAAGAAGATGATTCCTTAGTTGTATTACCCATT	661	Db
3744	ACAATTACCACATCTCAGAACGTCGACGATGAGGTCGATGACGTCATCATTGTGCCTATC	3685	Qy
660	GATCCACAAAAGAAGAAACACAAATACCAACTTCAGGCTCTTTATTAACAGAATTACAA	601	Db
3684		3633	Qy
600	ACTCCACCTCAACCAGATGTAACTCCATCTCCATTATCTGTAAGGGTAAGTGGTAGTTCA	541	Db
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540	ANCGAAGCTTTAAAATCTTACGAAAATTTTCTCCCCAGAAGCAAAAGTTACAACAGTTGTA	481	Db
3596	AATAACGCACTGGAATCTTACAAGAAGTTCCTGCCTGAAGGAACAGATGTCGC	3544	Qy
480	GAAGTAATAAAAATAAAAATTATACAGGTAATCTCCCAAGTGAAAATAATAAGAAAGTT	421	Db
3543	GAAGTCATTAAGAACAAGAACTACACCGGCAATAGCCCAAGCGAGAATAATACAGACGTG	3484	Ωу
420	GGAAAGAAAATTATCTTTCTTATCAAGTGGATTACATCATTTAATTACTGAATTAAAA	361	рь
3483	GAGAAGAAGAAGCTCAGCTACCTCTAGCGGACTGCATCACCTGATCGCCGAGCTCAAG	3424	Qy
360	301 TTAGAAAAATTTAGAGTATTAAGTAAAATAGATGGAAAACTCAATGATAATTTACATTTA	301	DЪ

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                                                                                                   Submitted (22-APR-1998) Molecular Institute, Socinstrasse 57, Basel
                                                                                                                                                                                                                                      Plasmodium falciparum.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 1141)
                                                                                                                                                                                                                                                                                                Plasmodium falciparum isolate (mspl) gene, partial cds. AF061141
                                                                                                                       Direct Submission
                                                                                                                                   Jiang,G.,
                                                                                                                                                                           Acta
                                                                                                                                                                                             Sequence diversity of the merozoite surface protein 1 of Plasmodium falciparum in clinical isolates from the Kilombero District,
                                                                                                                                                                                                                    Pluschke,G
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                                                                                                                                                                          Trop. 74 (1),
 /note="wild isolate"
71. .>1141
/gene="msp1"
71. .>1141
                                                                                                                                Daubenberger, C.A., Matile, H. and Pluschke, G
                                                             /organism="Plasmodium
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                                         /db_xref="taxon:5833"
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                                                                                          , Socinstrasse 57, I
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71. .>1141
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Eukaryota; Alveolata; Apicomplexa;
1 (bases 1 to 1142)
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Plasmodium falciparum.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 893)
Peterson,M.G., Coppel,R.L., McIntyre,P., Langford,C.J., Wood
Brown,G.V., Anders,R.F. and Kemp,D.J.
Variation in the precursor to the major merozoite surface ar
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INLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNPYDFEAIKKLINDDTKKDM
LGKLLSTGLVQNFPNTIISKLIEGKFQDMLNISQHQCVKKQCPENSGCFRHLDEREEC
                                                                                                                                                                                                                                                              /product="merozoite surface antigen 1 gene, 3+-end"
/protein_id="CAA84557.1"
/db_xref="G1:535252"
/db_xref="SPTREMBL:Q25923"
/db_xref="SPTREMBL:Q25923"
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KFRVLSKIDGKLNDNLHLGKKKLSFLSSGLHHLITELKEVIKNKNYTGNSPSENNKKV
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SNEYIIEDSFKLLNSEQKNTLLKSYKYIKESVENDIKFAQEGISYYEKVLAKYKDDLE
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LQQVVQSQNYDEEDDSLVVLPIFGESEDNDEYLDQVVTGEAISVTMDNILSGFENEYD
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                                                                                                      KCLLNYKQEGDKCVENPNPTCNENNGGCDADATCTEKDSGSSRKKITCECTKPDSYPL
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Sequence diversity of the merozoite
falciparum in clinical isolates from
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Submitted (22-APR-1998) Molecular
Institute, Socinstrasse 57, Basel
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Jiang,G., Daubenberger,C.A.,
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1 (bases 1 to 1116)
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67. .>1116
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67. .>1116
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67. .>1116
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/chromosome="9"
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/isolate="HN6.24"
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           Ranford-Cartwright, L.C., Balfe, P., Carter, R. and Walliker, D. Direct sequencing of enzymatically amplified DNA of alleles merozoite surface antigen MSA-1 gene from the malaria parasi Plasmodium falciparum
                                                                                               Submitted (10-MAY-1990) Ranford-Cartwright Animal and Population Genetics, University Road, Edinburgh, EH9 3JN, Scotland
                                                                                                                                                                                                                                                                 1009 bp DNA linear INV 19-S. Plasmodium falciparum merozoite surface antigen (MSA-1) gene fragment (clone HB3A).
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See <X52963> for MSA-1 clone :
Location/Qualifiers
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/protein_id="AAC69735.1"
/db_xref="GI:3821965"
/translation="MKITEFILCSFLFFIINTOCVTHESYQELVKKLEALEDAVLTGYG
LFHKEKMYLNEGTSGTAVTTSTPGSKGSVTSGGSGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGAVAVA
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/note="p190;
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/chromosome="9"
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/isolate="IFA9.2"
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                                                                                                                                     Submitted (22-APR-1998)
                                                                                                                                                   Direct Submission
                                                                                                                                                               Jiang, G., Daubenberger, C.A., Matile, H. and Pluschke
                                                                                                                                                                                                       Acta Trop.
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                                                                                                                                                                                                                                            Sequence diversity of the merozoite surface protein 1 of Plasmodium falciparum in clinical isolates from the Kilombero District,
                                                                                                                                                                                                                                                                      Pluschke, G
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Jiang, G., Daubenberger, C.A., Matile, H. and
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/translation="MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYS
LEQKEKMVLNEGTSGTAVTTSTPQSGGSVTSGGGSGGSVASVASVGSGSGSNSRRTMPS
DNSSDSDAKSYADLKHRVQNYLFTIKELKYPELFDLTNHMLTLCDNIHGFKYLIDGYE
EINELLYKLHFYYDLLRAKLNDACANSYCQIPFNLKIRANELDVLKKIVEGYRKPLDN
IKDNYGKMEDYIKKNKTTTANINELIEGSEKTIDQNKNADNEEGKKKLYQAQYNLFIY
NKQLQEAHNLISVLEKRIDALKKNENIKKLLGKINEIKNPPPANSGNTPNTLLDKNKK
IEEHEEKIKE"

455 a 134 c 158 g 355 t
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TGTCAAATTCCATTCAATTTGAAGATCAGAGCCAACGAGTTGGACGTATTGAAGAAGTTG
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GCTCAATATAATCTTTTTACTTTACAATAAACAATTACAAGAAGCACATAATTTAATAAGC
                                                                       TATATTAAAAAGAATAAGAAGACCATCGAGAACATTAACGAGCTGATCGAAGAATCCAAA
                                                                                                                                                                                                                    GTCTTCGGATATCGCAAGCCTCTCGACAACATCAAGGACAATGTGGGAAAGATGGAAGAT
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733; Conserv
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68.7%;
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Pred. No. 8.2e
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3.2e-101;
nes 298;
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KEYWORDS
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TITLE
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MEDLINE
PUBMED
                              Query Match
Best Local :
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                Matches
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                748;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 1157)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (mspl) gene,
AF061135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (22-APR-1998) Molecular Institute, Socinstrasse 57, Basel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jiang, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence diversity of the merozoite surface protein 1 of Plasmodium falciparum in clinical isolates from the Kilombero District,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pluschke, G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jiang,
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                              Similarity
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                                                                                         489
                Conservative
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FIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLDK
NKKLEEHEKEIKEIAKTIKFNIDSLFTD"
143 c 155 g 370 t
                                                                                                                                              activity
                                                                                                                                                                                                                                                                                                              /product="merozoite
72. .>1157
                                                                                                                                                                                                                                                                                                                                                                                      /note="wild isolate"
72. .>1157
                                                                                                                                                                                                         /product="merozoite surface protein
/protein_id="AAC69734.1"
/db_xref="GI:3821963"
                                                                                                                                                                                                                                                                                                                                                         /gene="msp1"
72. .>1157
                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:5833"
/chromosome="9"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Plasmodium
/isolate="IFA9.16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Daubenberger, C., Huber, W.,
                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                 /gene="msp1"
/note="p190; surface protein with spectrin
                                                                                                                                                                                                                                                                                                                                        /gene="msp1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
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                           10.3%;
               0,
             Score 508.2; DB 3;
Pred. No. 8.2e-101;
0; Mismatches 338;
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                                                                                                        AAGATTAATGAAATTAAGAATCCTCCGCCAGCCAACTCTGGGAACACCCCCTAACACGCTG
                                                                                                                                                 GTTTTAGAAAAACGTATTGACACTTTAAAAAAAAATGAAAACATTAAGGAATTACTTGAT
                                                                                                                                                                                                            GCTCAATATGATCTTTTTATTTACAATAAACAATTAGAAGAAGCACATAATTTAATAAGC
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Plasmodium falciparum isolate HN5 merozoite surface protein
(msp1) gene, partial cds.
AF061145
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Jiang, G., Daubenberger, C.A., Matile, H. and
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Sequence diversity of the merozoite
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 1123)
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RKPLDNIKDNVGKMEDYIKKNKTTIANINELIEGSKKTIDQNKNADNEEGKKKLYQAQ
YNLFIYNKQLQEAHNLISVLEKRIDTLKKNENIKKLLEDIDKIKTDAEKPTTGSKPNT
                                                                                                                                                                                                                                                                                                                                                                            activity"
                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="msp1"
/product="merozoite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Daubenberger, C., Huber, W., Matile, H.,
                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                         /note="p190; surface protein
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GCTTCAGGTGGTTCAGGTAATTCAAGACGTACAAATCCTTCAGATAATTCAAGTGATTCA
                                                                     TCTGTGGCCTCTGGGGGTTCCGTCGCCTCCGGCGGCAGCGTGGCATCAGGTGGCTCAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 1124)
Jiang,G., Daubenberger,C., Huber,W., Matile,H., Tanner,M. ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jiang, G., Daubenberger, C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence diversity of the merozoite surface protein 1 of Plasmodium falciparum in clinical isolates from the Kilombero District,
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32; Conservative
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/note="p190; surface protein with spectrin binding
activity"
                                                                                                                                                                                                                                                                                                                                                                             /translation="MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYS
LFQKEKMYLNEGTSGTAVTTSTPGSKGSGGGSGGSGGSVASVASGGSCNS
RRTNPSDNSSDSDAKSPADLKHRVQNYLFTIELKYPELPLTNHMLTLCDNIHFKY
LICYSEINELLYKLMSYDLLRAKLANDACANSYCQIPFNLKIRANELDYLKKIYFGY
RKPLDNIKDNVGKMEDYIKKNKTTIANINELIEGSKKTIDQNKNADNEEGKKKLYQAQ
YNLFIYNKQLQEAHNLISVLEKRIDTLKKNENIKKLLEDIDKIKTDAEKPTTGSKPNT
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/product="merozoite
72. .>1124
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135 c 166 g
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/protein_id="AAC69743.1"
/db_xref="GI:3821981"
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72. .>1124
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/chromosome="9"
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/isolate="HN3"
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
1 (bases 1 to 1149)
Submitted
                 Jiang,G., Daubenberger,C.A., Matile,H. and Pluschke,G. Direct Submission
(22-APR-1998)
 Molecular
Immunology,
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/protein_id="AAC69737.1"
/protein_id="AAC69737.1."
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/translation="MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYG
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/chromosome="9"
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/gene="mspl"
/product="merozoite
73. .>1167
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73. .>1167
                                                                                              /note="wild isolate
73. .>1167
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/chromosome="9"
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/isolate="IFA9.10"
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GTAGGAAAAATGGAAGATTACATTAAAAAAAAATAAAACAACCATAGCAAATATAAATGAA
                                                                               AATGAACTCCTGTACAAGTTGAATTTCTACTTCGACTTGCTAAGGGCCAAACTGAATGAC
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38; Conservative
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LTLCDNHHGFKYLIDGYEENIKEINENIKHLIDIDKIKTD
NEEGKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKKLLEDIDKIKTD
AEKLTTGSKFNPUFPENKKEVEGHEERIKEI"

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/note="p190; surface
activity"
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Pred. No. 6.4e-99;
0; Mismatches 329;
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Sequence diversity of the merozoite surface protein 1 of Plasmodium for clinical isolates from the Kilombero District,
                                                                                                                                                                                                                                                                                                              Submitted (22-APR-1998)
Institute, Socinstrasse
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Plasmodium falciparum
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/translation="mkiifflcsflffiinTqcvthesyqelvkklealedavlTgyg
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                                                                                             activity
                                                                                                                                                                           /gene="msp1"
71. .>1129
                                                                                                                                                                                                                                                                                                                                                      Daubenberger, C.A., Matile, H. and Pluschke, G
                                                                               /codon_start=1
                                                                                                          /gene="msp1"
/note="p190;
                                                                                                                                     /product="merozoite
71. .>1129
                                                                                                                                                              /gene="msp1"
                                                                                                                                                                                                        71. .>1129
                                                                                                                                                                                                                   /note="wild isolate"
                                                                                                                                                                                                                                /isolate="IFA19"
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                                                                                                                                                                                                                                                                        ∕organism="Plasmodium
                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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GTACTGGAGAAGCGCATAGACACCCTCAAGAAGAATGAAAATATCAAAGAACTGCTCGAC
                                  GCCCAGTACGACCTGTCCATCTATAACAAACAGCTTGAAGAAGCCCATAACCTCATCAGC
                                                                                TATATTAAAAAGAATAAGAAGACCATCGAGAACATTAACGAGCTGATCGAAGAATCCAAA
                                                                                                                                                            GTCTTCGGATATCGCAAGCCTCTCGACAACATCAAGGACAATGTGGGAAAGATGGAAGAT
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                     GCTCAATATGATCTTTCTATTTACAATAAACAATTAGAAGAAGCACATAATTTAATAAGC
                                                                    TGTCAAATACCTTTCAATCTTAAAATTCGTGCAAATGAATTAGACGTACTTAAAAAAATT
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                                                         CTGGACAAGAACAAGAAGATAGAGGAGCACGAGAAAGAGATCAAAGA 1076
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 AATGAAGGAACAAGTGGAACAGCTGTTACAACTAGTACACCTGGTTCAGGTGGTTCAGTT
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Direct Submission
Submitted (21-MAY-2002) Faculty of Medicine, Chulalongkorn Submitted (21-MAY-2002) Faculty of Medicine, Chulalongkorn University, Rama4, Pathumwan, Bangkok 10330, Thailand On May 21, 2002 this sequence version replaced gi:309700.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum Eukaryota; Alveolata; 1 (bases 1 to 1002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (p190) gene, partial om M77716 M77716.2 GI:21040170 T-cell epitope; major
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Plasmodium falciparum clone
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<1. .>1002
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                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="erythrocytic"
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M77723.2 GI:21040184
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Plasmodium falciparum.
4 Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa:
1 (bases 1 to 1002)
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Plasmodium falciparum clone 835B
(p190) gene, partial cds.
M77723
          Apicomplexa;
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major
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             ATCAATGAACTCCTGTACAAGTTGAATTTCTACTTCGACTTGCTAAGGGCCAAACTGAAT
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Submitted (21-MAY-2002) Facult
University, Rama4, Pathumwan,
On May 21, 2002 this sequence
Location/Qualifiers
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Pred. No. 3.2e-98;
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umwan, Bangkok 10330, Thailand
quence version replaced gi:309712.
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                                                                                                         Direct Submission
Submitted (21-MAY-2002) Faculty of Medicine, Chulalongkorn
University, Rama4, Pathumwan, Bangkok 10330, Thailand
On May 21, 2002 this sequence version replaced gi:309696.
                                                                                                                                                                                        Jongwutiwes, S., Tanabe, K., Nakazawa, S., Yanagi, T. Sequence variation in the tripeptide repeats and P190 (MSA-1) of Plasmodium falciparum from field Mol. Biochem. Parasitol. 51 (1), 81-89 (1992)
                                                                                                                                                                                                                                                    Plasmodium falciparum.
Plasmodium falciparum
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                                                                                        Location/Qualifiers
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INELIEGSKKTIDQNKNADNEEGKKKLYQAQYNLFIYNKQLQEAHNLISVLEKRIDTL
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/codon_start=1
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M77724.2 GI:21040186

P1-cell epitope; major merozoite surface antigen; Plasmodium falciparum

Plasmodium falciparum

Plasmodium falciparum

Eukaryota; Alveolata; Apicomplexa; Haemosporida; 1 (bases 1 to 1002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (21-MAY-2002) Faculty of Medicine, Chulalongkorn University, Rama4, Pathumwan, Bangkok 10330, Thailand On May 21, 2002 this sequence version replaced gi:309714.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jongwutiwes, S., Tanabe, K., Nakazawa, S., Yanagi, T. and Kanbara, H. Sequence variation in the tripeptide repeats and T cell epitopes P190 (MSA-1) of Plasmodium falciparum from field isolates Mol. Biochem. Parasitol. 51 (1), 81-89 (1992)
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B. burgdorferi ant
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                                                               Recombinant production of complete gp190/MSP-1 Plasmodium surface protein - useful in anti-malaria vaccines, also stabilising genes reducing their AT content
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monoclonal antibody; passive immunisation; parasite; ss.
     This sequence encodes a
                                 Example 1; Fig 3c; 48pp; German
                                                                                                                                WPI; 1998-240088/21.
P-PSDB; AAW54145.
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                                     AAGAAGTTGGTCTTCGGATATCGCAAGCCTCTCGACAACATCAAGGACAATGTGGGAAAG
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        CTGTACAAGTTGAATTTCTACTTCGACTTGCTAAGGGCCAAACTGAATGACGTTTGCGCC
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1980	CTGAAGAACGTGGAGTTAAAACATAATATACATGTGCCGAATAGTTATAAGCAGGAGAAAT	1921	Qy
1980		1921	Db
1920 1920	CAAGTGCAGAAGGTGCTCCTCATGAACAAGATTGATGAACTCAAGAAGACTCAACTCATT		Qy Db
1860 1860	ACAAAAGACGAAAATAAACCAGATGAGAAGATCCTGGAGGTCTCCGATATTGTTAAAGTC	1801 1801	ОУ
1800	ATCGAGACGCTTGTTGAGAACATTAAGAAGGATGAAGAACAGTTGTTTGAGAAGAAGATT	1741	Qy
1800		1741	Db
1740	ATTGTTGTGGAGAAGAACTAAAGTATTACAAGAATCTCATAAGTAAG	1681	Qy
1740		1681	Db
1680	CATAATCTTGAGAAGCTCACCAAAGCTCTTAAGTATATGGAGGACTATTCTCTGCGGAAC	1621	Qу
1680		1621	Db
1620	TCTTACAAAGTGGAGAAACTGACACACCATAATACCTTTGCATCCTATGAGAATTCTAAG	1561	Qy
1620		1561	
1560	TCCAAATTCAACAATAACATCGACCTGACCAACTTCGAGAAAATGATGGGAAAACGGTAC	1501	Qy
1560		1501	Db
1500	AGCAAAAGTCTAAACGATATCACTAAAGAGTATGAAAAGCTGCTGAACGAGATCTATGAT	1441	Qy
1500		1441	Db
1440	GAGAAGATCAAAATTGAGAAGAAGAAATTGAGAGTGACAAGAAAAGTTACGAAGACCGC	1381	Оу
1440		1381	
1380	GAACCCTCTAAGAATATCTACACAGACAATGAGAGAAAGAA	1321	Qy
1380		1321	Db
1320	AACGCTCTCAACGAGCTCAATAGCTTCGGTGACTTGATTAACCCCTTCGATTATACGAAA	1261	Qy
1320		1261	Db
1260	ACCGAACCTAATGAATATCCCCAATGGTGTGACGTACCCTCTGTCTTATAACGATATCAAC	1201	Qy
1260		1201	Db
1200	TACTTGAGAGAGAATAAAGAATATAGACATCTCCGCCAAAGTCGAGACAAAGGAATCA	1141	Фр
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1140 1140	GCCAAAACCATTAAGTTCAACATAGATTCTCTCTTTACTGATCCCCTTGAGCTGGAGTAC	1081	Qy Db
1080	AACACGCTGCTGGACAAGAACAAGAAGATAGAGGAGCACGAGAAAGAGATCCAAAGAGATC	1021	Qy
1080		1021	Db
1020	CTGCTCGACAAGATTAATGAAATTAAGAATCCTCCGCCAGCCA	961	Qy
1020		961	Db
960	CTCATCAGCGTACTGGAGAAGCGCATAGACACCCTCAAGAAGAATGAAAATATCAAAGAA	901 901	Qy Db

	3120	CTCTTCGACAAGAAGAAGACAGTCGGCAAGTATAAGATGCAGATCAAGAAGTTGACTCTG	3061	Qy
	3060	AAGACACTGCAACTGAGCTTCGACCTGTACAACAAGTACAACTGAAACTG	3001	Db
	3060	GAAGACACTGCAACTGAGCTTCGACCTGTACAACAACTACAACTGAAACTGGAGAG	300	Qy
	3000	ATCAACTCTCTTAACGATGAATCTAAACGTAAGAGCTGGAAGAGGACATCAATAAGCTG	2941	Дb
	3000	TCAACTCTCTTAACGATGAATCTAAACGTAAGAAGCTGGAAGAGGACATCAATAAC	2941	Qy
	2940	GACAGCGACACATTCTATAACGAGAGCTTCACTAACTTCGTGAAATCTAAAGCCGATGAT	2881	DP GA
	88	TCTACCAAGAACTTATTGGACAGAAATCGTCCGAGAACTTCTACGAGAAGATACTGA	82	g Db
	2880	ATCTACCAAGAACTTATTGGACAGAAATCGTCCGAGAACTTCTACGAGAAGATACTGAAA	8	Qy
	2820	AACCTTAATAACTCACTGAAACTGTTTGAGAACATCCTGTCTCTCGGCAAGAATAAGAAC	2761	Db
	2820	CTTAATAACTCACTGAAACTGTTTGAGAACATCCTGTCTCTCGGCAAGAATAAC	276	Qy
	2760 2760	TCTCTCACACCTCAAGACAAGCCCGAAGTGAGCGCTAACGACGACACCTCTCACTCGACCC	2701 2701	B 63
	2700	AAGCTAAGAAGTCTCCCACCTCTGTTAAAACTCTCTCTCT	2641	В
	2700	GAAGCTAAGAAGGTCTCCACCTCTGTTAAAACTCTCTCTC	2641	Qy
	2640	GAGATGGTCTGCAACCTGTATAAACTCAAAGACAACGACAAGATTAAGAACCTTCTGGAG	2581	Db
	2640	AGATGGTCTGCAACCTGTATAAACTCAAAGACAACGACAAGATTAAGAACCTTCTGG	2581	Qy
	55		ίň	Db
	2580	CTATGTTCGATAGCCTCAACAATTCTCTCTCTCAACTGTTCATGGAGATATATGAGAA	2521	Qy
	2520	TCCTCTTGTGATCCACTGGACCTGCTGTTCAATATCCAGAACAACATTCCCGTTATGTAT	2461	Db
	2520	CCTCTTGTGATCCACTGGACCTGCTGTTCAATATCCAGAACAACATTCCCGTTATGT	2461	Qy
	46	ACTATGAACGAGAAGATTCTTAAACAGTACAAGATAACCAAGGAAGAGGAGAGTAAACTG	. 4	Db 42
	4	ТАТGAACGAGAAGATTCTTAAACAGTACAAGATAACCAAGGAAGAGGAGGAGTAAACT	- 4	٥ ا
	2400	TVETATIONSTITUCTIGAMINGATICCTACAMICTIGUCACAMATATATICCTICGTCTCTCACAGG	2341	B &
		CACCABUICTIBIBANI MAKAABAKCUBABAAI BI CABCAAACI BBACIACI IBABA	, o	
	ŭ ŭ	CCACCAGCTCCTGTGAATAACAAGACCGAGAATGTCAGCAAACTGGACTACCTTGAGAAG 	2281	P 9
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	2280	GCAGGCACAGCCTCCAGTGCCAGTGCCCGTTCCAGAGGCTAAAGCTCAAGTGCCTAC	222	Qγ
	2220 2220	GGACAACAGGCCGGTTCAGCTCTCGAAGGCGATAGCGTGCAAGCTCAAGCACAAGAGCAG	2161 2161	р О
	16	CAGATAACTCCGAGCCTTCCACAGAAGGAGAGATAACCGGACAGGCTACCACCAAGC	10	Ъ
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:	2100 2100	ATGCCCAAAGTCGAGAGCCTGATCAACGAAGAGAAGAAGAACATTAAAACTGAAGGACAG	2041	DP QA
	2040	AAGCAGGAACCATACCTCATCGTACTCAAGAAAGAGATAGACAAACTGAAAGTGTTC	1981	DЬ
	2040	AGGAACCATACTACCTCATCGTACTCAAGAAAGAGATAGACAAACTGAAAGTGT	1981	Qy

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                                                        malaria; MSP-1; merozoite surface protein;
onal antibody; passive immunisation; parasit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Fig 3c; 48pp; German.
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P-PSDB; AAW54145.
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                                             ACTATCAAAGAACTCAAATATCCTCAACTCTTTGATTTAACTAATCATATGTTAACTTTG
                                                             ACTATCAAGGAGCTGAAGTACCCACAGTTGTTCGACCTCACTAATCATATGCTGACACTG
                                                                                                  AGCGATTCCGACGCCAAGTCCTACGCCGACCTCAAGCACCGAGTGAGAAACTATCTCCTC
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1560	AACAATAACATCGACCTGACCAACTTCGAGAAAATGATGGGGAAAACGGTAC	1501	Qy
1500	TCTAAGTCTTAAATGATATAACAAAAGAATATGAAAAATTACTTAATGAAATTTATGAT	1441	Db
1500	AGCAAAAGTCTAAACGATATCACTAAAGAGTATGAAAAGCTGCTGAACGAGATCTATGAT	1441	Qy
1440	GAAAAAATTAAAATAGAAAAAAAAAAATTGAATCTGATAAAAAATCTTACGAAGACAGA	1381	Db
1440	GAGAAGATCAAAATTGAGAAGAAGAAAATTGAGAGTGACAAGAAAAGTTACGAAGACCGC	1381	Qy
1380	GAACCAAGTAAAAACATATATACTGATAATGAAAGAAAAAATTCATAAATGAAATTAAG	1321	Ф
1380	AACCCTCTAAGAATATCTACACAGACAATGAGAGAAAGAA	1321	Qy
1320	AAAA	1261	Db
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ຸ ່ນ	TACTTGAGAGAGAATAAGAATATAGACATCTCCGCCAAAGTCGAGACAAAGGAATCA	1141	P 04
-	CAAAACTATTAAATTTAATATTGATAGTTTATTTACTGATCCACTTGAATTAGAATAC	0	DЬ
4	GCCAAAACCATTAAGTTCAACATAGATTCTCTCTTTTACTGATCCCCTTGAGCTGGAGTAC	0	Ş
1080	ACTCTCCTTGATAAGAACAAAAAATCGAGGAACACGAAAAAGAAATAAAAGAATT	1021	рь
1080	AACACGCTGCTGGACAAGAACAAGAAGATAGAGGAGCACGAGAAAGAGATCAAAGAGATC	1021	Qy
1020	TTACTTGATAAGATAAATGAAATTAAAAATCCCCCACCGGCCAATTCTGGAAATACACCA	961	Дb
1020	CTGCTCGACAAGATTAATGAAATTAAGAATCCTCCGCCAGCCA	961	Qy
960	TTAATAAGCGTTTTAGAAAAACGTATTGACACTTTAAAAAAAA	901	ф
960	CTCATCAGCGTACTGGAGAAGCGCATAGACACCCTCAAGAAGAATGAAAATATCAAAGAA	901	Qy
900	TTATACCAAGCTCAATATGATCTTTCTATTTACAATAAACAATTAGAAGAAGCACATAAT	841	В
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660	TGACTATTGTCAAATTCCATTCAATTTGAAGATCAGAGCCAACGAGTTGGACGTATTG	601	Qy
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GAC	ACAAGCCC	2701	Qy
TCCACATCTGTAAAAACTCTTTCAAGTTCATCAATGCAACCAT	AAGCGAAAAAAGTATCCACATCTG	9	Db
TCCACCTCTGTTAAAACTCTCTC	AAGAAGGTCTCCACCTCTG	64	Qy
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TACCAGTACCAGTACCAGAAGCAAAAGCACAAGTCCCAACA 2	AGCACAACCACCAGTACCAC	2221	Db
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ATCTGCTTTAGAAGGAGATTCAGTACAAGCACAAGCACAAGAAC	GACAACAAGCAGGATCTGCTT	2161	Db
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CATCAACCGAAGGAGAAATAACAGGACAAGCAACTACAAAAC	ATCAAC	2101	Db
CAGAAGGAGAGATAACCGGACAGGCTACCACCAAGC	AGATAACTCCGAGCCTTCCAC	2101	Qy
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NGCCTGATCAACGAAGAGAAGAAGAACATTAAAACTGAAGGA	CCCAAAGTCGAGAGCCTGATC	0	Qy
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TACCTCATCGTACTCAAGAAAGAGATAGACAAACTGAAAGTGTT	CAGGAACCATACTACCTCATCG	9	Qγ
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TGAGAACATTAAGAAGGATGAAGAACAGTTGTTTGAGAAGAAGA	GAGACGCTTGTTGAGAACATT	7	Qγ
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486	Db Db	3781 CAGGTGGTCACCGGTGAGGCTGTCACTCCCTTCCGTGATTGAT	0у з
486	Db Db		
480	Qy	3721 GATGACGTCATCATTGTGCCTATCTTCGGCGAGAGCGAGGAGGACTACGATGACCTCGGC 3780	Qy 3
474	Db	HIIIIII	
474	Qy	3661 ACTCATGTCGGAGCCGAGTCCAATACAATTACCACATCTCAGAACGTCGACGATGAGGTC 3720	Ωуз
468	Db		
468	Qy	GTGGTGTCTGAATCTGGCTCCGACACACTGGAGCACTCTCAACCTTAAGAAGCCTGTGTTT	
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456	Db	3401 AARGANTIKATIKATIKATURA (TILI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	ر م م
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450	Db	3421 TTRGABARGABARAATTATCATTAGTAGAGTGGATTAGAGTGATTAGTGGTGABTGA 3480	B 5
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444	Db		
444	Qy	ACCOTOGAGAACTTOAAGGTCOTGTTOTAAGOTTOGAAGGOAAGGTTOGAAGGAGAAACOTGAAAG	
438	Db		
438	Qy	3301 GAGTCTTCTCCTGGAAGACTCTCTCCGAGGAGGAGCATCCAGACCGAGGATAACTACGCC 3360	
432	Db		
432	Qy	3241 CTGGAGAACACCAAGATTCTTCTCAAACACTACAAAGGCCTCGTCAAGTATTATAATGGC 3300	Ωуз
426	Db		
426	Qy	3181 AACTTCTCAGTGTTCTTCAACAAGAAGAAGGAAGCCGAGATCGCCGAGACAGAGAACACT 3240	Qy 3
420	Db	3121 TTAAAAGAACAATTAGAATCAAAATTGAATTCACCTAATAACCCCAAAGCATGTATTACAA 3180	D b 3
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41,		3061 TTATTTGATAAAAAGAAAACAGTTGGTAAATATAAAATGCAAATTAAAAAACTTACTT	Db 3
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408	Qy	3001 AAGAAGACACTGCAACTGAGCTTCGACCTGTACAACAAGTACAAACTGAAACTGGAGAGA 3060	Оуз
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ى 0 (D 5	TCCTGTC	Qy 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence encoding the P195 protein of Plasmodium falciparum (AANSO530) and a peptide comprising at least one of its epitopes (see AAP50777) are claimed. Also claimed is a vaccine for inducir immunity to malaria comprising the novel peptide or P195 or a peptide comprising at least one epitope when derived from the new peptide comprising at least one epitope when derived from the new peptide comprising at least one epitope when derived from the new peptide comprising at least one epitope when derived from the new peptide comprising at least one epitope when derived from the new peptide comprising at least one epitope when derived from the new peptide comprising at least one epitope when derived from the new peptide comprising at least one epitope when derived from the new peptide comprising at least one of its epitopes.
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028 CTGTACAACAAGTACAAACTGAAACTGGAGAGACTCTTCGACAAGAAGAAGAAGACAGTCGGC 308 	Qу
968 CGTAAGAAGCTGGAAGAGGACATCAATAAGCTGAAGAAGAACACTGCAACTGAGCTTCGAC 3	Оy
2908 TTCACTAACTTCGTGAAATCTAAAGCCGATGATATCAACCTCTCTTAACGATGAATCTAAA 2967	Оy
2848 TCGTCCGAGAACTTCTACGAGAAGATACTGAAAGACAGCGACACATTCTATAACGAGAGC 2907 	Оу
2788 GAGAACATCCTGTCTCCGGCAAGAATAAGAACATCTACCAAGAACTTATTGGACAGAAA 2847 	Оу
28 GTGAGCGCTAACGACGACACCTCTCACTCGACCAACCTTAATAACTCACTGAAACTGTTT 278	Qy Db
2668 AAAACTCTCTTCCAGCTCCATGCAACCACTGTCTCTCACACCTCAAGACAAGCCCGAA 2727 	Qy Db
2608 AAAGACAACGACAAGATTAAGAACCTTCTGGAGGAAGCTAAGAAGGTCTCCACCTCTGTT 2667	Дy
2548 CTCTCTCAACTGTTCATGGAGATATATGAGAAGGAGATGGTCTGCAACCTGTATAAACTC 2607	Оy
2530 GATAGCCTCAACA	Оу
2470 GATCCACTGGACCTGCTGTTCAATATCCAGAACAACATTCCCGTTATGTATCTATGTTC 2529 	Оу
2410 GAGAAGATTCTTAAACAGTACAAGATAACCAAGGAAGAGGAGAGTAAACTGTCCTCTTGT 2469 	Db Qy

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MSA-1 (N-terminal p83 of C-terminal gp42) genes, or a combination of these in non-essential regions of their genomes are claimed. These poxviruses (pref. with a virulence reducing genomic deletion or disruption) can be used as vaccines against malaria and for the prodn. of Plasmodium immunogens. These viruses
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                                                                                                                           AAQ80911 is the P. falciparum MSA-1 gene cDNA sequence. New recombinant poxviruses containing either the SERA, ABRA, Pfhsp70, AMA-1, Pfs25, Pfs16, CSP, PfSSP2, LSA-1, LSA-1 repeatless, MSA-1.
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region - useful in vaccines
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	AAAAGAAGAAGTTGTACCAGGCCCAGTACGACCTGTCCATCTATAACAACAGCTTGAA 888 	829 GAAA 901 GGAA	D Qy
	GAGCTGATCGAAGAATCCAAAAAAGACCATAGACAAAAATAAGAATGCAACCAAGGAGGAA 828 	769 GAGC 841 GAAT	Db Qy
	AATGTGGGAAAGATGGAAGATTATATTAAAAAGAATAAGAAG	709 AATG 781 AATG	DB Qy
	TGGACGTATTGAAGAAGTTGGTCTTCGGATATCGCAAGCCTCTCGACAACATCAAGGAC 708 	649 TTGG 721 TTAG	Db Qy
	GACGTTTGCGCCAATGACTATTGTCAAATTCCATTCAATTTGAAGATCAGAGCCAACGAG 648 	589 GACG 661 GATG	Db Qy
	ATCAATGAACTCCTGTACAAGTTGAATTTCTACTTCGACTTGCTAAGGGCCAAACTGAAT 588 	529 ATCA 601 ATTA	Db Qy
	ATGCTGACACTGTGTGATAACATTCATGGCTTCAAATATCTGATTGACGGTTACGAAGAG 528 	469 ATGC 541 ATGT	ОУ
	AACTATCTCCTCACTATCAAGGAGCTGAAGTACCCACAGTTGTTCGACCTCACTAATCAT 468 	409 AACT 481 AATT	ОУ
	-ACTCTAGCGATTCCGACGCCAAGTCCTACGCCGACCTCAAGCACCGAGTGAGA 408 	356 421 CCAGCTG	ОУ
	CGAAGAACCAATCCATCTGACA355	334 CGAA 361 AGTC	р _Q
	GCCTCCGGCGGCAGCGTGGCATCAGGTGGCTCAGTGGCAAGCGGGGGTTCCGGGAACAGT 333	274 GCCT 301 GGTA	Qу
	TCTAAAGGGTCTGTGGCTAGCGGTGGCTCCCGGTGGGGTCTGTGGGGGTTCCGTC 273	214 TCTA 241 ACAA	DP 64
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,	ACCGGATACAGCCTGTTCCAGAAGGAGGAGATGGTGCTGAATGAA	130 ACCG 121 ACAG	Оβ
	ACCCACGAATCCTATCAGGAGCTGGTTAAGAAACTGGAAGCTTTGGAAGATGCCGTCCTT 129 	70 ACCC 61 ACAC	Ф
	ATGAAAATCATTTTCTTCCTGTGTTCATTTCTGTTTTTTATCATCAATACTCAGTGCGTG 69 	10 ATGA 1 ATGA	р
16;	25.5%; Score 1262; DB 16; Length 5181; imilarity 56.0%; Pred. No. 1.9e-296; Conservative 0; Mismatches 1995; Indels 291; Gaps 16	ry Match t Local s ches 2910	Que Bes Mat
	lticomponent, multistage vaccines due to their expression te, liver stage, blood stage and sexual stage proteins. 181 BP; 2287 A; 684 C; 707 G; 1503 T; 0 other;	provide multi of sporozite, Sequence 5181	8 X C C C

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Qy	Db	Qy	DЬ	Qy	Db	Qу	Db	Qy	Db	Qy	Ъ	Qy	ДЬ	Qy	DЬ	Qy	DЬ	Qy	Db	0	Db	Qy	Db	Qy	DЪ	Qy	Db	Οy	Db	Qy	Db	Qy	Qу	Дb	Qy
1951 CATGTGCCGAATAGTTATAAGCAGGAGAATAAGCAGGAACCATACTACCTCCTCATCGTACTC 2			TCCTTAGAAGTATATGATATTGTAAAATTACAAGTACAAAAAGTTTTATTAATTA		1861 AGTGAAAACAAAATTCTAGAAAAAAATTTTAAAGGACTAACACATTCAGCAAATGCT 1		1801 TATACTTTGAAAACTGGCCTCGAAGCTGATATAAAAAATTAACAGAAGAAATAAAGAGT 1		1741 TCATATCTTGAAGATTATTCTTTAAGAAAAGGAATTTCTGAAAAAAGATTTTAATCATTAT 1		1681 AATAAATTTTCATCCTCTAATAATTCTGTATATAATGTTCAAAAAATTAAAAAAGGCTCTT 1			1531 AACTTCGAGAAAATGATGGGAAAACGGTACTCTTACAAAGTGGAGAAACTGACACCAC 1	1561 TATGAAGAATTACTTGAAAAATTTATGAAATGAAATTTAATAATAATTATTTGACAAAGAT 1		1501 AATCACACAAAAGAACAAAATAAAAAATTACTTGAAGATTATGAAAAAGTCAAAAAAGGAT 1						1321 TTACCACTCACTGATATTCATTATCATTAGCTGCAGATAAGATAAAAAATTCATATGGT 1		1261 GATCCTACGAAATCTGTTCAAATACCAAAAGTTCCTTATCCAAATGGTATTGTATATCCT 1		1201 GAATTAGAATATTTAAGAGAAAAAAAATAAAAAAGTTGATGA		1141 ATAAAAGAAATTGCCAAAACTATTAAATTTAACATTGATAGTTTATTTA		1081 GGAAATACACCAAATACTCTCCTTGATAAGAACAAAAAATCGAGGAACACGAAGAAAAA 1		949 AATATCAAAGAACTGCTCGACAAGATTAATGAAATTAAGAATCCTCCGCCAGCCA		GAAGCCCATAACCTCATCAGCGTACTGGAGAAGCGCATAGACACCCCTCAAGAAGAATGAA
2010	2037	1950	1977	1890	1917	1830	1860	1770	1800	1710	1740	1650	1680	1590	1620	1530	1560	1470	1500	1410	1440	1350	1380	1290	1320	1239	1260	1187	1200	1128	1140	1068	1008	1020	948

	CTG 3012	2953 AACGATGAATCTAAACGTAAGAAGCTGGAAGAGGACACTGAATAAGCTGAAGAAGACACTG	Qy
-	rTG 3114	3055 TATTTTAATGATGATATCAAACAATTCGTAAAATCTAATTCAAAAGTAATTACAGGTTTG	Db
	CTT 2952	2893 TTCTATAACGAGAGCTTCACTAACTTCGTGAAATCTAAAGCCGATGATATCAACTCTCTT	Qy
-	ACC 3054	2995 ACCATTTCTACAACAGAGATGGAAAAATTTTATGAGAATATTTTAAAAAAATAAT	Db
٠٠	ACA 2892	2833 CTTATTGGACAGAAATCGTCCGAGAACTTCTACGAGAAGATACTGAAAGACAGCGACACA	Qy
•	TTA 2994	2935 TTGAAAGGTATTGTTAGTCTCTTAAATCTTGGAAATAAAACTAAAGTACCTAATCCATTA	Db
.0	3AA 2832	2776 CTGAAACTGTTTGAGAACATCCTGTCTCTCGGCAAGAATAAGAACATCTACCAAGAA	Qy
-	SAT 2934	2875 GGTCCTGCTGTAGTTGAAGAAAGTCATGATCCCTTAACAGTATTGTGTATTAGTAACG	DЬ
0.	FCA 2775	2721GCCCGAAGTGAGCGCTAACGACGACACCTTCTCACTCGACCAACCTTAATAACTCA	Qy
	TCT 2874	2815 CAAAACCAACAATCAAATGCATCCTCTACCAATACCCAAAATGGTGTAGCTGTATCATCT	DЬ
J	2720	2682 CAGCTCCATGCAACCACTGTCTCTCACACCTCAAGACAA	Qy
_	rcc 2814	2755 ACATCCAGTCCTGGAAATACAACCGTAAATACTGCTCAATCCGCAACTCACAGTAATTCC	Dβ
,	ГТС 2681	2658CACCTCTGTTAAAACTCTCTCTTC	Qy
-	TCT 2754	2695 GAGGAAAATCACATCAAAAAATTATTAGAGGAGCAAAAACAAATAACTGGAACATCAT	DЬ
•	2657	2611 GACAACGACAAGATTAAGAACCTTCTGGAGGAAGCTAAGAAGGTCTC	Qy
-	AAA 2694	2635 CAACATCTCTTTTTGAATTATTATATCAAAAGGAAATGATTTATTATTTACATAAACTAAAA	Ф
Ū	AAA 2610	2551 TCTCAACTGTTCATGGAGATATATGAGAAGGAGATGGTCTGCAACCTGTATAAACTCAAA	Qy
-	 TA 2634	2575 ANTATTCAAAATAACATACCTGCTATGTATTCATTATATGTATG	Db
Ü	CTC 2550	atccagaacaacattcccgttatgt	VΩ
-	II TTT 2574	2515 AATCTTACTCCAGAAGAAGAAATGAATTAAAATCATGTGATCATTAGATTTATTAT	Db
Ŭ	TTC 2490	2431 AAGATAACCAAGGAAGAGGAGAGTAAACTGTCCTCTTGTGATCCACTGGACCTGCTGTTC	Qy
-	II TAT 2514	2455 TGTCATAAATATTTTAGTATCAAACTCTAGTATGGACCAAAAATTATTAGAGGTATAT	망
	TAC 2430	2371 TGCCACAAATATATCCTCGTCTCTCACAGCACTATGAACGAGAAGATTCTTAAACAGTAC	Qy
•	 ATA 2454	2395 GCCTTGACAAAAACAGTTTATCTAAAGAAATTAGATGAATTTTTAACTAAATCATAT.	Db
	ATC 2370	2311 AATGTCAGCAAACTGGACTACCTTGAGAAGCTCTATGAGTTCCTGAATACATCCTACATC	Qy
•	CAA 2394	2335 CCAAAAGAAGTAAAAGTTGTTGAAAAATTCAATAGAACATAAGAGTAATGACAATTCAC	DЬ
Ū	3AG 2310	2251 GTTCCAGAGGCTAAAGCTCAAGTGCCTACACCAGCTGCTGTGAATAACAAGACCGAG	Qy
_	[] CCA 2334	2275 GAAACAGAAGAACAGAAGAACAGTAGGACACAACAGCAGTAACAATAACATTA	Db
Ū	CC 2250	2191 GATAGCGTGCAAGCTCAAGCACAAGAGCAGAAGCAGGCACAGCCTCCAGTGCCAGTGCCC	Qy
•	3AA 2274	2216 AAGAT-GGGGGTCACTCCACACACACTTATCCCAATCAGGAGAAACAGAAGTAACAG	DЪ
J	3GC 2190	2131 GAGATAACCGGACAGGCTACCACCAAGCCCGGGACAACAGGCCGGTTCAGCTCTCGAAGGC	Qy
•	CTG 2215	2156 AAGAACAAGCTGTCTTATCAAGTATTACACAACCTTTAGTTGCAGCAAGCGAAACAACTG	рb
•	3GA 2130	2071 GAGAAGAACATTAAAACTGAAGGACAGTCAGATAACTCCGAGCCTTCCACAGAAGGA	Qy
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맑 Q В QΥ В Qy рь δÃ д Qy ф Qy 멍 Qy 밁 γQ В οy 밁 Qy В Š 밁 δÃ Вb δÃ В ρŅ Вþ Qy В δ В δõ В δõ 밁 3472 3172 4189 3592 3232 3073 3115 3994 3874 4009 3814 3892 3694 3832 3642 3772 3652 3493 3532 3373 3313 3253 3352 3292 CTTGAAAGCAAACTCAACTCACTGAACAATCCGAAACACGTACTGCAGAACTTCTCAGTG TTAGAATCTGATTTAATGCAATTTAAACATATATCCTCAAATGAATACATTATTGAAGAT TTGGAGAGCGACTTGATTCCCTATAAAGACCTGACCTCCTCTAACCTACGTTGTCAAGGAC GTCAACGTGAAGGACATTCTGAACAGCCGCTTTAATAAGAGAGAAAATTTCAAGAACGTC CAATTACAAAATTATGACGAAGAAGATGATTCCTTAGTTGTATTACCCCATTTTTGGAGAA ACATCTCAGAACGTCGACGATGAGGTCGATGACGTCATCATTGTGCCTATCTTCGGCGAG ACCTAAGAA------GCTTGCATCTACTCATGTCGGAGCCGAGTCCAATACAATTACC CAACCAGATGTAACTCCATCTCCATTATCTGTAAGGGTAAGTGGTAGTTCAGGATCCACA TTAAAATCTTACGAAAATTTTCTCCCAGAAGCAAAAGTTACAACAGTTGTAACTCCACCT TTCAAGGTCCTGTCTAAGCTCGAAGGCAAGCTGAAGGACAACCTGAACCTGGAGAAGAAG TTCTTCAACAAGAAGAAGGAAGCCGAGATCGCCGAGACAGAGAACACTCTGGAGAACACC TTAGAATCAAAATTGAATTCACTTAATAACCCACATAATGTATTACAAAACTTTTCTGTT AAGAAGACAGTCGGCAAGTATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAG ACC - - - GAAACACAAAAAATGCATTAAATGATGAAATTAAAAAATTAAAAGATACTTTA TTAAATTTGAACGATATCTTAAATTCACGTCTTAAGAAACGAAAATATTTCTTAGATGTA AAAGAAGAAACACAAATACCAACTTCAGGCTCTTTATTAACAGAATTACAACAAGTAGTA -CACTGTGGTGTCTGAATCTGGCTCCGACACACTGGAGCAGTCTCA 4053 3171 4188 4128 4068 4008 3951 3693 3641 3771 3711 3651 3492 3591 3432 3531 3471 3411 3252 3192 3291 3132 4248 3993 3933 3873 3813 3753 3891 3831 3596 3552 3372 3312 3351 3231

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                             AAT97956
                                                   AAT97956 standard; DNA; 1950
                                                                                                                      TTAATACTCATGTTAATATTATACAGTTTCATTTAA
                                                                                                                                    CTGATCCTCATGCTGATCCTGTACAGCTTCATCTAA 4929
                                                                                                                                                                                                                                             GAGGAAGACAGCGGCTCTAACGGAAAGAAATCACATGCGAGTGTACTAAGCCCGACTCC 4833
                                                                                                                                                                                                                                                                                               AACCCAAACCCTACCTGCAATGAAAACAATGGCGGGTGTGACGCCGATGCTAAATGCACC
                                                                                                                                                                                                                                                                                                                                    CAACACCAATGCGTAAAAAAACAATGTCCAGAAAATTCTGGATGTTTCAGACATTTAGAT
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Best Local Similarity
Matches 1297; Conserv
                                                                                                                                                                                                                              The present sequence encodes a chimeric protein that contains a mammallan signal and anchor sequence, and a merozoite surface antigen-1 (MSA-1) carboxy terminal peptide. The C-terminal fragment of MSA-1 provides a more specific response than the complete MSA-1, and attachment of anchor and signal sequences improve the immunogenicity of the protein better than the use of an adjuvant. The chimeric protein, and expression vectors (analogues that express MSA-1 without either signal or anchor peptides), particularly in the form of recombinant vaccinia virus, are used in vaccines to prevent or treat malaria caused by Plasmodium falciparum. The vaccinia vector expresses the antigen fragment for many days, or even years, generating a long-lasting immune response (humoral and/or cell-mediated) against the merozoite form of the paragite. in humans or other actuals
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recombinant vaccinia virus; Plasmodium falciparum; ancl
response; humoral; cell-mediated; merozoite; ss.
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                         P-PSDB; AAY09372
                                             WPI; 1999-288313/24
                                                                                                                                                                            15-MAY-1998;
20-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Merozoite
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX56008 standard;
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                                                                                                                                                                                                                                                                                       29-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum
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                                                                                                                               (GENZ )
                                                                                        LH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             merozoite surface protein;
                                                                                                                                 GENZYME TRANSGENICS
                                                                                                                                                                                                                                                                                                                                                                                                                                      engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      surface protein MSP-1-42
                                                                                        Meade H;
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97US-0062592
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This novel, modified nucleic acid encodes the 42 kDa C-terminal portion (see AAY09372) of malaria merozoite surface protein MSP-1 (MSP-1-42), an important target for the development of a vaccine against plasmodium falciparum. The nucleic acid sequence has been modified compared to the native sequence of MSP-1-42 (see AAX56009) second that 306 nucleotide positions have been replaced to lower the AT content (from 76 to 49.7%) and to eliminate 10 mRNA instability motifs while maintaining the same protein amino acid sequence. These alterations allow MSP-1-42 to be expressed in mammalian cell culture and in transgenic mice. Native MSP-1-12 is known to be difficult to express in cell culture systems, mammalian cell culture systems or in transgenic animals. The invention allows capression of MSP-1-42 protein in the milk of transgenic animals, and also provides a DNA vaccine comprising a vector containing the callered MSP-1-42 sequence. Claim Modified malarial 1; Fig 1; 35pp; English. protein for use in anti-malarial vaccines

Matches Query Match Sequence 1065 BP; 324 A; 254 C; 280 G; 207 T; 0 other; Local Similarity Conservative 15.1%; 81.3%; 0; Mismatches Score 744.2; DB 20; Pred. No. 9.3e-171; 198; Length Gaps 0

Qy 밁 Ωy 4099 241 TACGTGGTCAAGGATCCCTACAAGTTCCTGAACAAGGAGAAGAGAGATAAGTTCCTGAGC 4158 30Ó

301 AGTTACAACTATATCAAGGACTCCATCGACACCGATATCAATTTCGCTAATGATGTGCTG AGTTACAACTACATCAAGGATAGCATTGATACCGATATCAACTTCGCCAACGATGTCCTG

360

4159 GGGTATTACAAGATCCTGAGCGAAAAATACAAGTCTGACCTTGACTCTATTAAAAAAGTAT 4218

4279 421

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CTCAACTATACTTACGAGAAGAGCAATGTGGAAGTTAAAATCAAGGAGCTGAACTACCTC CTGAACTACACATATGAGAAGAGCAACGTGGAGGTCAAGATCAAGGAGCTGAATTACCTG 600

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Q В Š 4459 GACCTGTCTACCGATTATAACCACAACAATCTCCTGACCAAGTTTCTGTCCACTGGCATG AAAACAATCCAAGACAAGCTGGCAGATTTCAAGAAAAATAACAATTTCGTCGGGAATTGCA **AAGACCATCCAGGATAAGCTGGCCGATTTCAAGAAGAACAACAACTTCGTCGGGATCGCC** 4518 660

GATCTGAGCACCGATTACAACCACAACCACGCTGCCGAACTTCCTGAGCACCGGTATG

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RRESULT 9
AAXX25586
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XX AXA AAXX
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XX MSP
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                                                                                                                                                                                                                                                                                                                                                                                Chen
                                       This novel, modified nucleic acid encodes a 42 kDa C-terminal part (see AAY05832) of malaria merozoite surface protein MSP-1 (MSP-1-42), an important target for the development of a vaccine against Plasmodium falciparum. The nucleic acid sequence has been modified compared to the native sequence of MSP-1-42 (see AAX25587) such that 306 nucleotide positions have been replaced to lower the AT content (from 76 to 49.7%) and to eliminate 10 mRNA instability
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motifs while maintaining the same protein amino acid These alterations allow MSP-1-42 to be expressed in \boldsymbol{\pi}
                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-MAY-1998;
20-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSP-1;
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DB; AAY05832.
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                                                                                                                                                                                                           12; Fig 1; 43pp;
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n engineering;
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                                                                                                                                                                                                                                                                          recombinant
                                                                                                                                                                                                                                                         vaccine
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97US-0062592
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protein expression;
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                                                                                                                                                                                                                                                                            nucleic
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This novel, modified nucleic acid encodes a 42 kDa C-terminal part (see AAY09374) of malaria merozoite surface protein MSP-1 (MSP-1-42), an important target for the development of a vaccine against Plasmodium falciparum. The nucleic acid sequence has been modified compared to the native sequence of MSP-1-42 (see AAX56009) such that the AT content has been reduced and 10 mRNA instability motifs eliminated while maintaining the protein amino acid sequence. In addition, a sequence encoding a 15-amino acid beta-casein signal peptide has been added to the 5' end of the sequence, and N262Q
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DB; AAY09374.
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              GCGGCTGTTTCAGGCATCTGGACGAGCGCGAAGAGTGCAAGTGTCTCCTGAACTACAAAC
                                                                    TGCAGGGCATGCTGAACATCTCCCAGCACCAATGCGTGAAGAAACAGTGCCCCCAGAATA
                                                                                                                            CTGGCATGGTGTTCGAAAACCTCGCCAAAACAGTGCTGAGCAATCTGCTCGACGGCAACC
                                                                                                                                                                                  GAATTGCAGACCTGTCTACCGATTATAACCACAACAATCTCCTGACCAAGTTTTCTGTCCA
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                                                                                                             GAATCGCCGATCTGAGCACCGATTACAACCACAACAACCTGCTGACCAAGTTCCTGAGCA
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{\tt GCGGATGCTTCAGACACCTGGATGAGAGGGAGGAGTGCAAGTGCCTGCTGAACTACAAGC}
                                                       {\tt TGCAGGGAATGCTGCAGATCAGCCAGCACCAGTGTGTGAAGAAGCAGTGTCCCCAGAACA}
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No. 3.3e-170;
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AAGAAGGAGATAAGTGCGTGGAGAACCCCAAACCCTACCTGCAATGAAAAACAATGGCGGGT

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RESULT 11
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               motifs eliminated while maintaining the protein amino acid sequence. In addition, a sequence encoding a 15-amino acid beta-casein signal peptide has been added to the 5' end of the sequence, and N262Q and N181Q mutations have been introduced to eliminate w-glycosylation sites. These alterations allow MSP-1-42 to be expressed in the mammary gland (i.e. milk) of transgenic mice. The invention provides modified recombinant nucleic acid sequences and
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                                                                              (MSP-1-42), an important target for the development of a vaccine against Plasmodium falciparum. The nucleic acid sequence has been modified compared to the native sequence of MSP-1-42 (see AAX258s) such that the AT content has been reduced and 10 mRNA instability
                                                                                                                                             Claim
                                                                                                                                                              New modified recombinant nucleic malarial DNA vaccine
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20-OCT-1997;
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n engineering; protein expression;
enic animal; mutant; ss.
for increasing the mRNA levels and s that are difficult to express in c
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GCGGCTGTTTCAGGCATCTGGACGAGCGCGAAGAGTGCCAAGTGTCTCCTGAACTACAAAC
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derived from lower organisms such as parasites, bacteria and viruses that have DNA coding sequences of high AT content or which have mRNA instability motifs or rare codons relative to the recombinant expression system to be used. The invention allows expression of MSP-1 in the milk of transgenic animals, and also provides a DNA vaccine comprising a vector containing the altered
                                                                                                                                                                                                                                                                                                                         preferred difficult protein candidates for expression are those
                                                                                                                                                                                                                                                                                                                                                                           cell culture systems or in transgenic animals.
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25-MAY-1999;
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                                                                                                                                                                                                                                              The present invention relates to non-natural variants of a C-terminal fragment of a Plasmodium merozoite surface protein-1 (MSP-1). The non-natural variants have reduced affinity for at least 1 antibody capable of blocking a second antibody that inhibits the proteolytic cleavage of Plasmodium MSP-1_4_2, and has the same affinity for at least cleavage of Plasmodium MSP-1_4_2, and has the same affinity for at least MSP-1_4_2, compared to natural MSP-1_1_9. The non-natural variants of the present invention are useful for immunising a mammal against malaria, and can be used to treat malaria. The present sequence is the MSP-142
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AAX56009 ID AAX56009 standard; cDN/ XX

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                                                                                                                                                                                                This nucleic acid encodes a 42 kDa C-terminal portion (see AAY09373) of malaria merozoite surface protein MSP-1 (i.e. MSP-1-42), an important target for the development of a vaccine against plasmodium falciparum. The 3' end of the sequence has been modified to include a 6xHis tag. The nucleic acid sequence has been modified (see AAX56008) according to a method of the invention in order to improve expression in mammalian host cells and in transgenic animals. In the modified coding sequence, 306 nucleotide positions have been replaced to lower the AT content (from 76 to 49.7%) and to eliminate 10 mRNA instability motifs. The encoded amino acid sequence is unaltered. In another modified sequence (see AAX56021), a signal peptide sequence has been added and two N-glycosylation sites eliminated. The invention allows expression of MSP-1-42 protein in the milk of transgenic animals, and also
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                               CTCTATCTGAAACCTCTGGCAGGCGTCTATAGGTCTCTCAAGAAACAGCTGGAGAATAAC
                                                                                                                GCAGTAACTCCTTCCGTAATTGATAACATACTTTCTAAAATTGAAAATGAATACGAGGTT
          AATTTCAAGAACGTCTTGGAGAGCGACTTGATTCCCTATAAAGACCTGACCTCCTCTAAC
                                                   GTGATGACCTTCAATGTCAACGTGAAGGACATTCTGAACAGCCGCTTTAATAAGAGAGAA
                                                                        merozoite surface
n engineering; prot
enic animal; ss.
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                                                                                                                                                                                                                     a DNA vaccine comprising a vector containing the sequence.
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MSP-1; merozoite surface protein; malaria; vaccine; protein engineering; protein expression; codon usag
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Cof mmalaria merozoite surface protein MSP-1 (i.e. MSP-1-42), an

Cimportant target for the development of a vaccine against

Class dimportant target for the development of a vaccine against

Class dimportant target for the development of a vaccine against

Class dimportant target for the development of a vaccine against

Class difficultied (see AAX25586) according to a method of the invention

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                                                                                                                                                                                                                                                                                                                                                                                              rare codons relative to the recombinant expression system to be ed. The invention allows expression of MSP-1 protein in the milk transgenic animals, and also provides a DNA vaccine comprising a
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                                                                                                                                                                                                                      AATTTCAAGAACGTCTTGGAGAGCGACTTGATTCCCTATAAAGACCTGACCTCCTCTAAC
                                                                                     GTGATGACCTTCAATGTCAACGTGAAGGACATTCTGAACAGCCGCTTTAATAAGAGAGAAA
                                                                                                                                                       CTCTATCTGAAACCTCTGGCAGGCGTCTATAGGTCTCTCAAGAAACAGCTGGAGAATAAC
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                                                                                                                                     AATTTCAAAAATGTTTTAGAATCAGATTTAATTCCATATAAAGATTTAACATCAAGTAAT
                                                                   GTTATGACATTTAATGTTAATGTTAAGGATATTTTAAATTCACGATTTAATAAACGTGAA
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97US-0062592
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74.3%;
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Pred. No. 8.7e-142;
0; Mismatches 273;
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                                         Merozoite surface protein;
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                                                                                                                           standard;
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13-MAY-1999;
25-MAY-1999;
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                                    ATCAACGATAAGCAAGGCGAGAATGAAAAATATCTGCCCTTCCTGAATAACATCGAAACC
                                                                                  GGTTACTACAAGATCTTGTCTGAGAAGTACAAGTCTGGACTTGGATTCCATCAAGAAGTAC
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01-DEC-1999;
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                                                            Producing malaria vaccine, useful for treatment or forms of malaria in humans, by expressing immunogen
                                       Example
                                                                                     P-PSDB;
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                                                                                                                          ) UNIV HAWAII.
) UNIV CHINESE
) QUEEN EMMA FO
                                      ω
                                                                                                                                                                                                                                                                                                  vaccine;
                                                     malaria in humans,
in a baculovirus s
                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                           Lap-Yin
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                                                                                                                                                                                                                                                                                  falciparum
                                                                                                                                                       ; 99US-0165178.
; 99US-0168327.
; 2000US-0226861.
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                                                                                                                                                                                        2000WO-US31064
                                                                                                                                                                                                                                                                                                                        major merozoite
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                                                                                                                           EMMA FOUND
                                       88-89;
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                                                                                                                                                                                                                                                                                                         protein-1;
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                                                     s, by expressing system -
                                                                                                                                   KONG
                                                                                                                                                                                                                                            "major merozoite
                                                                                                                                                                                                                                     of 42kDa"
                                       English
                                                                                                                                                                                                                                                                                                                        surface protein-1 fragment of 42kDa.
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                                                            immunogenic merozoit
                                                                                                                                                                                                                                             surface
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The present sequence encodes a major merozoite surface protein-1 C-terminal fragment of 42kba (MBP1-42). This fragment is linked melittin signal peptide, and then expressed in a in a silkworm/baculovirus system. The protein is used to prepare a

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  malaria vaccine, which is used to treat or prevent malaria, caused any of the four species of Plasmodium that infect humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1128 BP;
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                                                    CACCAATGCGTGAAGAAACAGTGCCCCCAGAATAGCGGCTGTTTCAGGCATCTGGACGAG
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              CGCGAAGAGTGCAAGTGTCTCCTGAACTACAAACAAGAAGGAGAGATAAGTGCGTGGAGAAC
                                                                                                                                                                                AACCACAACAATCTCCTGACCAAGTTTCTGTCCACTGGCATGGTGTTCGAAAACCTTCGCC
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                                                                                                                                                                   ACGAAAAAGATATGCTTGGCAAATTACTTAGTACAGGATTAG---TTCAAAATTTTCCT
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                                                                                                                                       AAAACAGTGCTGAGCAATCTGCTCGACGGCAACCTGCAGGGCATGCTGAACATCTCCCAG
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Pred. No. 3.0
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Matches 391
                                                                                                                                               The DNA encodes a region of a polypeptide. The region contains one epitope of the 190kD precursor of the major merozoite surfac of P.falciparum.
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                                                                                                                                 Sequence 660 BP; 281
                                                                                                                                                                                 Disclosure; ; pp; German
                                                                                                                                                                                                New immunogenic polypeptides - derived from Plasmodium falciparum 190~\mathrm{kD} surface antigen precursor, useful in vaccines, and encoding DNA sequences
                                                                                                                                                                                                                                                 Ulrich C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAN81148;
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                                                                                                        Score 308.8; DB 9
Pred. No. 7.1e-65;
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                                                                                                 Indels
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                       New immunogenic polypeptides - derived from Plasmodium falciparum 190 kD surface antigen precursor, useful in vaccines, and encoding DNA sequences
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P-PSDB; AAP80547.
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                                                                                                                          Sequence 1068 BP;
                                                                                                                                                                                                                                                                         Disclosure; ; 5pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ulrich C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-MAR-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA sequence
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                         Score 308.8; DB 9;
Pred. No. 9e-65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric; Plasmodium vivax; merozoite surface protein; MSP1; Plasmodium falciparum; malaria; vaccine; immunity; epitope;
  14-FEB-1996;
                                                  14-FEB-1997;
                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                         misc_feature
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                                                                                                   21-AUG-1997.
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/note= "sequence contains 2 in frame stop codons at the 3'-end"
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anchoring sequence"

p19

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ART94550
ID AAT9450
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Matches
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        Plasmodium Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is the nucleotide sequence encoding a recombinant protein compris nucleotides encoding amino acids 1613-1705 of the Plasmodium falciparu merozoite surface protein 1 (MSPI) 19 kD C-terminal fragment (pl9), linked to a sequence encoding a glycosylphosphatidylinositol membrane anchoring sequence pl9 is the C-terminal fragment of the 42 kD MSPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YNYU)
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                                                                                                                                                                                                                                                                                                              4703
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                                                                                                                                                                                                                                                                                                                                                                              4583 TGAACATCTCCCAGCACCAATGCGTGAAGAAACAGTGCCCCCAGAATAGCGGCTGTTTCA 4642
                                                                                                                                                                                                                                                                                                                                                                                                                                                               The recombinant protein can be used for the production of anti-malarial vaccines, where the p19 fragment provides a high level of protective immunity since it includes epitopes not presented in the p42 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roth
                                      Plasmodium
                                                                PfMSP1(p19)A
                                                                                     25-MAR-1998
                                                                                                        AAT94550
                                                                                                                         AAT94550 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 1B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein-1
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                                                                                                                                                                                                                                                  TCTCCTTCCTGATCCTCATGCTGATCCTGTACAGCTTCATCTAATA
                                                                                                                                                                                                                                                                                        AGTGCGTGGAGAACCCAAACCCTACCTGCAATGAAAACAATGGCGGGTGTGACGCCGATG 4762
                                                                                                                                                                                                                                                                                                                               Plasmodium species.
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DB; AAW22592.
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                                                                                                                                                                                                              AACCCGACTCGTACCCGCTGTTCGACGGCATCTTCTGCAGCTCCTCTAACTTCTTGGGCA
                                                                                                                                                                                                                        AGCCCGACTCCTATCCACTCTTCGACGGGATTTTTTTGCTCCAGCTCTAATTTCCTGGGCA
                                                                                                                                                                                                                                                                                                                                                                    TCAACATCTCGCAGCACCAATGCGTGAAAAAAACAATGTCCCGAGAACTCTGGCTGTTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nt protein containing Plasmodium merozoite surface p42 fragment - useful in antimalarial vaccines, s for diagnosis and protein purification
                                             Plasmodium vivax;
                 falciparum
                                     falciparum;
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                                                                coding
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                                                                 sequence
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                                                                                   entry)
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81.7%;
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                                      malaria;
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                                               merozoite
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Pred. No. 7.1e
0; Mismatches
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                                    vaccine; immunity; epit
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es 64;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB;
                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                 vaccines, where immunity since i
                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 1B; 85pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     purification
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant protein containing the fragment - useful in anti-malarial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-425033/39
P-PSDB; AAW36103.
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                                                                                                                                                                                                                                                                                                                                                  from Plasmodium species.
                                                                                                                                                                                                                                                                                                                  recombinant protein can be used for the production of cines, where the p19 fragment provides a high level of unity since it includes epitopes not presented in the production.
TCTCCTTCCTGATCCTCATGCTGATCCTGTACAGCTTCATCTAATA 4931
                                                                                                                                                        AGCCCGACTCCTATCCACTCTTCGACGGGATTTTTTGCTCCAGCTCTAATTTCCTGGGCA
                                                                  CCAAATGCACCGAGGAGGACTCGGGCAGCAACGGCAAGAAAATCACGTGTGAGTGTACCA
                                                                                                                          AGTGCGTGGAGAACCCAAACCCTACCTGCAATGAAAACAATGGCGGGTGTGACGCCGATG
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Pred. No. 7.1e-50;
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codons at
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TCTCGTTCTTGTTGATCCTCATGTTGATCTTGTACAGCTTCATTTAATA

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prodn. of antigens of Plasmodium species, esp. recombinant DNA methods giving polypeptide(s) against malaria or for diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 737
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DB; AAP50304.
                     GCCGTTACAACCAGCACACCCGGTTCTAAAGGGTCTGTGGCTAGCGGTGGCTCCGGTGGG
GCTGTTACAACTAGTACACCTGGTTCAGGTGGTTCAGGTTACTTCAGGTGGTTCAGGTGGT
                                                                                                       ACCCACGAATCCTATCAGGAGCTGGTTAAGAAACTGGAAGCTTTGGAAGATGCCGTCCTT 129
                                                                                                                                                                                                                                                      ATGAAGATCATATTCTTTTTATGTTCATTTCTTTTTTTTATTAAAATACACAATGTGTA
                                                                                                                                                                    ACACATGAAAGTTATCAAGAACTTGTCAAAAAAACTAGAAGCTTTAGAAGATGCAGTATTG
                                                                                  ACAGGTTATAGTTTATTTCAAAAGGAAAAAATGGTATTAAATGAAGGAACAAGTGGAACA
                                                                                                                                                                                                                                                                                                                                           359;
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                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 253 A; 90 C; 124 G; 270 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
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Best Query Match Matches

Local Similarity nes 335; Conser

Conservative

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Score 240.2; Pred. No. 3.6e 0; Mismatches

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Indels Length

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RESULT 22
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                                  The sequence encodes a polypeptide which contains the unique sequence of the surface antigen of P. falciparum, but lacks the immunodominant repeat sequences which may allow the parasite to evade and decoy the immune system. The DNA for the stage-specific late schizoint-merozoite antigen 31-1 in p31-1 (W08503725) was modified to delete the entire sequence coding for the repitope. The expression plasmid, 31-1 Repeated Delete, was introduced into E.coli K12 to produce the modified peptide. The transformant has been deposited in the Deutsche Sammlung von Microorganismen as E.coli K12 (98G936c1) (p31-1 Repeat Delete)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ss;
Sequence
                                                                                                                                                                              Disclosure; ; p; English.
                                                                                                                                                                                                       surface antigen sequence
                                                                                                                                                                                                                 Peptide(s) for prodn. of
                                                                                                                                                                                                                                                                               Shaw A,
                                                                                                                                                                                                                                                                                                         (BEHW ) BEHRINGWERKE
                                                                                                                                                                                                                                                                                                                                  26-JUN-1986;
                                                                                                                                                                                                                                                                                                                                                         20-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                  03-FEB-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Malaria; stage-specific late schizont-merozoite antigen 31-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-1 Repeated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTGTGGCCTCTGGGGGGTTCCGTCGCCTCCGGCGCGCAGCGTGGCATCAGGTGGCTCAGTG
                                                                                                                                                                                                                                                         1988-030152/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTCATGGCTTCAAATATCTGATTGACGGTTACGAAGAGAGATCA 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAACTCAAATATCCCGAACTCTTTGATTTAACCAATCATATGTTAACTTTGTGTGATAAT' 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGCTGAAGTACCCACAGTTGTTCGACCTCACTAATCATATGCTGACACACTGTGTGATAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAAGCGGCGGTTCCGGGAACAGTCGAAGCAACCTGTGACAACTCTAGCGATTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTTCAGGTGGTTCAGGTAATTCAAGACGTACAAATCCTTCAGATAATTCAAGTGATTCA
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  899
                                                                                                                                                                                                                                                                              Humbert Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                          to treat and
 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           protozoan
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 A; | 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                           parasite; repitope
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                      31-1 Repeat Delete). The peptide was prevent protozoan parasitic infection
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 115 G;
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 0 other;
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New immunogenic polypeptides - derived from Plasmodium falciparum 190 kD surface antigen precursor, useful in vaccines, and encoding DNA sequences
                                                P-PSDB;
                                                              WPI; 1988-272339/39.
                                                                                                                          (HOFF ) F HOFFMANN-LA ROCHE & CO.
                                                                                                                                                         19-MAR-1987;
                                                                                                                                                                                      08-MAR-1988;
                                                                                                                                                                                                                                                   EP283829-A
                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                           Polypeptide p190-2b; P.falciparum; merozoite; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                         DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                        11-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAN81150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAN81150 standard; DNA; 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 613
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                                                AAP80546
                                                                                           Gentz H,
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(HOFF ) F. HOFFMANN-LA ROCHE &
                              19-MAR-1987;
                                                           08-MAR-1988;
                                                                                        28-SEP-1988
                                                                                                                     EP283829-A
                                                                                                                                                                                                                                             Polypeptide p190-2a; P.falciparum; merozoite;
                                                                                                                                                                                                                                                                                                                                        AAN81149;
                                                                                                                                                                                                                                                                                                                                                                     AAN81149 standard; DNA;
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                                                           88EP-0103564
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Pred. No. 6.5e-39;
0; Mismatches 137;
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20-APR-2000; 2000WO-GB01558
                                                                                                                                              Plasmodium
                                                                                                                                                                                           Merozoite surface protein; protazoacide; vaccine;
                                                                                                                                                                                                                                       Merozoite surface protein-119 coding sequence
                                                                                                                                                                                                                                                                                                                                                                                        AAC68977 standard; DNA; 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3634 C
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0; Mismatches 137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0 other;
                                                                                                                                                                                             malaria; ss
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RESULT 26
AAT80404
ID AAT80
XX AAT80
AC AAT80
XX 25-MA
DT 25-MA
XX PIMSP
XX Chime
XX Plasm
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Best Local :
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13-MAY-1999;
25-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              surface
malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to non-natural variants of a C-terminal fragment of a Plasmodium merozoite surface protein-1 (MSP-1). The non-natural variants have reduced affinity for at least 1 antibody capable of blocking a second antibody that inhibits the proteolytic cleavage of Plasmodium MSP-1_4_2, and has the same affinity for at least one third antibody that inhibits the proteolytic cleavage of Plasmodium MSP-1_4_2, and has the same affinity for at least one third antibody that inhibits the proteolytic cleavage of Plasmodium MSP-1_4_2, compared to natural MSP-1_1_9. The non-natural variants of the present invention are useful for immunising a mammal against malaria, and can be used to treat malaria. The present sequence is the MSP-119
              Chimeric; Plasmodium vivax; merozoite surface protein; MSP1; plasmodium falciparum; malaria; vaccine; immunity; epitope; s
                                                                                                                                                                                                                                                                                               4808
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                                                                                                                                                                                                                                        4868 CTAATTTCCTGG 4879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB;
                                                     PfMSP1(p19)S coding sequence
                                                                                  25-MAR-1998
                                                                                                                                         AAT80404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel variants of the C-terminal fragment of Plasmodium merozoite surface protein-1, useful as vaccines for treating or preventing malaria -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Holder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity es 241; Conserv
                                                                                                                                                                                                                                                                                  CATGCGAGTGTACTAAGCCCGACTCCTATCCACTCTTCGACGGGATTTTTTGCTCCAGCT
                                                                                                                                                                                                                                                                                                                                       AACAAGAAGGAGGAGATAAGTGCGTGGAGAACCCCAAACCCTACCTGCAATGAAAACAATGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-015762/02.
                                                                                                                                                                                                              CTAACTAAGTGG
                                                                                                                                                                                                                                                                                                                            GATGCGACGCTGACGCTAAGTGCACCGAAGAAGACTCTGGTTCTAACGGAAAGAAGATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATAGCGGCTGTTTCAGGCATCTGGACGACGAGCGCGAAGAGTGCAAGTGTCTCCTGAACTACA
                                                                                                                                                                                                                                                                     CTTGCGAATGTACTAAGCCAGACTCTTACCCTTTGTTCGATGGAATCTTCTGTTCTTCCT
                                                                                                                                                                                                                                                                                                                                                                                AGCAGGAAGGTGATAAGTGTGTTGAGAACCCAAACCCTACCTGTAACGAGAACAACGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTCCGGATGTTTCAGACATCTGGACGAGAGAAGAATGTAAGTGTCTGTTGAACTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Birdsall B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
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                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333 BP; 107
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                                                                                  (first
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99US-0311817.
99CA-2271451.
                                                                                                                                          DNA;
                                                                                entry)
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77.28;
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                                                                                                                                          387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;
                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 198.4; DB 22; Pred. No. 3.7e-38; "ismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 T; 0 other;
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Plasmodium vivax.

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                                                                                                               Query Match
Best Local Similarity
Matches 226; Conserv
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Chimeric -
                                                                                                                                                                         This is the nucleotide sequence encoding a chimeric protein comprising nucleotides encoding amino acids 1-32 of the Plasmodium vivax merozoite surface protein 1 (MSP1) linked to the nucleotide sequence encoding the 19 kD C-terminal fragment (p19) of MSP-1 from Plasmodium falciparum. p19 is the C-terminal fragment of the 42 kD MSPI from Plasmodium species. The recombinant protein can be used for the production of anti-malarial vaccines, where the p19 fragment provides a high level of protective immunity since it includes epitopes not presented in the p42 fragment.
                                                    4643
                                                                                              4583
                                                                                                                                                                                                                                                                                                                                                                     Roth
                                                                                                                                                                                                                                                                                                                                                                                                                                   14-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                          Sequence 387 BP;
                                                                                                                                                                                                                                                                        Disclosure; Fig 1C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mat_peptide
                                                                                                                                                                                                                                                                                                       Recombinant protein containing Plasmodium merozoite surface protein-l p42 fragment - useful in antimalarial vaccines, a
                                                                                                                                                                                                                                                                                                                                                                                Barnwell JW,
                                                                                                                                                                                                                                                                                                                                                                                                   (INSP ) INST
(UYNY ) UNIV
                                161
                                                                         101
                                                                                   TGAACATCTCCCAGCACCAATGCGTGAAGAAACAGTGCCCCCAGAATAGCGGCTGTTTCA 4642
                                                                                                                                                                                                                                                                                                                                        1997-425034/39.
DB; AAW22592.
AGTGCGTGGAGAACCCCAAACCCCTGCAATGAAAACAATGGCGGGTGTGACGCCGATG
                                           GACACTTGGACGAGAGAGGAGGGTGTAAATGTCTGCTGAACTACAAACAGGAGGGCGACA
                                                                        TCAACATCTCGCAGCACCAATGCGTGAAAAAAACAATGTCCCGAGAACTCTGGCTGTTTCA 160
                                                                                                                                                                                                                                                                                               for
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                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    NEW YORK STATE
                                                                                                                                                                                                                                                                                                                                                                                                              PASTEUR
                                                                                                                                                                                                                                                                                                                                                                              Longacre-Andre
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/product= PfMSP1(p19)S
/note= "sequence contains 2
/the 3' end"
                                                                                                                                                                                                                                                                                              diagnosis
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97..102
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58..381
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                                                                                                                                                          116 A; 94 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
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                                                                                                                          3.9%;
                                                                                                                                                                                                                                                                        85pp; French.
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                                                                                                                          Score 194.8; DB Pred. No. 3e-37;
                                                                                                                                                          96 G; 81 T;
                                                                                                                Mismatches
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                                                                                                                                                          0 other;
                                                                                                                                     DB 18;
                                                                                                                52;
                                                                                                                                                                                                                                                                                                                                                                               Nato
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RESULT 27
AAT94549
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                                   Recombinant protein of fragment - useful in
                                                          WPI; 1997-425033/39
P-PSDB; AAW36102.
                                                                                                     (INSP ) INST
(UYNY ) UNIV
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                                                                                                                                                                                                                                                                     misc_feature
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Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                    Chimeric; Plasmodium vivax; merozoite surface protein; MSP1; p19; Plasmodium falciparum; malaria; vaccine; immunity; epitope; ss.
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            Disclosure; Fig 1C;
                             purification
                                                                                 Barnwell JW, Roth C;
                                                                                                                              14-FEB-1996;
                                                                                                                                             14-FEB-1997;
                                                                                                                                                            21-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACCCGACTCGTACCCGCTGTTCGACGGCATCTTCTGC
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                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum
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                                                                                                        NEW YORK STATE
                                                                                                                PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                           coding sequence
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                                                                                       Longacre-Andre
                                                                                                                              96FR-0001822
                                                                                                                                              97WO-FR00290
                                                                                                                                                                                                                                               /note=
97..102
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58..381
                                                                                                                                                                                                                                                                                                                /product= PfMSP1(p19)S
/note= "sequence"
                                                                                                                                                                                                                 103..381
                                                                                                                                                                                                                                                                                                    1..57
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1..96
                                                                                                                                                                                         /note= "sequence derived sequence"
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                                                                                                                                                                                                                               /note= "sequence
                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                    containing the n anti-malarial
            85pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
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                                                                                                                                                                                                                        ce derived
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                                                                                         Mendis
                                     merozoite vaccines,
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                                                                                                                                                                                                                               genérated restriction
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                                 protein-1 p19
is and protein
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This is the nucleotide sequence encoding a chimeric protein comprising

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RESULT 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 226
The invention relates to a variant DNA sequence useful in DNA vaccines The DNA sequence encodes a naturally occurring protein such as C3d whiby virtue of third base redundancy and other variations permissible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleotides encoding amino acids 1-32 of the plasmodium vivax merozoite surface protein 1 (MSP1) linked to the nucleotide sequence encoding the 19 kD C-terminal fragment (p19) of MSP-1 from plasmodium falciparum. p19 is the C-terminal fragment of the 42 kD MSP1 from Plasmodium species. The recombinant protein can be used for the production of anti-malarial vaccines, where the p19 fragment provides a high level of protective immunity since it includes epitopes not presented in the p42 fragment.
                                                                           Novel variant DNA sequence useful in DNA vaccine, encodes occurring protein and comprises a sequence non-identical occurring DNA sequence encoding the protein -
                                                                                                                                                                                                                                                                                    WO200177324-A1
                                                                                                                                                                                                                                                                                                            Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                      C3d;
                                                                                                                                                                                                                                                                                                                                                                          Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                   12-FEB-2002
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                                                  Example 13; Page 65;
                                                                                                                                                        Steward
                                                                                                                                                                                (ADPR-)
                                                                                                                                                                                                         08-APR-2000;
                                                                                                                                                                                                                                 09-APR-2001; 2001WO-GB01599
                                                                                                                                                                                                                                                           18-OCT-2001
                                                                                                                                                                                                                                                                                                                                                 pUC105-01 vector; immunostimulant; vaccine; immunisation; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                            AAD22459
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD22459 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101
                                                                                                                               2002-010909/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCCCGACTCCTATCCACTCTTCGACGGGATTTTTTTGC 4860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTGCGTGGAGAACCCAAACCCTACCTGCAATGAAAACAATGGCGGGTGTGACGCCGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACACTTGGACGAGAGAGAGGAGTGTAAATGTCTGCTGAACTACAAACAGGAGGGCGACA
                                                                                                                                                                                                                                                                                                                                     immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AACCCGACTCGTACCCGCTGTTCGACGGCATCTTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCAAATGCACCGAGGAGGACTCGGGCAGCAACGGCAAGAAAATCACGTGTGAGTGTACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGTGCGTGGAGAACCCCAACCCGACCTGTAACGAGAACAACGGCGGCTGTGACGCAGACG
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                                                                                                                                                                                ADPROTECH LTD
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                                                                                                                                                        Cox VF;
                                                                                                                                                                                                                                                                                                                                   response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 116
                                                                                                                                                                                                         2000GB-0008582
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.9%;
81.3%;
                                                  87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; 94 C;
                                                                                                                                                                                                                                                                                                                                      ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 194.8;
Pred. No. 3e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                        insert in pUC105-01 vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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to naturally
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RESULT 29
AAD22460
QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 230; Conserv
                                                                                                                                                                                                                                     Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       within an amino acid codon, is non-identical to the naturally occurring DNA sequence encoding that protein. The DNA sequence is useful in a DNA immunisation vector to encode one or more naturally occurring human or non-human proteins with immunomodulatory properties. The DNA sequence is useful for inducing an immune response to an antigen in a human or animal. A pharmaceutical composition is useful for introducing a DNA sequence encoding a naturally occurring protein into a human or animal by administering the pharmaceutical composition in useful for introducing a DNA sequence encoding the pharmaceutical composition into the human or animal, where the administration results in a therapeutic effect on the human or animal. The present sequence is Plasmodium falciparum prMSP1.19 insert in pUC105-01 vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4585 AACATCTCCCAGCACCAATGCGTGAAGAAACAGTGCCCCCAGAATAGCGGCTGTTTCAGG
           WO200177324-A1
                                                             misc_feature
                                                                                                    mat_peptide
                                                                                                                             sig_peptide
                                                                                                                                                                                                                                                                Chimeric
                                                                                                                                                                                                                                                                                                                               PfMSP1.19-human C3d3 DNA coding sequence from pVK104-01 vector.
                                                                                                                                                                                                                                                                                                                                                           12-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                             AAD22460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4705 TGCGTGGAGAACCCAAACCCTACCTGCAATGAAAACAATGGCGGGTGTGACGCCGATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                           immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 CCAGACTCTTACCCTTTGTTCGATGGAATCTTCTTGTTCTTCCTTAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCGACTCCTATCCACTCTTCGACGGGATTTTTTGCTCCAGCTCTAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAATGCACCGAGGAAGACAGCGGCTCTAACGGAAAAGAAAATCACATGCGAGTGTACTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATCTGGACGAGAGAAGAATGTAAGTGTCTGTTGAACTACAAGCAGGAAGGTGATAAG
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                                                                                                                                                                                                                                                                                           response;
                                                                                                                                                                                                                                                                                                     immunostimulant;
                                                                                                                                                                                                                                                                 .
                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309 BP; 94 A;
                                                                                                                                                                                                                                     Homo sapiens:
Plasmodium falciparum
Unidentified
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                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                             /product=
                                                                                                 /*tag= | l
73..3147
                                                                                                                                /partial
                                   /*tag=
/note=
                                                                                                                                                                                                Location/Qualifiers
1..3147
                                                                                                                                                       /product= "Human C3d3-PfMSP1.19 protein"
/note= "CDS does not include stop codon"
                                                                                                                                                                                                                                                                                       mulant; vaccine; immunisation;
pVK104-01 vector; ds.
                                                                                        /*tag=
                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
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                                  "Antigen
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Pred. No. 3e-3
0; Mismatches
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                                     sequence
                                                                           human C3d3
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3e-37;
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                                                                           protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
                                                                                                                                                                                                                                                                                                        therapeutic; C3d,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309;
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RESULF 30
AAD22461
ID AAD22
XX AAD22
AC AAD22
XX 12-FE
XX Human
XX Human
XX Human
XX Immun
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Best Local Sin
Matches 230;
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                                                                                                                                                                                                                                                                                                                                                                                                  4645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunisation vector to encode one or more naturally occurring human or non-human proteins with immunomodulatory properties. The DNA sequence is useful for inducing an immune response to an antigen in a human or animal. A pharmaceutical composition is useful for introducing a DNA sequence encoding a naturally occurring protein into a human or animal by administration in the pharmaceutical composition into the human or animal, where the administration results in a therapeutic effect on the human or animal. The present sequence is plasmodium falciparum PfMSP1.19-human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                    12-FEB-2002
                                                                                                                                         AAD22461 standard;
                                                                                                                                                                                                                                      4825
                                                                                                                                                                                                                                                                                                                                                                                                                                                     4585 AACATCTCCCAGCACCAATGCGTGAAGAAACAGTGCCCCCAGAATAGCGGCTGTTTCAGG 4644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3147 BP; 869 A; 754 C; 834 G; 690 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a variant DNA sequence useful in DNA vaccines. The DNA sequence encodes a naturally occurring protein such as C3d which by virtue of third base redundancy and other variations permissible within an amino acid codon, is non-identical to the naturally occurring DNA sequence encoding that protein. The DNA sequence is useful in a DNA requence according that protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 16; Page 66-68; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel variant DNA sequence useful in DNA vaccine, encodes na occurring protein and comprises a sequence non-identical to occurring DNA sequence encoding the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-APR-2000;
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                                                    Human C3d3 DNA-PfMSP1.19 coding sequence from pVK104-02 vector.
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                immune
                                                                                                                                                                                                           313
                                                                                                                                                                                                                                                                                                                    193
                                                                                                                                                                                                                                                                                                                                                                        133
                                                                                                                                                                                                                                                                                                                                                                                                                           73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                        CCCGACTCCTATCCACTCTTCGACGGGATTTTTTTGCTCCAGCTCTAATT
                                                                                                                                                                                                                                                                                                                                                                                    CCAGACTCTTACCCTTTGTTCGATGGAATCTTCTGTTCTTCCTCTAACT
                                                                                                                                                                                                                                                             AACATTGCCCAACACCAATGCGTTAAGAAGCAATGTCCACAAAACTCCGGATGTTTCAGA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002-010909/01.
                                                                                                                                                                                                                                                                                        AAATGCACCGAGGAAGACAGCGGCTCTAACGGAAAGAAAATCACATGCGAGTGTACTAAG
                                                                                                                                                                                                                                                                                                                                            TGCGTGGAGAACCCAAACCCTACCTGCAATGAAAACAATGGCGGGTGTGACGCCGATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA coding sequence from vector pVK104-01.
                             immunostimulant;
               response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cox VF;
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                                                                                   (first
           mulant; vaccine; immunisation; therapeutic; C3d;
pVK104-02 vector; ds.
                                                                                                                                         DNA;
                                                                                   entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 194.6; DB Pred. No. 9.9e-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as C3d which,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           naturally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Best Local
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Chimeric - I
Chimeric - I
 4765
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Qγ 뫄 δÃ В δÃ В δÃ

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4585 AACATCTCCCCAGCACCAATGCGTGAAGAAAACAGTGCCCCCAGAAATAGCGGCTGTTTCAGG 4644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3147 BP; 869 A; 754 C; 834 G; 690 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a variant DNA sequence useful in DNA vaccines. The DNA sequence encodes a naturally occurring protein such as C3d which, by virtue of third base redundancy and other variations permissible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 16; Page 69-71; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel variant DNA sequence useful in DNA vaccine, encodes naturally occurring protein and comprises a sequence non-identical to natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-APR-2001; 2001WO-GB01599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C3d3 DNA coding sequence from vector pVK104-02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ADPR-) ADPROTECH LTD
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AAATGCACCGAGGAAGACAGCGGCTCTAACGGAAAAGAAAATCACATGCGAGTGTACTAAG
                                                                                                                                                                                              TGCGTGGAGAACCCCAAACCCTACCTGCAATGAAAACAATGGCGGGTGTGACGCCGATGCT
                                                                                                                                                                                                                                                                                    AACATTGCCCAACACCAATGCGTTAAGAAGCAATGTCCACAAAACTCCGGATGTTTCAGA
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                                                       TGTGTTGAGAACCCAAACCCTACCTGTAACGAGAACAACGGTGGATGCGACGCTGACGCT
                                                                                                                                                                       CATCTGGACGAGAGAGAATGTAAGTGTCTGTTGAACTACAAGCAGGAAGGTGATAAG
                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein and comprises a sequence non-identical to naturally DNA sequence encoding the protein {}^{\bullet}
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Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cox VF;
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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/product= "
2845..3142
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73..3147
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/note= "CDS does not include stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Antigen sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                              Score 194.6;
Pred. No. 9.9
                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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RESULT 31
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 Query Match
Best Local
                                                            sequence encoding a naturally occurring protein into a human or animal by administering the pharmaceutical composition into the human or animal, where the administration results in a therapeutic effect on the human or animal. The present sequence is Plasmodium falciparum PfMSP1.19 mutant DNA used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                   Novel variant DNA sequence useful in DNA vaccine, encodes naturally occurring protein and comprises a sequence non-identical to naturally occurring DNA sequence encoding the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4825
                                                                                                                            immunisation vector to encode one or more naturally occurring human or non-human proteins with immunomodulatory properties. The DNA sequence is useful for inducing an immune response to an antigen in a human or animal. A pharmaceutical composition is useful for introducing a DNA
                                                                                                                                                                                within an amino acid codon, is non-identical to the naturally occurring DNA sequence encoding that protein. The DNA sequence is useful in a DNA
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                                       Sequence
                                                                                                                                                                                                                                                            Example 13; Page 72; 87pp; English.
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Local Similarity
                                                                                                                                                                                                                                    invention relates to a variant DNA sequence useful in DNA vaccines
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                                       71 C;
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Score
Pred.
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191.4; DB 2
No. 1.8e-36;
                                       74 T; 0 other;
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d change
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from Cys t
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Chimeric
      Novel variant DNA sequence useful in DNA vaccine, encodes naturally occurring protein and comprises a sequence non-identical to naturally occurring DNA sequence encoding the protein
                                                                                                                                                                                                                                                                                                                                 CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Mutant PfMSP1.19-human C3d3 DNA coding sequence from pVK104-03 vector.
                                                  WPI; 2002-010909/01
                                                                                                                 08-APR-2000; 2000GB-0008582
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                                                                                                                                                                                                                                                                                                                                                                                                                   Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAATGCACCGAGGAAGACAGCGGCTCTAACGGAAAGAAATCACATGCGAGTGTACTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                         immunostimulant; vaccine; immunisation; therapeutic; C3d; response; pVK104-03 vector; ds.
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                                                                                            ADPROTECH LTD
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Plasmodium falciparum
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73..3147
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                                                                                                                                                                                                    "Antigen sequence"
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                                                                                                                                                                                                                                                                                                 "Human C3d3-PfMSP1.19 protein"
DS does not include stop codon"
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                                                                                                                                                                                                                                      C3d3
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                                                                                                                                                                                                                                   protein"
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RESULT 33
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Chimeric -
Chimeric -
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                                                                                            sig_peptide
                                                                                                                                                                                                                                                                                                                                        immune
                                                                                                                                                                                                                                                                                                                                                        Human;
                                                                                                                                                                                                                                                                                                                                                                                         Human C3d3-PfMSP1.19 mutant DNA coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      12-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD22464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD22464 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4585 AACATCTCCCAGCACCAATGCGTGAAGAAAACAGTGCCCCCAGAATAGCGGCTGTTTCAGG 4644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACATTGCCCAACACCAATGCGTTAAGAAGCAAATTCCACAAAACTCCGGATGTTTCAGA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGACTCTTACCCTTTGTTCGATGGAATCTTCTGTTCTTCCTCTAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATCTGGACGAGAGAGAAGAATGGAAGTGTCTGTTGAACTACAAGCAGGAAGGTGATAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCGACTCCTATCCACTCTTCGACGGGATTTTTTGCTCCAGCTCTAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATGCACCGAGGAAGACAGCGGCTCTAACGGAAAGAAAATCACATGCGAGTGTACTAAG 4824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCGTGGAGAACCCAAACCCTACCTGCAATGAAAACAATGGCGGGTGTGACGCCGATGCT 4764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGTGCACCGAAGAAGACTCTGGTTCTAACGGAAAGAAGATTACTTGCGAATGTACTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTGTTGAGAACCCAAACCCTACCTGTAACGAGAACAACGGTGGATGCGACGCTGACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228;
                                                                                                                                                                                                                                                                                                                                                        immunostimulant; vaccine; immunisation;
                                                                                                                                                                                                                                                                                                                                    response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3147 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page
                                                                                                                                                                                                                                                      Homo sapiens.
Plasmodium falciparum
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.9%;
nilarity 78.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73-75;
        /product=
                                                                                                /partial
1..72
                                                                                                                                   /product= "Human
/note= "CDS does
                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    PVK104-04
                                                                     /*tag=
                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            870 A; 754 C;
                                                     .3147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87pp;
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                  "Mature human
                                                                                                                                                                                                                                                                                                                                 vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 191.4;
Pred. No. 6e-3
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            834 G;
                                                                                                                                                     C3d3-PfMSP1.19
                                                                                                                                     not include
                                                                                                                                                                                                                                                                                                                                    ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6e-36;
                  C3d3-PfMSP1.19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T; 0 other;
                                                                                                                                   stop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61;
                                                                                                                                                                                                                                                                                                                                                      therapeutic;
                                                                                                                                                     protein"
                                                                                                                                                                                                                                                                                                                                                                                           from pVK104-04 vector
                                                                                                                                     codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4873
                protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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22-OCT-1991 AAN50354; AAN50354

(first entry)

Storage-specific, plasmid p31-1.

late schizont merozoite malaria

antigen

insert

AAN50354 RESULT 34

standard;

DNA;

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Invention relates to a variant DNA sequence useful in DNA vaccines. The DNA sequence encodes a naturally occurring protein such as C3d which, by virtue of third base redundancy and other variations permissible within an amino acid codon, is non-identical to the naturally occurring DNA sequence encoding that protein. The DNA sequence is useful in a DNA immunisation vector to encode one or more naturally occurring human or non-human proteins with immunomodulatory properties. The DNA sequence is useful for inducing an immune response to an antigen in a human or animal. A pharmaceutical composition is useful for introducing a DNA sequence encoding a naturally occurring protein into the human or animal by administering the pharmaceutical composition into the human or animal. The present sequence is plasmodium falciparum PfMSP1.19-human or animal. The present sequence is plasmodium falciparum PfMSP1.19-human or animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   occurring occurring
 3085
                                   4825
                                                                    3025
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                                                                                                                                                                                                                                                                           2845
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               C3d3 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel variant DNA sequence useful in DNA vaccine, encodes naturally occurring protein and comprises a sequence non-identical to natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Steward M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-APR-2000; 2000GB-0008582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ADPR-) ADPROTECH LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200177324-A1
                   CCCGACTCCTATCCACTCTTCGACGGGATTTTTTTGCTCCAGCTCTAATT 4873
 CCAGACTCTTACCCTTTGTTCGATGGAATCTTCTGTTCTTCCTCTAACT
                                                                    AAGTGCACCGAAGAAGACTCTGGTTCTAACGGAAAGAAGATTACTTGCGAATGTACTAAG
                                                                                                  AAATGCACCGAGGAAGACAGCGGCTCTAACGGAAAGAAATCACATGCGAGTGTACTAAG 4824
                                                                                                                                                       TGCGTGGAGAACCCAAACCCTACCTGCAATGAAAACAATGGCGGGTGTGACGCCGATGCT
                                                                                                                                                                                                        CATCTGGACGAGAGAGAATGGAAGTGTCTGTTGAACTACAAGCAGGAAGGTGATAAG
                                                                                                                                                                                                                                        AACATTGCCCAACACCAATGCGTTAAGAAGCAAATTCCACAAAACTCCGGATGTTTCAGA 2904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002-010909/01
                                                                                                                                     {	t TGTGTTGAGAACCCAAACCCTACCTGTAACGAGAACAACGGTGGATGCGACGCTGACGCT}
                                                                                                                                                                                                                                                                                                                                              228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Page
                                                                                                                                                                                                                                                                                                                                                                                                             3147
                                                                                                                                                                                                                                                                                                                                                                                                                                           coding sequence from vector pVK104-04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA sequence encoding the
                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001WO-GB01599
                                                                                                                                                                                                                                                                                                                                                                                                             BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76-78;
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                                                                                                                                                                                                                                                                                                                                                                                                             870 A; 754 C; 834 G; 689
                                                                                                                                                                                                                                                                                                                                                         3.9%;
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                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                          Pred. No. 6e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            Score 191.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                            6e-36;
                                                                                                                                                                                                                                                                                                                                                                                                             T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                            DB 24;
                                                                                                                                                                                                                                                                                                                                            61;
                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                       4764
                                                                    3084
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AATO5868
ID AATO5
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XX L14-AU
DT 114-AU
XX Chick
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local S
 Chicken
                             Chicken leucocytozoan; immunisation; vaccinat
                                                                     Chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The DNA sequence encodes a Plasmodium falciparum, plasmodium vivax plasmodium malariae and plasmodium ovale antigen which may be used in the diagnosis of malaria and as a vaccine against malaria. Nucleotides 293-422 and 429-530 are used in the preparation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prodn. of antigens of Plasmodium species, esp. recombinant DNA methods giving polypeptide(s) against malaria or for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W08503725-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium
                                                                                              14-AUG-1996
                                                                                                                         AAT05868;
                                                                                                                                                  AAT05868 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              monoclonal antibodies against the malaria antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 5; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mach B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-FEB-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-FEB-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-AUG-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Malaria; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BIOJ )
                                                                                                                                                                                                                   198
                                                                                                                                                                                                                                              262
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                                                                                                                                                                                                                                                                                                                                                                                           TATCAGGAGCTGGTTAAGAAACTGGAAGCTTTGGAAGATGCCGTCCTTACCGGATACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1985-223371/36
                                                                                                                                                                                                                              GGGGGTTCCGTCGCCTCCGGCGCAGCGTGGCATCAGGTGGCTCAG 307
                                                                                                                                                                                                                                                                                              AGCACACCCGGTTCTAAAGGGTCTGTGGCTAGCGGTGGCTCCGGTGGGTCTGTGGCCTCT
                                                                                                                                                                                                                                                                                                                          TTATTTCAAAAGGAAAAAATGGTATTAAATGAAGGAACAAGTGGAACAGCTGTTACAACT
                                                                                                                                                                                                                                                                                                                                                   CTGTTCCAGAAGGAGAAGATGGTGCTGAATGAAGGGACGAGTGGCACGGCCGTTACAACC
                                                                                                                                                                                                                                                                                                                                                                             TATCAAGAACTTGTCAAAAAACTAGAAGCTTTAGAAGATGCACTATTGACAGGTTATAGT
                                                                                                                                                                                                                  GTTGCTTCAGGTGGTTCAGGTGGCTCAGTTGCTTCAGGTGGTTCAG
                                                                                                                                                                                                                                                                     AGTACACCTGGTTCAGGTGGTTCAGTTACTTCAGGTGGTTCAGGTGGTTCAGTTGCTTCA
leucocytozoan
                                                                 leucocytozoan DNA encoding immunogenic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAP50303
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 87
                           vaccination;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=  a
/label= malaria antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasmid
                                                                                                                                                 DNA; 3399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; 49 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McGarvey M,
                                                                                                                                                                                                                                                                                                                                                                                                                                             2.4%;
                                         immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p31-1;
                             SS
                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 119.2; DB 6;
Pred. No. 6.8e-19;
0; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 G;
                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cheung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ยู่
                                        recombinant vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shaw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                243
                                                                  for vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                0,
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                                                                                                                                                                                                                                1978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT05868 encodes a chicken leucocytozoan immunogenic protein, this DN or a fragment of it can be used in a recombinant vaccine to immunise against chicken leucocytozoan disease. The DNA is used in a vector and operatively linked to an expression regulatory sequence as in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                           2038
                                                                                                                                                                                                                                                                                   1918 GAAGAAGTAATACATGAAGAAGAAAAAGAAGAAGTAACACATGAAGAAATAGAAAAAGAA
                                                                                                                                                                                                                                                                                                                                      1858 GTAATACATGAAGAAGAAAAAAGAAGTAACACATGAAGAAATAGAAAAAAGAAGAGCAT
                                                                                                                                                                                                                                                                                                                                                                                         1798 CATGAAGAAGAAAAAGAAGAAGTAACACATGAAGAAAAAAGAAAAAGAAGAAGAGCATGAAGAA 1857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB;
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(KITA ) KITASATO KENKYUSHO SH.
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nes 563; Conserv
                                                                                    GAAAGAGATCAAAGAGATĆGCCAAAACCATTAAGTTCAACATAGATTCTCTCTTTTACTGA 1121
                                      TCCCCTTGAGCTGGAGTACTACTTGAGAGAGAAGAATAAGAATATAGACATCTCCGCCAA 1181
                                                                                                                                       CAACTCTGGGAACACCCCTAACACGCTGCTGGACAAGAACAAGAAGATAGAGGAGCACGA 1061
                                                                                                                        ATAGAAAAAGAAGAAGCATGAAGAAGTAATACATGAAGAAGAAAAAAGAAGTAACACAT
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use as insert in a recombinant vaccine
against chicken leucocytozoan disease"
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                Plasmodium vivax
                                                         antigen-antibody
                                                                     Merozoite surface
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                                                                                                 vivax merozoite
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                                                         composite;
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                                                                     ,malaria; blood;
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                                                                                                 protein
                                                      Immunosorbent Assay;
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Matches 234; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents a DNA encoding the Plasmodium vivax merozoite surface protein (MSP) C-terminal region. The C-terminal region of the merozoite surface protein has a strong antigenicity in malarial diseases. For diagnosis of malaria, recombinant proteins with enhanced antigenicity, obtained by addition of fusion proteins to surface protein C-terminal regions, can be reacted with serum or blood of a Plasmodium infected patient. Antigen-antibody composites will be formed, and these recombinant antigens provide a quick and reliable diagnosis of malaria, with good sensitivity and selectivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
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25-APR-2000;
20-MAY-2000;
                                                                                                                                                                                                                                                                                                                                               4488 TCTCCTGACCAAGTTTCTGTCCACTGGCATGGTGTTCGAAAACCTCGCCAAAACAGTGCT 4547
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P-PSDB; AAU00669.
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                                                                                                                                                                                                                                                                                                                   189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene encoding merozoite surface protein of Plasmodium vivax, \boldsymbol{u}_{\boldsymbol{i}} producing protein for diagnosis of malaria and for vaccination
                                                                                                                                                                                                                                                                    GAGCAATCTGCTCGACGGCAACCTGCAGGGGCATGCTGAACATCTCCCAGCACCAATGCGT
                                                                                                                                                                                                         GAAGAAACAGTGCCCCCAGAATAGCGGCTGTTTCAGGCATCTGGACGAGCGCGAAGAGTG
                                                                                 CTGCAATGAAAACAATGGCGGGTGTGACGCCGATGCTAAATGCACCGAGGAAGACAGCGG
                CTCTAACGGAAAGAAATCACATGCGAGTGTACTAAGCCCGACTCCTATCCACTCTTCGA
                                                                                                                          GAGATGCTTGTTAAACCTTTAAAGAAGAAGGCGGCAAGTGTGTGCCCAGGATCGAATGTGAC
                                                              TTGTAAGGATAACAATGGTGGTTGTGCCCCCTGAAGCTGAATGTAAAATGACGGACAGC--
                                                                                                                                                         CAAGTGTCTCCTGAACTACAAACAAGAAGGAGATAAGTGCGTGGAGAACCCAAACCCCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                            618 BP; 207 A; 114 C; 147 G; 150 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                Conservative
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2000KR-0022041.
2000KR-0027305.
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· AATAAAATCGTCTGTAAATGTACAAAAGAAGGTTCTGAGCCACTCTTTGA
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4848

CGGGATTTTTTGCTCCAGCTCTAATTTCCTGGGCATCTTCCTTGCTGATCCTCATGCT

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cc vaccine. A novel expression vector contains a sequence encoding an cc immunogenic merozoite surface antigen-1 peptide (MSA-1), and a cc mammalian signal (AAM34595-96) and/or anchoring sequence (AAM34598). CC The signal peptide contains 3 regions, a first or c region at the cc carboxy end of the peptide which serves as the cleavage site for a cc signal peptidase enzyme, a second or h region which is N-terminal to cc The c region (and highly hydrophobic), and a third region or n region cc The vectors (or analogues that express MSA-1 without either signal or can are used in vaccines to prevent or treat malaria caused by car used in vaccines to prevent or treat malaria caused by cc Plasmodium falciparum. The chimeric proteins can also be used in cc vaccines. The vaccinia vector expresses the antigen fragment for many cc days, or even years, generating a long-lasting immune response (humoral and/or cell-mediated) against the merozoite form of the parasite, in thumans or other animals.
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Matches 124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 19; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        merozoite surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Davidson EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal peptide; malaria; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding signal peptide 2 which is used in a malaria vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT93729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT93729 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Malaria vaccine - comprises expression vector expressing fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-393372/36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lmmune response; humoral; cell-mediated; merozoite; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     597 TTTCCT 602
                                                                                                                                     Local Similarity
61
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              ACCCACGAATCCTATCAGGAGCTGGTTAAGAAACTTGGAAGCTTTGGAAGATGCCGTCCTT 129
                                                                           ATGAAAATCATTTTCTTCCTCTGTTCATTTCTGTTTTTTATCATCAATACTCAGTGCGTG
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ACACATGAAAGTTATCAAGAACTTGTCAAAAAACTAGAAGCTTTAGAAGATGCAGTATTG
                                                           ATGAAGATCATATTCTTTTTATGTTCATTTCTTTTTTTTATTATAAAATACACAATGTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         recombinant vaccinia virus;
                                                                                                                       Conservative
                                                                                                                                                                                   BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-US01395
                                                                                                                                                                                 65 A; 16 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                     2.0%;
75.2%;
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                                                                                                                       0,
                                                                                                                                  Score 99.4
Pred. No.
                                                                                                                                                                                 24 G; 60 T; 0 other
                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     merozoite
                                                                                                                                                   99.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum;
                                                                                                                                     3.3e-14;
                                                                                                                                                   DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     surface antigen-1 peptide;
                                                                                                                     41;
                                                                                                                     Indels
                                                                                                                                                   Length
                                                                                                                                                     165;
                                                                                                                     0;
                                                                                                                                                                                                                                             (humoral
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RESULT 38
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                                                                                     stage major merozoite surface antigen (MSP-1) immunogenic peptide, cpl15MSP-1 (see AMS0527). The invention relates to a malaria vaccine comprising an expression vector, preferably a defective venezuela equine encephalitis (DVEE) viral vector system, which expresses pl15MSP-1 or its immunogenic fragment raises a humoral and/or cell-mediated response to the erythrocytic merozoite malaria antigen, protecting the patient from a subsequent malaria infection. The DVEE viral vector system continues to express antigen in the patient for a pariod of days, months or even years. Inclusion of a signal peptide and/or an anchor peptide sequence in the pl15MSP-1 antigen produces an immunogenic response which is significantly (i.e. at least about 2 times and as much as 100 times or more) greater than the immunogenic response produced by pl15MSP-1 which does not contain the signal or anchor peptide sequence.
 Matches 124;
                                                               Sequence 165 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel vaccine for immunizing mammals against plasmodium falciparum infection, comprises a viral vector system expressing protein corresponding to specific domain of major merozoite surface protein of plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                               The present sequence is that of DNA encoding a typical mammalian signal peptide sequence (see AAM50529). Such a signal peptide sequence may be incorporated into chimeric proteins of the invention that also include the plasmodium falciparum erythrocytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Merozoite surface antigen; 1; MSP-1; pl15MSP-1; antigen; immu malaria; vaccine; Venezuela equine encephalitis virus; DVEB; vector; immunisation; Plasmodium falciparum; signal peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAI70929 standard;
                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 20; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAM50529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Davidson E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAY-2000; 2000US-202430P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding signal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) UNIV GEORGETOWN.
                Similarity
Conservative
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                                                             65 A; 16 C;
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                Pred.
                                                             24 G;
                             Score
Mismatches
                99.4;
No. 3.
                                                               60 T; 0 other;
                .3e-14;
                              DB 24;
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 Indels
                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                        surface protein
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                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                       capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                              4730
                                                                                      1307
                                                                                                                                   4670
                                                                                                                                                                                                                                                                                                 Sequence 5688 BP; 1925 A; 1719 C; 1147 G; 897 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 31102; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila; developmental biology;
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                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                       ATAACGATATCAACAACGCTCTCAACGAGCTCAATAGCTTCGGTGACTTGATTAACCCCT 1306
TCAACGAAATCAAGGAGAAGATCAAAATTGAGAAGAAAATTGAGAGTGACAAGAAAA 1426
                                          AAAATAACATCCAAAGCCAGAATGAGAACAACAACCAAAATAACATCCAAAGCAAGAATC
                                                                                  TCGATTATACGAAAGAACCCTCTAAGAATATCTACACAGACAATGAGAAGAAGAAGTTTA 1366
                                                                                                                              ATGAGAACAGCAACCACAATAACAACGAGAACATCCAAAGCAAGAATGAGAACAACC
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Pred. No. 6.4e-10;
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                    23-MAR-2001; 2001WO-US09231
                                                                27-SEP-2001.
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melanogaster genomic polynucleotide SEQ

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biology; cell signalling;

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Matches 377; Conserv
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11-JUL-2000; 2000US-0614150
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                         TTGAGAAGAAGATTACAAAAGACGAAAATAAACCAGATGAGAAGATCCTGGAGGTCTCCG
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                                                                                                                                                                                                            AAQ87587-89 encode polypeptides having a whole or partial epitope of a structural protein of Leucocytozoan protozoa (see AAR70491-93). The polypeptides and DNA encoding them are useful in the production of vaccines for the treatment of leucocytozoanosis of fowl.
                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                             Claim 1;
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P-PSDB; AAR70491.
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                                                ATATTGTTAAAGTCCAAGTGCAGAAGGTGCTCCTCATGAACAAGATTGATGAACTCAAGA
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                                                                                                                                                                                                                                                                                           Page 12-14; 20pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               macular degeneration, arteriosclerosis, anaemia, cancer, acute my leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid comprising frag
for diagnosis and treatment
cytosine methylation -
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01-SEP-2000;
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                                    CTCCGCCAAAGTCGAGACAAAGGAATCAACCGAACCTAATGAATATCCCAATGGTGTGAC
                                                                                                                                    GGAGCACGAGAAAGAGATCAAAGAGATCGCCAAAACCATTAAGTTCAACATAGATTCTCT
                                                                                                                                                                                                                                   TAACAAACAGCTTGAAGAAGCCCATAACCTCATCAGCGTACTGGAGAAGCGCATAGACAC
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                                                           GTACCCTCTGTCTTATAACGATATCAACAACGCTCTCAACGAGCTCAATAGCTTCGGTGA
                                                                                     TCCGCCAGCCAACTCTGGGAACACCCCTAACACGCTGCTGGACAAGAACAAGAAGATAGA
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42.6%;
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RESULT 43
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New recombinant multivalent protein deriyed from more than one stage in
                              P-PSDB;
                                                                                                  31-JAN-2000; 2000US-0179213
                                                                                                                                          02-AUG-2001.
                                                                                                                                                             WO200155181-A2
                                                                                                                                                                                                                                 Plasmodium vivax.
                                                                                                                                                                                                                                             Synthetic
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                                                                                                                      29-JAN-2001; 2001WO-US02937
                                                                                                                                                                                                                                                                                                                                                     AAH47054 standard; DNA;
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                              2001-514557/56
DB; AAB85697.
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                                                           Xiao L,
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/product= "ViVaclp"
                                                                                                                                                                                                             Location/Qualifiers
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                                                           Zhou
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                                                                                                                                                                                                                                                                                           encoding recombinant protein ViVaclp
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                                                                               SERVICES
comprising antigenic determandity a life cycle of Plasmodium
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          determinants
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                                                                                                                                                                                                                                                                                                                                                                                                                                             5344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by Plasmodium parasites, such as P. vivax. (I) is especially useful in the treatment, prevention and reduction of malarial infection, as research or diagnostic reagents for the detection of Plasmodium species in a biological sample, and for conferring immunity against multiple stages of the malarial parasite. The antibodies produced are useful for the detection or measurement of antigenic epitopes derived from one or more stages in a life cycle of a parasite, particularly P. vivax. The
                                                           CDS
                                                                                                                                                                                                                                                                  AAH47055;
                                                                                                                                                                                                                                                                                                   AAH47055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5164 AGCTCCGAGCACACGTATAGACACCAATGTGCCTGATAATGCAGCCTGCTATAGGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine comprising the recombinant proteins, is cost-effective, health promoting intervention for controlling, preventing or treating the incidence of malaria. The present sequence represents a synthetic gene ViVacl encoding the recombinant protein ViVaclp, a multivalent and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                than one stage in a life cycle of a Plasmodium vivax parasite. (I) is useful as a vaccine for stimulating an immune response, specifically a protective immune response that confers increased resistance to infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful as a vaccine for infection -
                                                                                                                        Synthetic
                                                                                                                                                     protozoacide;
                                                                                                                                                                                                   Synthetic gene ViVac2
                                                                                                                                                                                                                                    29-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         multistage vaccine against P. vivax.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to recombinant multivalent proteins (I) that stimulate an immune response to Plasmodium vivax. (I) comprises antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9;
                                                                                                         Plasmodium
                                                                                                                                                                       Multivalent
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                                                                                                                                                                                                                                                                                                                                                                                CCCTTTGAGGGAGTTTTC 5421
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                                                                                                                                                                                                                                                                                                 standard;
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                                                                                                          vivax.
                                                                                                                                                                  protein; immune response; Plasmodium vivax; parasite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                         vaccine;
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                                                                                                                                                                                                   encoding recombinant protein ViVac2p
                                                                                                                                                         malaria;
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                           "ViVac2p"
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Pred. No. 7
                                                                                                                                                                                                                                                                                                 ВP
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                                                                                                                                                         recombinant;
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                                                                                                                                                         ViVac2;
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                  AAA70099
                                                  AAA70099 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant multivalent protein comprising antigenic determinants derived from more than one stage in a life cycle of Plasmodium vivax, useful as a vaccine for treating, preventing and reducing malarial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to recombinant multivalent proteins (I) that mulate an immune response to Plasmodium vivax. (I) comprises an
                                                                                                                                                                                                                                                                                                                                               TTGGACGGAACGGAAGATGGAGATGCTTGTTAACCTTTAAAGAAGAAGGCGCCAAGTGT
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                                                                                                                                         CCCTTTGAGGGAGTTTTC
                                                                                                                                                                           GACTCCTATCCACTCTTC
                                                                                                                                                                                                                                            TGCACCGAGGAAGACAGCGGCTCTAACGGAAAGAAATCACATGCGAGTGTACTAAGCCC
                                                                                                                                                                                                                                                                              GTGCCAGCATCGAATGTGACTTGTAAGGATAACAATGGTGGTTGTGCCCCTGAAGCTGAA
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                                                                                                                                                                                                         TGTAAAATGACGGACAGCAATAAAATCGTCTGTAAATGTACTAAAGAAGGTTCTGAGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2077 A; 1168 C; 1534 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             against P. vivax.
                                                    DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 6101;
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                                                                                                                                                                                                                                                                                         Also described are: (1) nucleotide sequences (II) encoding (1); and (2) vaccines against P. falciparum infection comprising (I) or (II). (I) and (II) are useful for the development of vaccines against P. falciparum infection. (1) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand complexity of the parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new
                                                                                                                                                                                                                                      Best
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                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                            1610 AGAATTCTAAGCATAATCTTGAGAAGCTCACCAAAGCTCTTAAGTATATGGAGGACTATT 1669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteins encoded by chromosome 2 of the human malarial parasite, plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection - \frac{1}{2}
                                                                                                                                                                                                                                                                                         Sequence 3579 BP; 1904 A; 398 C; 552 G; 725 T; 0
                                                                                                                                                                                                                                                                                                                        and protein sequences given in the present invention, specifically mentioned within the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 457-458; 577pp; English
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                                                                                                                                                                                                                                                                                                                                                            drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide
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                                                                                                                                                                                                                                    Local Similarity
ATCAGAAAAAGATAAAGAAGAATCAGAAAAAAGACAAAAGAAAAAAACTGAAGAAGATGAAGA
                                   TCGAAAACGAGATCGAGACGCTTGTTGAGAACATTAAGAAGGATGAAGAACAGTTGTTTG
                                                                                                       AGAAAACAAAGAAGAAACAGAAAGTAGACGAAAAAAAAACAGAAAAAAGCCGAAGAAGTT
                                                                       AGAAGAAGACAAAGAAGAATCAGAAAAAGACAAAGAAGAATCAGAAAAAAGATAAAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) HOFFMAN S.
) CARUCCI D.
) GARDNER M.
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                                                                                                                                                                                                                   Conservative
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protozoacide; infection; insecticide;
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The meth is used: (1), for diagnosis and/or prognosis of side effects of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1485
                                                                                                                                                                                                                                                                                                                                                                                                                                             Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA -
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05-SEP-2000; 2000DE-1044543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphi SNP; cell differentiation; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; DNA;
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therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABG13410-ABG54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in
disclosure of the invention.
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Sequence 646 BP; 118 Α, 46 C; 97 G; 385 T; 0 other;

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AACAATACGAATAACGATAACAATCAAAATAACGATAAC
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Pred. No. 8
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RRESULT 47
RAGA6953
ID ABQ44
AC ABQ4
AC ABQ4
AC ADQ1
DT 12-J
XX
DE Olig
XX
Huma
KW drug
KW drug
KW gast
KW gast
KW SNP;
XX
SS Homc
                               Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism snp; cell differentiation; ds.
                                                                                                          Oligonucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel method for determining the degree of comethylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers comember, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers comember, of oligomers the degree of hybridisation to both classes is determined from the complete on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (1) for diagnosis and/or prognosis of side effects of concertion of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide cystems etc., particularly by detecting mutations or single nucleotide cypes and for investigating call differentiation. The method allows the methylation status of many C residues to be determined simultaneously.

Canadian and continues of many C residues to be determined simultaneously.

Canadian and continues of the degree of cytosine methylation described in the described in the described in the hybridistic of the prognic DNA sequences used to illustrate the content of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA -
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05-SEP-2000; 2000DE-1044543
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                                   TACTCTTACAAAGTGGAGAAACTGACACCATAATACCTTTGCA---TCCTATGAGAAT 1614
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AACGATAACAATACGAATAACGATAACAATCAAAATAACGATAACAATACGAATAAAAAT
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Pred. No. 8
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ARESULT 48
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                  methylation of a particular cytosine in a motification of the genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic CDNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the Classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of the central nervous, cardiovascular, gastrointestinal and respiratory cystems etc., particularly by detecting mutations or single nucleotide types and for investigating cell differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6e-06;
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91

Query Match Best Local Similarity

1.48;

Score 68.6; DB 24; Pred. No. 2.6e-06; 0; Mismatches 524;

Indels Length

9;

Gaps

2

DB 24;

Conservative

690 TCTCGACAACATCAAGGACAATGTGGGAAAGATGGAAGATTATATTAAAAAAGAATAAGAA 749

31 TCTTACTAAAATTACTAATAAAAACGAATACGAATATAAAATACGAATAAAAATACTAATAA

90

750 GACCATCGAGAACATTAACGAGCTGATCGAAGAATCCAAAAAAGACCATAGACAAAAATAA 809

AACGAATAAAAATACGAATAAAAATACTAATAAAAACGAATAAAAATACGAATAAAAATAC

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RESULT 49
ABQ39491
ID ABQ39491
XX ABQ39
XX ABQ39
XX ABQ39
XX ABQ39
XX ABQ39
XX ABQ39
XX ABQ39
XX Huma
KW Huma
KW Gast
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                                                                        systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP'S); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                    is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA -
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05-SEP-2000; 2000DE-1044543
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   969 BP; 645 A; 93 C; 54 G; 177 T; 0 other;
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RESULT 50
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             Synthetic
                                        Multivalent protein; immune response; Plasmodium vivax; parasite; protozoacide; vaccine; malaria; recombinant; ViVaclp; ds.
                                                                                  Synthetic gene ViVac2bias nucleotide sequence
                                                                                                                29-OCT-2001
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                                                                                                                                                                        AAH47056 standard; DNA; 5643
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RESULT 51
AAA65171
ID AAA65
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AC AAA65

AAA65171 standard;

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AAA65171;

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Best Local S
Matches 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protective immune response that confers increased resistance to infection by Plasmodium parasites, such as P. vivax. (I) is especially useful in the treatment, prevention and reduction of malarial infection, as research or diagnostic reagents for the detection of Plasmodium species in a biological sample, and for conferring immunity against multiple stages of the malarial parasite. The antibodies produced are useful for the detection or measurement of antigenic epitopes derived from one or more stages in a life cycle of a parasite, particularly P. vivax. The vaccine comprising the recombinant proteins, is cost-effective, health-promoting intervention for controlling, preventing or treating the incidence of malaria. The present sequence represents the nucleotide sequence of a synthetic gene ViVAc2bias.
                                                                                                                                                                                                                                                                                                                      5376
5604
                                                                             5556
                                                                                                                                                                                               4710
                                                                                                                                                                                                                                       5436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to recombinant multivalent proteins (I) that stimulate an immune response to Plasmodium vivax. (I) comprises antigenic determinants, fragments or conservative substitutions, derived from more than one stage in a life cycle of a Plasmodium vivax parasite. (I) is useful as a vaccine for stimulating an immune response, specifically a protective immune response that confers increased resistance to infection
                                                                                                                                                                                                                                                                                                                                                         4590 CTCCCAGCACCAATGCGTGAAGAAACAGTGCCCCCAGAATAGCGGCTGTTTCAGGCATCT 4649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful as infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5643 BP; 1584 A; 1197 C; 1503 G; 1359 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant multivalent protein comprising antigenic determinants derived from more than one stage in a life cycle of Plasmodium vivax, useful as a vaccine for treating, preventing and reducing malarial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JAN-2000; 2000US-0179213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JAN-2001; 2001WO-US02937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                   CTCCTATCCACTCTTCGACGGGATTTTTTGCTCC 4863
                                                                                                                                                                            GGAGAACCCAAACCCTACCTGCAATGAAAACAATGGCGGGTGTGACGCCGATGCTAAATG
                                                                                                                                                                                                                                                            CTCCGAGCACACTTGTATCGACACTAACGTGCCAGATAACGCTGCTTGTTACAGATACTT
TTCTGAGCCACCCTTCGAGGGAGTTTTCTGTTCC
                                                                             TAAGATG----
                                                                                                                  CACCGAGGAAGACAGCGGCTCTAACGGAAAGAAAATCACATGCGAGTGTACTAAGCCCGA
                                                                                                                                                                                                                                       GGACGGAACTGAGGAGGTGGAGATGTTTGTTGACTTTCAAGGAGGAGGGTGGTAAGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-514557/56
                                                                                                                                                            GCCAGCTTCCAACGTGACTTGTAAGGATAACAACGGTGGTTGTGCTCCAGAGGCTGAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Page 56-59; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    1.4%;
                                                                           - ACTGACTCCAACAAGATCGTCTGTAAGTGTACTAAGGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 67.2; DB 22; Pred. No. 1.4e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 5643;
                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Query Match
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7690
                                  1538
                                                                                                                                    7570
                                                                                                                                                                                                   7510
                                                                                                                                                                                                                                                                                                   1298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polynucleotide encoding a polypeptide which has a activity and comprising a RNA-dependent RNA polymerase of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                кеу
                                                                                                                                                                                                                                                                                                                                                                  1238 CTCTGTCTTATAACGATATCAACAACGCTCTCAACGAGCTCAATAGCTTCGGTGACTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 suppression of genes.
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                                AGAAAATGATGGGAAAAC
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                                                                 AGCTGCTGAACGAGATCTATGATTCCAAATTCAACAATAACATCGACCTGACCAACTTCG
                                                                                                                                                                 ACAAGAAAAGTTACGAAGACCGCAGCAAAAGTCTAAACGATATCACTAAAGAGTATGAAA
                                                                                                                                                                                                   AGAAGTTTATCAACGAAATCAAGGAGAAGATCAAAATTGAGAAGAAGAAATTGAGAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               crassa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers 2447..6655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2089 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAPIENZA
                                  1555
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Pred. No. 5.1e
0; Mismatches
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nes 158;
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Best Local
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                                                                                                                                                                                                                                                                                                                         The present invention provides a number of human immune system associa genes which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
                                                                                                                                                                                 1197 ATCAACCGAACCTAATGAATATCCCCAATGGTGTGACGTACCCTCTGTCTTATAACGATAT 1256
                                                                                                                                                                                                                                                                                         diseases. The
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid comprising fractor diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiinflammatory; cancer; eye disease; arteriosclerosis;
acute_myeloid leukaemia; |Alzheimer's disease; AIDS; epil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiarteriosclerotic;
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                    leukaemia, Alzheimer's rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurofibromatosis; rheumatoid arthritis;
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Local r
278;
                                                              GAAAGAACCCTCTAAGAATATCTACACAGACAATGAGAGAAGAAGAAGTTTATCAACGAAAT
                        CAAGGAGAAGATCAAAATTGAGAAGAAGAAAATTGAGAGTGACAAGAAAAGTTACGAAGA
                                                                                                                             CAACAACGCTCTCAACGAGCTCAATAGCTTCGGTGACTTGATTAACCCCTTCGATTATAC
                                                                                                                                                          AACAAACGAACCTAATTTAAATTCCTATCGCTATCACTATAAACTATAAACTTAAACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens.
                                                                                                    immune system disease;
                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                               14006 BP; 3278 A; 155 C; 3257 G;
                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 1931;
                                                                                                                                                                                                                                                                                                                                                                                                                                     methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Piepenbrock
                                                                                                                                                                                                                                                                                                 Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                            Conservative
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2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001WO-EP07537
                                                                                                                                                                                                                                                                                      present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                fragment of chemically modified 
pent of diseases associated with
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                                                                                                                                                                                                            0;
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0; Mismatches
                                                                                                                                                                                                                       Score 63.8;
Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence Listing; German.
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                                                                                                                                                                                                                                     DB 24;
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AAV207000
ID AAV20
AC AAV20
XX AAV20
AC AAV20
XX 17-AU
XX Open
KW Open
KW antib
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XX Crypt
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                                                                                                                                                                                  Gut J,
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detection; diagnosis; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Open reading frame; ORF; antigen; GP900; cryptosporidium; antibody; prophylaxis; treatment; inhibition; retardation; detection; diagnosis; human; ds.
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                                        Anti-Cryptosporidium antibody - used detection, diagnosis, prophylaxis or
                                                                                                                  P-PSDB;
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DB; AAW48299.
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                                                                                                                                                                                  Leech J,
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                                        to develop products for treatment of Cryptosporidium
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Best Local Similarity
Matches 249; Conserv
                                                     GP900; NINC isolate; glycoprotein; antibody; cryptosporidiosis; competitive inhibition; attachment; invasion; ligand binding; sporozoite; merozoite; diarrhoea; protozoacide; open reading frame; ORF; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence is that encoding the GP900 antigen which may be used in the production of anti-Cryptosporidium antibodies. These can be used for the prophylaxis, treatment, inhibition or retardation of a Cryptosporidium infection in humans or in animals such as calves. They can also be used for the detection and diagnosis of related
Key
                                                                                                                                                                                                                                                                                        1155
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                          Cryptosporidium
                                                                                                                    ORF encoding a portion of Cryptosporidium parvum NINC isolate GP900
                                                                                                                                                    28-OCT-2000
                                                                                                                                                                                AAA61849;
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                                                                                                                                                                                                                                                                                        CAACTACTACTACTACAACC
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                                                                                                                                                                                                                                                                                                                                                    CAACAACAACAACAACAACAACAACAACAACTACCACGAAAACCAACAACAACAACAACAA 1154
                                                                                                                                                                                                                                                                                                                                                                               AGACAAGCTGGCAGATTTCAAGAAAAATAACAATTTCGTCGGAATTGCAGACCTGTCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATCAAGGACTCCATCGACACCGATATCAATTTCGCTAATGATGTGCTGGGGTATTACAA 4169
                                                                                                                                                                                                                                                                                                                      CGATTATAACCACAACAATCTCC 4492
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                                                                                                                                                                                                              standard;
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                            parvum
Location/Qualifiers
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Pred. No. 0.00053;
0; Mismatches 314;
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Best Local :
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29-MAY-1992;
03-APR-1995;
14-AUG-1996;
                                                                                                                                                                                                                                                                                                      agriculture. GP900 fragments, fusion proteins and antibodies may also used for the diagnosis of Cryptosporidium parvum infections, and for the detection of the parasite in the environment. The present sequence represents the open reading frame (ORF) encoding a portion of the GP90 protein of the NINC isolate of Cryptosporidium parvum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          competitively inhibit sporozoite or merozoite attachment or invasion, and are also useful for the generation of anti-GP900 antibodies. The antibodies also inhibit sporozoite or merozoite attachment/invasion and additionally inhibit the binding of GP900 ligands to GP900. GP900 proteins, fragments and antibodies may therefore be used to treat or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cryptosporidium parvum, DNA encoding it, GP900 fragments, and fusion proteins comprising GP900 fragments. The invention also relates to the administration of GP900 or fragments thereof to a host to elicit anti-GP900 antibody production, and to a method of cryptosporidiosis treatment or prophylaxis comprising administration of anti-GP900 antibodies to an individual. Cryptosporidium parvum GP900 and GP900 fragments are able to competitively inhibit sporozoite or merozoite attachment or invasion, and
                                   4050
                                                                                                     3990
                                                                                                                                                                                                                                                                                                                                                                                         prevent cryptosporidiosis. Infection with Cryptosporidium is a common cause of diarrhoea in humans and causes life-threatening diarrhoea in immunocompromised persons. Cryptosporidiosis can be contracted from contaminated municipal water supplies (e.g., public swimming pools). It also a cause of disease in animals, resulting in financial losses in animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to the GP900 glycoprotein of the protozoan Cryptosporidium parvum, DNA encoding it, GP900 fragments, and fu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New GP900 protein fragments and fusion proteins of Cryptosporidium parvum, useful for detecting the presence of the parasite, and diagnosing or treating Cryptosporidium infections by competitive inhibition of the function of GP900 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUN-2000
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                                                                                                                                                                      3930 CAATGTCAACGTGAAGGACATTCTGAACAGCCGCTTTAATAAGAGAGAAAATTTCAAGAA 3989
                                                                                                                                                                                                                                                                         Sequence
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CGTCTTGGAGAGCGACTTGATTCCCTATAAAGACCTGACCTCCTCTAACCTACGTTGTCAA 4049
                                                                                                                                      GGACCCATACAAGTTCCTCAATAAAGAGAAGAGGGATAAATTTCTGTCTAGTTACAACTA 4109
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)B; AAB11727.
                                                                   ) UNIV
                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                         5163 BP;
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                                                                                                                                                                                                          Conservative
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93US-0071880.
92US-0891301.
95US-0415751.
96US-0700651.
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/product= "Cryptosporidium parvum NINC isolate GP900"
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                    The present invention relates to a method of detecting Cryptosporidium biological and environmental samples, and of diagnosing cryptosporidiosis. This involves obtaining a sample and contacting it with Cryptosporidium GP900, P68 or cryptopain antigen, antibody, DNA or RNA, or its variant, mutant or fragment. The method is also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4470
                                                                                                                                          Detecting Cryptosporidium in biological and environmental samples and diagnosis of cryptosporidiosis involves, contacting the sample with Cryptosporidium GP900, P68 or cryptopain antigen, antibody, DNA or RNI
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                                                                                                                            GP900; NINC isolate; glycoprotein; antibody; cryptosporidiosis; competitive inhibition; attachment; invasion; ligand binding; sporozoite;
                                                                                                                                                                DNA encoding
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 3'UTR
                                                                                            Cryptosporidium
                                                                                                                  merozoite; diarrhoea; protozoacide;
                                                                                                                                                                                        28-OCT-2000
                                                                                                                                                                                                                 AAA61848;
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                                                                                                                                                                a portion of Cryptosporidium parvum NINC isolate GP900
                                                                                                                                                                                        (first entry)
                                                                                            parvum
       /product= "Cryptosporidium parvum NINC isolate GP900"
                                                                     Location/Qualifiers
                                  /partial
                                              /*tag=
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GGACCCATACAAGTTCCTCAATAAAGAGAAGAGGGATAAATTTCTGTCTAGTTACAACTA 4109 CGTCTTGGAGAGCGACTTGATTCCCTATAAAGACCTGACCTCCTCTAACTACGTTGTCAA 4049 CAACAACAACAACAACGACAACAACAACAACTACTACAACTACCACTACTACTACGA 673

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Matches Query Match

Local Similarity es 249; Conserv

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Score 60.6; DE Pred. No. 0.000 0; Mismatches

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                                                                                                                                                                                                                          CC Cryptosporidium parvum, DNA encoding it, GP900 fragments and fusion CC administration of GP900 fragments. The invention also relates to the CC administration of GP900 or fragments thereof to a host to ellicit anti-CC or prophylaxis comprising administration of anti-GP900 antibodies to an individual. Cryptosporidium parvum GP900 and GP900 antibodies to an CC competitively inhibit sporozoite or merozoite attachment or invasion, and CC are also useful for the generation of anti-GP900 antibodies. The CC antibodies also inhibit sporozoite or merozoite attachment or invasion and CC antibodies also inhibit sporozoite or merozoite attachment or invasion and CC antibodies also inhibit sporozoite or merozoite attachment/invasion and CC antibodies also inhibit the binding of GP900 ligands to GP900. GP900 proteins, fragments and antibodies may therefore be used to treat or prevent cryptosporidiosis. Infection with Cryptosporidium is a common CC cause of diarrhoea in humans and causes life-threatening diarrhoea in CC immunocompromised persons. Cryptosporidiosis can be contracted from CC contaminated municipal water supplies (e.g., public swimming pools). It is also a cause of disease in animals, resulting in financial losses in CC agriculture. GP900 fragments, fusion proteins and antibodies may also be
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01-JUN-1993;
29-MAY-1992;
03-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New GP900 protein fragments and fusion proteins of Cryptosporidium parvum, useful for detecting the presence of the parasite, and diagnosing or treating Cryptosporidium infections by competitive inhibition of the function of GP900 -
                                                                       detection of the parasite in the environment. The represents genomic DNA encoding a portion of the NINC isolate of Cryptosporidium parvum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 16; Column 41-48; 59pp; English
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P-PSDB; AAB11727.
Sequence
                                                                                                                                                                                             agriculture. GP900 fragments, fusion proteins and antibodies may also be used for the diagnosis of Cryptosporidium parvum infections, and for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to the GP900 glycoprotein of the protozoan
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93US-0071880.
92US-0891301.
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Query Match

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                                                  detecting and identifying individual Cryptosporidium isolates based on
the genetic characteristics, and for diagnosis of prior or concurrent
Cryptosporidium infection. The present sequence is a C. parvum coding
sequence used in the exemplification of the invention.
                                                                                                                                                                                                               The present invention relates to a method of detecting Cryptosporidium biological and environmental samples, and of diagnosing cryptosporidiosis. This involves obtaining a sample and contacting it
                                                                                                                                                                                                                                                                                                                                                                                                         Detecting Cryptosporidium in biological and environmental samples and diagnosis of cryptosporidiosis involves, contacting the sample with Cryptosporidium GP900, P68 or cryptopain antigen, antibody, DNA or RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
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  Sequence
                                                                                                                                                             with Cryptosporidium GP900, P68 or cryptopain antigen, antibody, DRNA, or its variant, mutant or fragment. The method is also useful
                                                                                                                                                                                                                                                                                                                             Disclosure; Page 101-103; 157pp; English.
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neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
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    30-JUN-2000;
                                 02-JUL-2001;
                                                              03-JAN-2002
                                                                                            WO200200928-A2
                                                                                                                                                                                                                    antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                              Human immune system associated
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                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249;
                                                                                                                                                                                                                                                                   immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                           standard;
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bowel disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of human immune system associate genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AlDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with cytosine methylation \, -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 1670; 32pp + Sequence Listing; German
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GAAGAATAAGAATATAGACATCTCCGCCAAAGTCGAGACAAAGGAATCAACCGAACCTAA 1211
                                                                                                                                                                                                  TAAGTTCAACATAGATTCTCTTTACTGATCCCCTTGAGCTGGAGTACTACTTGAGAGA 115:
                                                                                                                                                                                                                               GGACAAGAACAAGAAGATAGAGGAGCACGAGAAAGAGATCAAAGAGATCGCCAAAACCAT 1091
                                                                                                                                                                                                                                                                                                                                           CCAGTACGACCTGTCCATCTATAACAAACAGCTTGAAGAAGCCCCATAACCTCATCAGCGT 911
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                                                                                  TGAATATCCCAATGGTGTGACGTACCCTCTGTCTTATAACGATATCAACAACGCTCTCAA
                                                                                                               GATTAATGAAATTAAGAATCCTCCGCCAGCCAACTCTGGGAACACCCCTAACACGCTGCT
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Similarity 42.2%;
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Pred. No. 0.00076;
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                                            surface protein (MSP). The C-terminal region of the merozoite surface protein has a strong antigenicity in malarial diseases. For diagnosis malaria, recombinant proteins with enhanced antigenicity, obtained by addition of fusion proteins to surface protein C-terminal regions, can reacted with serum or blood of a Plasmodium infected patient. Antigen-antibody composites will be formed, and these are detected by Enzyme Linked Immunosorbent Assay (ELISA). The recombinant antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2592
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                                                                                                                            The sequence represents a DNA encoding a Plasmodium vivax merozoite
                                                                                                                                                                              New
for
                                                                                                                                                                                                                P-PSDB;
                      provide a quick and reliable diagnosis
and selectivity.
                                                                                                                                                       Claim
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                                                                                                                                                                                                                                                    Park H;
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25-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigen-antibody composite;
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                                                                                                                                                                                                                                                                           (HUMA-)
                                                                                                                                                                            gene encoding merozoite surface protein of Plasmodium vivax, useful producing protein for diagnosis of malaria and for vaccination \boldsymbol{\cdot}
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DB; AAU00668.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vivax.
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2000KR-0022041
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/product= "P. vivax merozoite surface protein"
/note= "No start or stop codon"
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Query Match Best Local Similarity

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Score Pred.

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                     435 TGATGAGCAAAACAAAAT 452
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TOPOLOGY: linear
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TELEFAX: (212) 840-0712
TELEX: 42506 CURTMS
INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                         FILING DATE: 09-JUN-1994

CLASSIFICATION 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,783

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/852,305

FILING DATE: 18-MARR-1992

PRIOR APPLICATION DATA: US 07/852,305

FILING DATE: 18-MARR-1992

PRIOR APPLICATION UNMBER: US 07/672,183

APPLICATION NUMBER: US 07/672,183

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                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 45,506
TELECOMMUNICATION INFORMATION
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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                                                          Score 1265.2;
Pred. No. 0;
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US-09-690-625-5

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US-08-155-888-1

US-08-811-566-1

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TTGGACGTATTGAAGAAGTTGGTCTTCGGATATCGCAAGCCTCTCGACAACATC	649 721	DЪ
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AACTATCTCCTCACTATCAAGGAGCTGAAGTÂCCCACAGTTG	409 481	gb dy
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ACCEGATACASCCTETTCCAGAAGGAAGATGGTGCTGATA 	21	B 4
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2131 GAGATAACCGGACAGGCTACCACCAAGCCCGGACAACAGGCCGGTTCAGCTCTCGAAGGC 2190	Оу
2071 GAGAAGAAGATTAAAACTGAAGGACAGTCAGATAACTCCGAGGCCTTCCACAGAAGGA 2130	Qу
011 AAGAAAGAGATAGACAAACTGAAAGTGTTCATGCCCAAAGTCGAGAGCCTGATCAACGAA 2 	Qу
951 CATGTGCCGAATAGTTATAAGCAGGAGAATAAGCAGGAACCATACTACCTCATCGTACTC	Qу ДЪ
1891 ATTGATGAACTCAAGAAGACTCAATCTGAAGAACGTGGAGTTAAAACATAATATA 1950	ДУ
ATCCTGGAGGTCTCCGATATGTTAAAGTCCAAGTGCAGAAGGTGCTCCTCATGAACAAG	Др. Оу
771 GATGAAGAACAGTTGTTTGAGAAGAAGAAGATTACAAAAGACGAAAATAAACCAGATGAGAAG	Qу
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591 AATACCTTTGCATCCTATGAGAATTCTAAGCATAATCTTGAGAAGCTCACCAAGCTCTT	Q y
1531 AACTTCGAGAAAATGATGGGAAAACGGTACTCTTACAAAGTGGAGAAACTGACACACAC	Qy Db
1471 TATGAAAAGCTGCTGAACGAGATCTATGATTCCAAATTCAACATAACATCGACCTGACC 1530 	Оy
1411 GAGAGTGACAAGAAAAGTTACGAAGACCGCAGCAAAAGTCTAAACGATATCACTAAAGAG 1470	Qу Db
1351 GAGAGAAAGAAGTTTATCAACGAAATCAAGGAGAAGATCAAAATTGAGAAGAAGAAAATT 1410 	Qy Db
1291 GACTTGATTAACCCCTTCGATTATACGAAAGAACCCTCTAAGAATATCTACACAGACAAT 1350 	Qу
1240 CTGTCTTATAACGATATCAACAACGCTCTCAACGAGCTCAATAGCTTCGGT 1290	Db Oy
1188GACAAAGGAATCAACCGAACCTAATGAATATCCCAATGGTGTGACGTACCCT 1239	Qy Db
1129 GAGCIGGAGTACTACTIGAGAGAGAGAATAAGAATAAGAACATCICCGCCAAAGTCGA- 1187 	Db Cy

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TCTTAGATGTA 41	129 TTAAATTTGA	Db
TGAACAGCCGCTTTAATAAGAGAGAAAATTTCAAGAA	3934 GTCAACGTGAAGGACATTCTGAACAGCCGG	Qy
TITAAAAAAACAAATTGAAAAAAACATT	4069 TTAGCTGGAGTATATAGAAGCTTAAAAAAAA	Db
VGCTGGAGAATAACGTGATGACCTTC	3874 CTGGCAGGCGTCTATAGGTCTCTCAAGAA	Qy
TCAGGATTTGAAAATGAATATGATGTTATATATTTAAAACCT 4068	4009 ACAATGGATAATATCCTCTCAGGATTTGAA	Db
CAAAATCGAGAACGAATACGAAGTGCTCTATCTGAAACC	ATTCTG	Qy
ATTTAGATCAAGTAGTAACTGGAGAAGCAATATCTG	ATTTAGATO	Db
ACCTCGGCCAGGTGGTCACCGGTGAGGCTGI	AGGACTACGATGACCTCGGCC	Qy
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GCATCTACTCATGTCGGAGCCGAGTCCAATACAATTACC 36	642 ACCTAAGAAGCCTGCATC	, Q
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rgtctgaatctggctccgacacactggagcagt	3597	, Qy
CCCAGAAGCAAAAGTTACAACAGTT	AATCTTACGAAAATTTTCTCCCAG	Db
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PAATTCTCCAAGTGAAAATAATAAGAAAGTTAACGAAG	PAATTCTCC	Db
CAATAGCCCAAGCGAGAATAATACAGACGTGAATA	AGAACAAGAACTACACCGGCAATAGCCC	Qy
ATCATTTAATTACTG	TATCTTTATCAAGTGGATTAC	Db
ATCACCTGATCGCCGAGCTCAAGGAAG3	3433 AAGCTCAGCTACCTCTCTAGCGGACTGCAI	Qy
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FATCAATTCAAACAGAAGATAATTATGCCAATTTAGAAAAA 3531		Db
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GTCAAGTATTATAATGGCGAGTCTTCTCCT 3	253 AAGATTCTTCTCAAACACTACAAAGGCCT	Qy
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                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                             APPLICANT: Chang, Sandra
APPLICANT: Hui, George
APPLICANT: Barr, Philip
APPLICANT: Glbson, Helen
TITLE OF INVENTION: BACULOVIRUS PRODUCED PLASMODIUM
TITLE OF INVENTION: FALCIPARUM VACCINE
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                      NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Davis Hoxie Faithfull Hapgood
STREET: 45 Rockefeller pl.
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                                                        STREET: 45 ROCK
CITY: New York
STATE: N.Y.
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 212-586-1461 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                         4005
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4245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 11:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-757-2200
TELEPHAX: 212-586-1461
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                                                                                                         4185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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Pred. No. 7.3e-78;
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                       APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKMER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
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CORRESPONDENCE ADDRESS:
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                             PRIOR APPLICATION DATA:
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                                                                                                                                                                                                   COUNTRY: USA
ZIP: 22313-0299
                                                                  APPLICATION NUMBER: FILING DATE:
APPLICATION NUMBER: FILING DATE:
                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                       ADDRESSEE:
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APPLICANT: PETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: MEISON, RICHARD, C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCIDES, ANTIBODIES, PROTITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
FILLE REFERENCE: 480.19-4(HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
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                                                                                                                                                                                        Sequence 1, Application US/08700651B Patent No. 6015882
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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EARLIER FILING DATE: 1995-04-03 NUMBER OF SEQ ID NOS: 15

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SEQ ID NO 1
LENGTH: 5163
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Best Local Similarity
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                                                                                                                      APPLICANT: Petersen, C
TITLE OF INVENTION: PE
TITLE OF INVENTION: FC
TITLE OF INVENTION: SI
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                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA STREET: 385 Sherman Avenue, Suite 6
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                                                                                                              NUMBER OF SEQUENCES:
COMPUTER READABLE FORM:
                         STREET: 385 Sher
CITY: Palo Alto
STATE: CA
COUNTRY: USA
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PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,

THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
SPECIES INFECTIONS
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REGISTATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 488
TELECOMMUNICATION INFORMATION:
TELECHONE: 650-324-1677
1154
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ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
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CURRENT APPLICATION DATA:
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Local Similarity 44.2%;
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CAACTACTACTACTACAACC
                            CGATTATAACCACAACAATCTCC
                                                         CAACAACAACAACAACAACAACAACAACAACTACCACGAAAACCAACAACAACAACAA 1153
                                                                                    AGACAAGCTGGCAGATTTCAAGAAAAATAACAATTTCGTCGGAATTGCAGACCTGTCTAC
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Sequence 3, Application Patent No. 6071518
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Matches 249; Conserv
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LENGTH: 5318
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CURRENT APPLICATION NUMBER: US/08/700,651B

CURRENT FILING DATE: 1997-08-14
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APPLICANT: NELSON, RICHARD, C.
APPLICANT: GUT, JIRI
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Pred. No. 1.1e-05;
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US-08-928-361B-3
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Best Local Similarity
Matches 249; Conserv
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INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                          4110 TATCAAGGACTCCATCGACACCGATATCAATTTCGCTAATGATGTGCTGGGGTATTACAA 4169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC:DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                     4050 GGACCCATACAAGTTCCTCAATAAAGAGAGAGAGAGAGATAAATTTCTGTCTAGTTACAACTA 4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3930 CAATGTCAACGTGAAGGACATTCTGAACAGCCGCTTTAATAAGAGAGAAAATTTCAAGAA 3989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: | MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                    794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 385 Sner
CITY: Palo Alto
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REGISTRATION NUMBER: 30,518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                  AGTGAACGACAAAATCGACCTCTTCGTAATTCACCTGGAGGCCAAGGTCCTCAACTATAC 4349
CCACAACAACAACAACAACAACTACAACTACCAAGAAACCAACAACTACTACTA 1033
                                                                          GCAAGGCGAGAATGAAAAATATCTGCCCTTCCTGAATAACATCGAAAACCCTGTACAAGAC
                                                                                                                                                                                            GATCCTGAGCGAAAAATACAAGTCTGACCTTGACTCTATTAAAAAGTATATCAACGATAA 4229
                                                                                                                                                                                                                                    CGTCTTGGAGAGCGACTTGATTCCCTATAAAAGACCTGACCTCCTCTAACCTACGTTGTCAA 4049
                                                                                                                                                       'RY: USA
94306-1840
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DEDNESS: double
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EPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
THEIR FUNCTIONAL MUTANTS, VARLANTS, ANALOGS AND FRAGMENTS
FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
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                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                         TELEPAX: 650-324-1678
(INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5511 base pairs
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                      1094
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS: JONES & BIKSA
ANDRESSEE: PETERS, VERNY, JONES & BIKSA
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APPLICATION NUMBER: US 60/026,062

FILING DATE: 13-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 650-324-1677
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                                                                                                                                                                                                                                                                                       LENGTH: 5511 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Palo Alto
                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
ATACAAGTTCCTCAATAAAGAGAAGAGGGATAAATTTCTGTCTAGTTACAACTATATCAA 4115
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                                                              GGAGAGCGACTTGATTCCCTATAAAGACCTGACCTCCTCTAACTACGTTGTCAAGGACCC 4055
                                                                                                CCACGACAACTACAACCACCACCAACTACCAAGAAACCAACAACAACAACAACAACAACAA 1153
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                                                                                                                                                                      216;
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45.2%;
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THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
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                                                                                                                                                                                      Score 58.8; DB 3; Pred. No. 3.2e-05;
                                                                                                                                                                    Mismatches 262;
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                                                                                                                                                                   Gaps
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US-08-928-361B-1
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Query Match
Best Local Similarity
Matches 216; Conserv
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                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HTELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
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INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361
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CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
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                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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                                                                                                 TOPOLOGY: 1
MOLECULE TYPE:
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TELEPHONE: 650-324-1678
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                                                                                                                                                              TYPE:
                                                                                                                                        STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGACAAAATCGACCTCTTCGTAATTCACCTGGAGGCCAAGGTCCTCAACTATACTTACGA 4355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGAGAATGAAAAATATCTGCCCTTCCTGAATAACATCGAAACCCTGTACAAGACAGTGAA 4295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94306-1840
                                                                                                                                                          nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA
                                                                                                                                                                          7334 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MBER: US/08/928,361B
12-SEP-1997
                                                                                               DNA (genomic)
                    1.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS, THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES INFECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carolyn
                                                                                                                                                                                                                   1:
                                                                                                                                                                                                                                                                                                480.76-1(HV)
  Score 58.8; DB 3;
Pred. No. 3.8e-05;
0; Mismatches 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version
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                                      Length 7334;
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US-08-938-105-2
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                                                                                                                TELEFAX: (303) 863-02
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                              ATTORNEY/AGENT INFORMÁTION:
NAME: Crook, Wannell M.
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Leinwand, APPLICANT: Vikstrom,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3062
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                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3182 CTACTACTACAACCAAGAAACCAACAACAACTACCACTGCCACAACAACAACTACTAC 3239
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                                                                                                                                                                                                                                                                              FILING DATE: CLASSIFICATION:
TOPOLOGY: 1
                                                                                                                                                       TELEPHONE:
                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                             LENGTH:
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ucleic acid
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                                                                                                                                       (303) 863-0223
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                      Linear
                                                                                                                                                         (303) 863-9700
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                                                                                                                                                                                                                 31,071
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,452A
FILING DATE: 18-JUL-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2436
                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Clarke, Adrienne E
TITLE OF INVERVION: Plant Arabinogalactan Protein (AGP) Genes
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
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SEQUENCE
                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                         TELEFAX:
                                                                                                                    REGISTRATION NUMBER: 34,464
REFERENCE/DOCKET NUMBER: 27
                                                                                                                                                         NAME: Caruthers, Jennie M
                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Boulder
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                                                                           TELEPHONE:
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  CHARACTERISTICS
                                           49617824
                                                                                                                                                                                                                                                                                                                                                                                                                    Colorado
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5370 Manhattan Circle, Suite
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Du, He
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                                                             (303)499-8089
                                                                                                                                                                                                                                                                                                                                                                                                   United States
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gane, Alison M
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                                                                                (303)499-8080
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Pred. No. 0.0071
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Best Local Sim
Matches 202;
                                                         Sequence 25, Application Patent No. 5830747
                            GENERAL INFORMATION: APPLICANT: Chen,
                                                                                                                                                                                                                                                3445
                                                                                                                                                                                                                                                                                                                                                                       3325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature LOCATION: 41..112
OTHER INFORMATION: /note OTHER INFORMATION: corre
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               APPLICANT:
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 APPLICANT:
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               Shaio-Lim
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31 are
26 can
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corresponding to the peptide sequence by protein
microsequencing"
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28, 30, 32-37 are identical
by protein microsequencing"
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Pred. No. 0.00
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LOCATION: 25..31
OTHER INFORMATION: /note=
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OTHER INFORMATION: 26 can
US-08-798-744-25
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Best Local Similarity
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TELEX: 49617824
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 13-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/27
FILING DATE: 18-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Caruthers, Jennie M.
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Plant Arabinogalactan Protein (AGP) Genes
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OTHER INFORMATION:
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CITY: B
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TOPOLOGY: linear
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REGISTRATION NUMBER: 34,40
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31 are hydroxylated proline
26 can be T instead of A"
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28, 30, 32-37 are identical
by protein microsequencing"
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                                                                                                                    Score 49.6; DB Pred. No. 0.004; 0; Mismatches 2
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                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (303)499-8080
TELEFAX: (303)499-8089
                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/276,452A
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner,
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                                                                                                                               SEQUENCE CHARACTERISTICS
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                                FEATURE
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                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY
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                                                                                                                                                                                                                             NAME: Caruthers, Jennie M. REGISTRATION NUMBER: 34,464 REFERENCE/DOCKET NUMBER: 27
                                                                                                                                                                                                                                                                                          FILING DATE: 18 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
NAME/KEY: CDS
LOCATION: '60..1442
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Bacic, Antony
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N: 435
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Shaio-Lim
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Ala; 37 and 39 can also be undetermined
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corresponding to the peptide sequence by protein
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CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                   LOCATION: 60..128 OTHER INFORMATION:
                                                                                                                                                                                 NAME/KEY: misc_feature LOCATION: 135..179
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                             /note= "Amino acids 27 to 36, 38,
and 40 are identical to that in the
obtained by direct microsequencing"
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corresponding to the peptide sequence by protein
microsequencing"
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                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
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Best Local Similarity
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                                                                                                                                                                     COMPUTER READABLE FORM:
               PRIOR APPLICATION DATA:
                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                  APPLICATION NUMBER: FILING DATE: Herew
                                 CLASSIFICATION:
                                                                                                    SOFTWARE:
                                                                                                                    OPERATING SYSTEM: WINDOWS
                                                                                                                                       COMPUTER:
                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                       STREET:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                      E: Jane Massey Licata, Esq
210 Lake Drive East, Suite
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                                                  Herewith
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Epitope Ordering and Protein
Restriction Mapping
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Ala; 37 and 39 can
 08/294,133
                                                                 PCT/US95/10668
                                                                                                                                                   3.5 INCH, 1.44 Mb STORAGE
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Pred. No. 0.
                                                                                                                    FOR WORKGROUPS
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PCT-US95-10668-4
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                                                                                                                                                                                COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDDERFECT 5.1
CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1417 GACAAGAAAAGTTACGAAGACCGCAGCAAAAGTCTAAACGATATCACTAAAGAGTATGAA 1476
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REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: PENN-0137
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
                                                                         APPLICATION NUMBER: 08/294,133 FILING DATE: August 22, 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb
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TITLE OF INVENTION:
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                                                                                                                            PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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STRANDEDNESS: Single
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                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                      COUNTRY:
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Local Similarity 52.6%;
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210 Lake Drive East, Suite 201
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Pred. No. 0.0085;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6270771 GENERAL INFORMATION:
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Best Local Similarity
Matches 101; Conserv
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                                                                 TELEFAX: (703) 836-20 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: DRUILHE, Pierre TITLE OF INVENTION: DESTINE SEQUENCES SPECIFIC FOR THE TITLE OF INVENTION: HEPATIC STAGES OF P. FALCIPARUM BEARING EPITOPES CAPABLE TITLE OF INVENTION: OF STIMULATING THE T LYMPHOCYTES

NUMBER OF SEQUENCES: 46
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                                                                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 05-FEB-1
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                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
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                                               SEQUENCE CHARACTERISTICS
                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 24-NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: P.O. Box CITY: Alexandria
 STRANDEDNESS:
                                                                                                   TELEPHONE:
                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United States
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                               ENGTH:
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EDNESS: Single
              954 base pairs
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D. Box 1404
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Pred. No. 0.
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RESULT 18
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Best Local Similarity
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                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                               APPLICATION NUMBER: US 00 FILING DATE: 24-NOV-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: FR 9:
                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: GUERIN-MARCHAND,
APPLICANT: DRUILHE, Pierre
TITLE OF INVENTION: PEPTIDE
TITLE OF INVENTION: HEPATIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUBLICATION INFORMATION:
DOCUMENT NUMBER: WO 9
FILING DATE: 05-FEB-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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                                                                                                                        CLASSIFICATION:
                                                                                                                                      FILING DATE:
                                                                                                                                                    APPLICATION NUMBER: US/08/462,625
                                                                                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                                                                                         COUNTRY:
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P.O. Box 1404
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0
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LENGTH: 954 base pairs
TYPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1..954
PUBLICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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 ACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGA
               ACACCCTCAAGAAGAATGAAAATATCAAAGAACTGCTCGACAAGATTAATGA 980
                                                          ACAAGAGAGACTTGCTAAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAG
                                                                                        TCTATAACAAACAGCTTGAAGAAGCCCATAACCTCATCAGCGTACTGGAGAAGCGCATAG
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ilarity 45.7%;
Conservative
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RESULT 19 US-08-098-327E-34 ; Sequence 34, Ap Patent No. GENERAL INFORMATION:
APPLICANT: GUERIN
APPLICANT: DRUILH COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Do TITLE OF INVENTION: TITLE OF INVENTION: CURRENT APPLICATION DATA: NUMBER OF SEQUENCES: MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS COUNTRY: STATE: CITY: Alexandria STREET: ZIP: 22313-1404 4, Application US/08098327E 6270771 Virginia P.O. Box 1404 DRUILHE, Pierre GUERIN-MARCHAND, Claudine Patentin Release #1.0, States PEPTIDE SEQUENCES SPECIFIC FOR THE HEPATIC STAGES OF P. FALCIPARUM BEJOF STIMULATING THE T LYMPHOCYTES Swecker & Version Mathis BEARING EPITOPES

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                                                                                                                                                                                                                                                                  Sequence 34, Application US/08462625 Patent No. 6319502
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Best Local Similarity
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DOCUMENT NUMBER: WO 92/1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                        APPLICANT: DRUILHE, Pierre
TITLE OF INVENTION: HEPATIC STAGES OF P. FALCIPARUM BEARING
TITLE OF INVENTION: OF STIMULATING THE T LYMPHOCYTES
                                                                                                                                                                                                               APPLICANT:
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                                                                   STREET:
CITY: A
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TYPE: nucleic acid
STRANDEDNESS: single
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                                  COUNTRY:
                                                   STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                      ADDRESSEE:
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                RY: United States
22313-1404
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 READABLE
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                                                                                      P.O. Box 1404
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                                                                                                                                                                        RESULT 21
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                                                                                                                     Patent No.
                                                                                                                       Sequence 104, Application Patent No. 5559223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 161;
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                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 988 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
            TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containin NUMBER OF SEQUENCES: 113
                                               APPLICANT:
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PUBLICATION INFORMATION:
CORRESPONDENCE
                                                                                    APPLICANT: Saverio Carl Falco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOCUMENT NUMBER: WO 92/13884 PUBLICATION DATE: 20-AUG-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FR 9 FILING DATE: 05-FEB-1991
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                                                                                                                                                                                                                                                                ACACCCTCAAGAAGAATGAAAATATCAAAGAACTGCTCGACAAGATTAATGA 980
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                                               Sharon J. Keel
Janet A. Rice
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ADDRESS:
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05-JUN-1995
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                                                                                            3153
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CURRENT APPLICATION DATA:
APPLICATION MICROSOFT WATER
                               3213
                                                                                                                                                      3093 TAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAGCTTGAAAGCAAACTCAACTC
                                                                                                                                                                                                                   3033 CAACAAGTACAAACTGAAACTGGAGAGACTCTTCGACAAGAAGAAGACAGTCGGCAAGTA 3092
                                                                                                                                                                                                                                                                                  2973 GAAGCTGGAAGAGGACATCAATAAGCTGAAGAAGACACTGCAACTGAGCTTCGACCTGTA 3032
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APPLICATION NUMBER: 07/7
FILING DATE: 9 August 19
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy Disk
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302
                                                                                                                        182 GATGAAGAAGCTCGAAGAAGAAGATGAAGGTCATGGAGGAGAAGATGAAAAAGCTCGAAGA 241
                                                                                                                                                                                     122 GAAAAAGCTGGAAGAAAAGATGAAGGCTATGGAGGACAAGATGAAATGGCTTGAGGAAAA 181
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TELEFAX: 835420
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OTHER INFORMATION:
                                                                                                                                                                                                                                                    62 GAAACTGAAAGAGGAAATGAAGAAGCTCGAAGAGAAGATGAAGGTCATGGAGGAGAAGAT 121
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CELL TYPE: DH5 alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 3..326
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AGAGAAGAT 310
                                                             AAAGATGAAGGCAATGGAAGACAAAATGAAGTGGCTTGAGGAGAAAATGAAGAAGCTCGA
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1007 Market Street
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                                                                                                                                                                                                                                                                                                                                                                                              /function= "synthetic seed
/product= "protein"
/gene= "ssp"
/standard_name= "SSP-534"
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Best Local Similarity
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                                                                                                                                                                                                                               Matches
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                                                               3093
                                                                                                                  3033 CAACAAGTACAAACTGGAAACTGGAGAGAGACTCTTCGACAAGAAGAAGACAGTCGGCAAGTA 3092
                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB
TELECOMMUNICATION INFORMATION:
3153 ACTGAACAATCCGAAACACGTACTGCAGAACTTCTCAGTGTTCTTCAACAAGAAGAAGAAGGA 3212
                                                                                                                                                                                             2973 GAAGCTGGAAGAGGACATCAATAAGCTGAAGAAGACACTGCAACTGAGCTTCGACCTGTA 3032
                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 3..326
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
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APPLICATION NUMBER: 07/743,006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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                                                                                                                                                              62
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TELEX: 835420
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FILING DATE: 19920807
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OPERATING SYSTEM: M
SOFTWARE: Microsoft
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CELL TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                              GATGAAGAAGCTCGAAGAAGAAGAAGATGAAGGTCATGGAGGAGAAGAAGAAGAAGCTCGAAGA 241
                                                             TAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAGCTTGAAAGCAAACTCAACTC
                                                                                                                                                              GAAACTGAAAGAGGAAATGAAGAAGCTCGAAGAGAAGATGAAGGTCATGGAGGAGAAGAT 121
                                                                                               GAAAAAGCTGGAAGAAAAGATGAAGGCTATGGAGGACAAGATGAAATGGCTTGAGGAAAA
                                                                                                                                                                                                                               122;
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PE: DH5 alpha
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                                                                                                                                                                                                                               Conservative
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/product= "protein"
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Pred. No. 0.01'
0; Mismatches
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RESULT 24
5171843-8
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                                                                                                                                                                                                                  ;Patent No. 5171843
; APPLICANT: NUSSENZWEIG, VICTOR
; TITLE OF INVENTION: IMMUNOGENIC POLYPEPTIDE AND METHOD FOR
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5171843-10
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; APPLICANT: NUSSENZWI; TITLE OF INVENTION:
; PURIFYING IT
                ; SEQ
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Best Local Similarity
Matches 141; Conserv
                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 754,645
FILING DATE: 9-JUL-1985
APPLICATION NUMBER: 115,634
FILING DATE: 26-OCT-1987
APPLICATION NUMBER: 649,903
FILING DATE: 12-SEP-1984
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                ID NO.8
                                                                                                                                      NUMBER OF SEQUENCES: 13
CURRENT APPLICATION DAMBER: US/07/175,112
APPLICATION NUMBER: US/07/175,112
FILING DATE: 30-MAR-1988
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APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                            1929 CGTGGAGTTAAAACATAATATACATGTGCCGAATAGTTATAAGCAGGAGAATAAGCAGGA 1988
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FILING DATE: 9-JUL-1985
APPLICATION NUMBER: 115,634
FILING DATE: 26-OCT-1987
APPLICATION NUMBER: 649,903
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 LENGTH: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 12-SEP-1984
                                                                                                                                                                                                                                                                                                                               GCTTGTTGAGAACATTAAGAAGGATGAAGAACAGTTGTTTGAGAAGAAGATTACAAAAGA 1808
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nilarity 47.0%;
Conservative
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Pred. No. 0.03;
0; Mismatches 159;
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                                           ; ANTI-SENSE: PCT-US95-10668-1
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PCT-US95-10668-1
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Best Local Similarity
Query Match
Best Local Similarity
                                                                                                                                                     TELEFAX: (609) 779-84
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                              FILING DATE: August 22, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: WORDPERFECT CURRENT APPLICATION DATA:
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MEDIUM TYPE: DISKETT
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                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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                                                                                                         LENGTH:
                                                                            TOPOLOGY:
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                                                                                            STRANDEDNESS:
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                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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22, 1994
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1929 CGTGGAGTTAAAACATAATATACATGTGCCGAATAGTTATAAGCAGGAGAATAAGCAGGA 1988
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Epitope Ordering and Protein
Restriction Mapping
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Score 45.4
Pred. No.
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                 Length 198;
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PCT-US95-10668-2
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GENERAL INFORMATION:
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                                                                                                                                     Query Match
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INFORMATION FOR SEQ ID NO:
1426 AGTTACGAAGACCGCAGCAAAAGTCTAAAACGATATCACTAAAGAGTATGAAAAGCTGCTG 1485
                                                                         1366 ATCAACGAAATCAAGGAGAAGATCAAAATTGAGAAGAAGAAATTGAGAGTGACAAGAAA 1425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: A Method of Sequencing Prote
TITLE OF INVENTION: Epitope Ordering and Protein
TITLE OF INVENTION: Restriction Mapping
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                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PENN-0137 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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OPERATING SYSTEM:
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                                                                                                                                                                                                            TYPE: Nucleic Acid
STRANDEDNESS: Sing
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                                                                                                                        Local
                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                            NAME: Jane Massey Licata REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
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97; Conserv
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210 Lake Drive East, Suite 201
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2779-8488
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                                                                                                                    Score 45.4; DB 5; Pred. No. 0.016;
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RESULT 28 US-08-098-327E-32

Sequence 3 Patent No.

32, Application US/08098327E 5. 6270771

GENERAL INFORMATION:

APPLICANT: GUERIN-MARCHAND, Claudine APPLICANT: DRUILHE, Pierre TITLE OF INVENTION: PEPTIDE SEQUENCES TITLE OF INVENTION: HERATIC STAGES OF TITLE OF INVENTION: OF STIMULATING TH NUMBER OF SEQUENCES: 46

PEPTIDE SEQUENCES SPECIFIC FOR THE HEPATIC STAGES OF P. FALCIPARUM BEARING EPITOPES CAPABLE OF STIMULATING THE T LYMPHOCYTES

CORRESPONDENCE ADDRESS

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US-09-412-554A-3
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Conklin, Darrell APPLICANT: Ellsworth, Jeff L. TITLE OF INVENTION: FOLLISTATIN RELATED PROTEIN ZFSTA2 FILE REFERENCE: 98-50
                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: variation LOCATION: (1)...(2949) OTHER INFORMATION: Each N is independently any nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2949
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Degenerate oligonucleotide sequence OTHER INFORMATION: zfsta2 polypeptide of SEQ ID NO:2.
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                             TATAACAAACAGCTTGAAGAAGCCCATAAC
                                                               GARYTNACNCARGTNATHAARCARGARGARYTNGGNAARGAYYTNTTYGAYTGYACNYTN 654
TAYGTNYTNYTNAARTAYGAYGAYTTYAAY 684
                                                                                            AATGCAACCAAGGAGGAAGAAAGAAGAAGTTGTACCAGGCCCAGTACGACCTGTCCATC
                                                                                                                               YTNGTNGAYCARATGTTYAARTAYTTYGAYGCNGAYWSNAAYGGNYTNGTNGAYATHAAY 594
                                                                                                                                                             ACCATCGAGAACATTAACGAGCTGATCGAAGAATCCAAAAAAGACCATAGACAAAAAATAAG 810
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Pred. No. 0.
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US-08-462-625-32
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                              Sequence 32, Application US/08462625 Patent No. 6319502 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 950 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9
FILING DATE: 05-FEB-1991
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   APPLICANT:
                  APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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REFERENCE/DOCKET NUMBER: 010830-045
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PUBLICATION DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
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GUERIN-MARCHAND,
DRUILHE, Pierre
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24-NOV-1993
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Pred. No. 0
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US-08-462-625-32
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08 FILING DATE: 24-NOV-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: FR 9: FILING DATE: 05-FEB-1991
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: Virginia
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TELECOMMUNICATION INFORMATION:
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PUBLICATION INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGA
                                    ACACCCTCAAGAAGAATGAAAATATCAAAGAACTGCTCGACAAGATTAATGA 980
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O. Box 1404
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20-AUG-1992
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Pred. No. 0.058;
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US-08-098-327E-41
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Tocal Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: 010830-045
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: FR 9:
FILING DATE: 05-FEB-1991
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CURRENT APPLICATION DATA:
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                                                                                                                                    GTTACAAGAGCAGCAAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGA 158
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CGATTTAGAACAAGAGAGAGGCTGCTAAAGAAAGTTGCAAGAACAACAAGAGCGATTTAGA 278
                              AGAATGCAACCAAGGAGGAAGAAAAGAAGAAGTTGTACCAGGCCCAGTACGACCTGTCCA 868
                                                                  ACAACAAAGCGATCTAGAACAAGAGAGAGGTGCTAAAGAAAAGTTGCAAGAACAACAAAG
                                                                                                  AGACCATCGAGAACATTAACGAGCTGATCGAAGAATCCAAAAAGACCATAGACAAAAATA 808
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P.O. Box 1404
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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20-AUG-1992
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HEPATIC STAGES OF P. FALCIPARUM BEARING EPITOPES CAPABLE
OF STIMULATING THE T LYMPHOCYTES
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Pred. No. 0.075;
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                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 1..1482
PUBLICATION INFORMATION:
DOCUMENT NUMBER: WO 92/13884
PUBLICATION DATE: 20-AUG-1992
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REFERENCE/DOCKET NUMBER: 010830-045
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                        689 CTCTCGACAACATCAAGGACAATGTGGGAAAGATGGAAGATTATATTAAAAAAGAATAAGA 748
                                                                                                                                                                                             629 TGAAGATCAGAGCCAACGAGTTGGACGTATTGAAGAAGTTGGTCTTCGGATATCGCAAGC 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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GTTACAAGAGCAGCAAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGA
                                                                                                                          TAAAGAAAAGTTTGCAAGAACAACAAAGCGATTTTAGAACAAGATAGACTTGCTAAAGAAAA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGA 390
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o. 6270771
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P.O. Box 1404
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                                                                                                                                                                                                                                                               Conservative
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Pred. No. 0.
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Matches

Best Local Similarity

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Pred. No. 0.075; 0; Mismatches 192;

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US-08-462-625-41
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                                  US-08-462-625-41
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 Query Match
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                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/098,327
FILING DATE: 24-NOV-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
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                                                                                 LOCATION: 1..1482
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 836-6620
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TITLE OF INVENTION:
                                                                                                                                     FEATURE:
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                                                                                                                                                     MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM POTENT ULSK
COMPUTER: IBM C COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release ""
                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 39,300 REFERENCE/DOCKET NUMBER: 01
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FR 9 FILING DATE: 05-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                  PUBLICATION DATE:
                                                                   DOCUMENT NUMBER:
                                                                                                                    NAME/KEY: CDS
                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                     LENGTH:
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                                                                                                                                                                                  nucleic acid
EDNESS: single
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). Box 1404
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05-JUN-1995
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                                                WO 92/13884
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 Score 44.8;
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Length 1482;
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                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 836 6620
                                                                                                                                                                                                              APPLICATION NUMBER: FR 91 01286 FILING DATE: 05-FEB-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                            FILING DATE: 24-NOV-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM:
SOFTWARE: Patent1
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                                                                                                                                                         REGISTRATION NUMBER: 39, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/462,625 FILING DATE: 05-JUN-1995
STRANDEDNESS:
                                                                                                                                                                                                NAME:
                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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                                    LENGTH:
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                                  1482 base pairs
                                                                                                : (703) 836+6620
(703) 836-2021
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                               OPERATING STATEMENT OF THE PRICE OF TWARE: PATCHION Release #1.0, VEIN SOFTWARE: PATCHION DATA:
CURRENT APPLICATION NUMBER: US/08/257,073
FILLING DATE: 09-JUN-1994
CLASSIFICATION: 424
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/075,783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08257073 Patent No. 5766597
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Best Local Similarity
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DOCUMENT NUMBER: WO 9
PUBLICATION DATE: 20-
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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APPLICANT: de Taisne, Ch
APPLICANT: Tine, John A.
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                     PRIOR APPLICATION DATA:
                                                                      PRIOR APPLICATION DATA:
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                                                                                         APPLICATION NUMBER: US 0 FILING DATE: 11-JUN-1993
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                                    FILING DATE:
                                                     APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                  New York
: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             de Taisne, Charles
                                                                                                                                                                                                                                                                                                                              UNITED STATES OF AMERICA
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SYSTEM: PC-DOS/MS-DOS
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US 07/672,183

 Mismatches

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                                                                                                                                                                                                                       Version #1.30
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Best Local Similarity
Matches 97; Conserv
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 840-07
TELEX: 425066 CURTMS
INFORMATION FOR SEQ ID NO:
                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927
PILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Blasdale, John H. C.
REGISTRATION NUMBER: 31,895
                                           TELEFAX: 201-822-7039
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                  CURRENT APPLICATION DATA: APPLICATION NUMBER: PC FILING DATE: 19930805
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
              SEQUENCE CHARACTERISTICS:
LENGTH: 4766 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 201-822-7398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                 COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintos
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                   SOFTWARE: Microsoft Word 5.1a
                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 07940-1000
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: 4766 base pairs nucleic acid
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(212) 840-0712
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Best Local Similarity 41.8%;
Matches 332; Conservative
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MOLECULE TYPE: cl
ORIGINAL SOURCE:
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IMMEDIATE SOURCE:
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LOCATION: 3..4766
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                                 GGACAGTCAGATAA 2108
                                                                                                                                                                              CTGATGGATTAAAAAGAAAATGCAGAGCTAAAAAATAAAGAATTACGAAATAAAGGATCTG
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                                                                   GGATTAAAAGAAAATGTATATACAAATAATGATTTAAAGAATAACGATATTCAAAATAAA
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Best Local Similarity
Matches 185; Conserv
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/67
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Science & Technology Law Group
STREET: 268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1625 ATCTTGAGAAGCTCACCAAAGCTCTTAAGTATATGGAGGACTATTCTCTGCGGAACATTG 168
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TOPOLOGY: lir
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ARGARATHAARGGNMGNACNGTNGCNGTNGAYTGGGCNGTNGCNAARGAYAARTAYAARG 589
                                                                                   GNTTYGTNCARTTYAARAAYYTNYTNGARGCNGGNAARGCNYTNAARGGNATGAAYATGA
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RESULT 37
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Best Local :
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                                                                                                                                                                                                                                                                TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                              1685
                                                                                      1625 ATCTTGAGAAGCTCACCAAAGCTCTTAAGTATATGGAGGACTATTCTCTGCGGGAACATTG 1684
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                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: UCI
                                                                                                                                                                                                                                                                                                                                                        NAME: Osman Ph.D., Richard A REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                             GACAACAGGCCGGTTCAGCTCTCGAAGGCGATAGCGTGCAAGCTCAAGCACAAGAGCAGA 2221
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TNGCNAARAARYTNMGNAAYAARACNAARGARAARGGNAARAAYGARAAYWSNGART 289
                                                         AYGTNCARMGNGCNYTNAARGARATHACNACNTTYGARGGNTGYAARATHAAYGTNACNG
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                                                                                                                     185;
                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                (415)343-4342
(415)343-4342
--- TO NO: 2:
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                                                                                                                     Conservative
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102; Mismatches
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RESULT 38
US-09-098-487-2
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TELEFAX: (415)
INFORMATION FOR SEQ
                                                                                                                  FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard
REGISTRATION NUMBER: 36,627
                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415)343-4342
                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: COLLINS, TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                              MEDITER KEALDAND MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94104
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8 Bush Street, Suite 3200
  NO:
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US-08-559-896B-1
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                                                                                                                                                       Sequence 1, Application US/08559896B Patent No. 6310046
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Best Local Similarity
                                                                                        GENERAL INFORMATION:

APPLICANT: Patrick E. Duffy
APPLICANT: Christian F. Ockenhouse
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LENGTH: 2277 base pairs
                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                           TITLE OF INVENTION: SEQUESTRIN
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STRANDEDNESS: double
TOPOLOGY: linear
STREET:
                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACAACAGGCCGGTTCAGCTCTCGAAGGCGATAGCGTGCAAGCTCAAGCACAAGAGCAGA
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USA MRMC -
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                  John Moran
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MCMR-JA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
                                                                                                                                                                                                                                                                                                   1372
                                                                                                                                                                                                                                                                                                                                        1600
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LENGTH: 1956 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 619-2065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Microsoft WO CURRENT APPLICATION DATA:
1612
                                                                                                                                                                                                                                                              1660 GAGGACTATTCTCTGCGGAACATTGTTGTGGAGAAAGAACTAAAGTATTACAAGAATCTC
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Local Similarity 42.9%;
nes 217; Conservative
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TYPE: Nucleic acid
STRANDEDNESS: Double
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TOPOLOGY: Lin
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REGISTRATION NUMBER: 26
REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                 GTCTCCGATATTGTTAAAGTCCAAGT 1865
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                                                                                                                                                                                                                                                                                                                                      GCATCCTATGAGAATTCTAAGCATAATCTTGAGAAGCTCACCAAAGCTCTTAAGTATATG 1659
ATAACAAATATTGATATAAAAAATGT 1637
                                                                                                         CAGTTGTTTGAGAAGAAGATTACAAAAGACGAAAATAAACCAGATGAGAAGATCCTGGAG
                                                                                                                                                CAACATAAGAAGGAAAATCAAGTAGATGTTGTCAGGAAAAATATTCAGATTATTCAAGAG
                                                                                                                                                                                                                           AATGTTTCCAATATAGTGAATTTTTAAATTCAAAAGTAGGAAAAGATAACACACCAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                  AAAATGATGGGAAAACGGTACTCTTACAAAGTGGAGAAACTGACACCATAATACCTTT 1599
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                                                                      GAT AATATAAAAAAT AAAGGCCAAAAGGATAACACTGAAATGTTAGATAATAATAAGGAA
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                                                                                                   Query Match
Best Local S
Matches 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: CG.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8582
 3032
                                                              2972 AGAAGCTGGAAGAGACATCAATAAGCTGAAGAAGACACTGCAACTGAGCTTCGACCTGT 3031
                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 0
FILING DATE: 09-SEP-1994
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EILING NAME: 23-MAR-1994

APPLICATION NUMBER.

EILING NAME: 23-MAR-1994
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 9..1238
OTHER INFORMATION:
OTHER INFORMATION:
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                                 88
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
                                                                                                   Local Similarity
les 215; Conserv
                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Pace, Gary M.
REGISTRATION NUMBER: P-40,403
                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 1241 base pairs
ACAACAAGTACAAACTGAAACTGGAGAGAGACTCTTCGACAAGAAGAAGACAGTCGGCAAGT 3091
                               AGAAGGAGAAGGAGTGGAAGCTTACCGCCACCGAGAAGGGCCAAGATGAACAACTTCCTGG
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7 Skyline Drive
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VENTION: No. 5770696el Pesticidal Proteins and Strains EQUENCES:- 50
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Koziel, Michael G
Mullins, Martha A
                                                                                                   Conservative
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Kostichka, N. Kristy
Duck, Nicholas B
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                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                 0.98;
                                                                                                                                                                               /note= "Maize optimized DNA sequence encoding VIP2A(a) with the Bacillus secretion signal removed as contained in pCIB5527"
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                                                                                                 Score 43; DB Pred. No. 0.2; 0; Mismatches
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                                                                                                               DB 1; Length 1241; 0.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL
APPLICATION NUMBER: US 08/218,018
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/037,057
FILING DATE: 25-MAR-1993
                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 09-SEP-1994
                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                FILING DATE: 09-SEP-PRIOR APPLICATION DATA:
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                                                                                                                                                     CLASSIFICATION: 530
                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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Mullins,
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Duck, Nicholas B
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Michael G
, Martha A
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No. 5770696el Pesticidal Proteins and
                                                                                                                                                                                                                      Release #1.0,
                                                                                                                    US 08/314,594
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RESULT 42
US-08-471-044-39
; Sequence 39, Applicatic
; Patent No. 5840868
; GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1241 base pairs
TYPE: nucleic acid
 APPLICANT:
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MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3146 TCAACTCACTGAACAATCCGAAACACGTACTGCAGAACTTCTCAGTGTTCTTCAACAAGA 3205
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LOCATION: 9..1238
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Local Similarity 44.7%;
nes 215; Conservative
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                                                                                                                                                                                                                            CCAAGGCCGGCGTGATCCTGAACAACAGCGAGTACAAGATGCTGATCGACAACGGCTACA 567
                                                                                                                                                                                                                                                             CTAAGCTCGAAGGCAAGCTGAAGGACAACCTGGAGAAGAAGAAGAAGCTCAGCTACC
                                                                                                                                                                                                                                                                                                                       CCGAGGAGAGCATCCAGACCGAGGATAACTACGCCAGCCTCGAGAACTTCAAGGTCCTGT
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                                                  9, Application US/08471044
5840868
Warren,
Kóziel,
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Gregory
Michael
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US-08-471-044-39
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 0
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: |
APPLICATION NUMBER: US 08/218,018
FILING DATE: 23-MAR-1994
                               3032 ACAACAAGTACAAACTGAAACTGGAGAGACTCTTCGACAAGAAGAAGACAGTCGGCAAGT 3091
                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = | "Synthetic DNA"
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STREET: / ...
CITY: Hawthorne
TMATE: NY
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                                                                                                   2972 AGAAGCTGGAAGAGGACATCAATAAGCTGAAGAAGACACTGCAACTGAGCTTCGACCTGT 3031
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OTHER INFORMATION:
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                                                                                                                                      Local Similarity
nes 215; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 0 CLASSIFICATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV6 -
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compress: 7 Skyline Drive
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ACAACAAGAACGACATCAAGACCAACTACAAGGAGATCACCTTCAGCATAGCCGGCAGCT
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                                                                                                                                    Conservative
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Patent No. 5
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APPLICATION NUMBER: US 00
APPLICATION NUMBER: US 00
FILING DATE: 09-SEP-1994
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APPLICANT: Estruch, Juan J
TITLE OF INVENTION: NO. 5840868el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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                     FILING DATE: 23-MAR-PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                            PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/463,483
FILING DATE: 05-JUN-1995
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                                                                          APPLICATION NUMBER:
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Kostichka, N. Kristy
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Koziel, Michael G
Mullins, Martha A
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JMBER: US 08/037,057
25-MAR-1993
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8582
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LOCATION: 9..1238
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NAME: Pace, Gary M.
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Mismatches 260;
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RESULT 44 US-08-463-483A-39

Sequence 39, Application US/08463483A Patent No. 5849870 GENERAL INFORMATION: APPLICANT: Warren, Gregory W APPLICANT: Koziel, Michael G

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ADDRESSEE: CIBA-GEIGY CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL O
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TITLE OF INVENTION: No. 5849870el Pesticidal Proteins and Strains
                                                              3092 ATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAGCTTGA-----AAGCAAAC 3145
                                                                                                                                                                                                                                                                                                                                      2972 AGAAGCTGGAAGAGGACATCAATAAGCTGAAGAAGACACTGCAACTGAGCTTCGACCTGT 3031
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Spruill, W. Murray REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US UFILING DATE: 23-MAR-1994
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CLASSIFICATION: 530
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LOCATION: 9...
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TCGAGGACGAGATCAAGGACCTGAAGGAGATCGACAAGATGTTCGACAAGACCAACCTGA 267
                                                                                                                                                                                                                                                                       AGAAGGAGAAGGAGTGGAAGCTTACCGCCACCGAGAAGGGCAAGATGAACAACTTCCTGG 147
                                                                                                                                   ACAACAAGAACGACATCAAGACCAACTACAAGGAGATCACCTTCAGCATAGCCGGCAGCT
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215; Conserv
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Kostichka, N. Kristy
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/desc = "Synthetic DNA"
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25-MAR-1993
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Pred. No. 0.2;
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REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8615
                                                                                                                                               APPLICATION NUMBER: FILING DATE: 23-MAR-PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA
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MEDIUM TYPE: Floppy
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TITLE OF INVENTION: No. 5849870el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
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                                                                         ATTORNEY/AGENT INFORMATION: NAME: Spruill, W. Murray
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                APPLICATION NUMBER: ÚS 08/037,057 FILING DATE: 25-MAR-1993
                                                                                                                                                                                                                       APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                          CLASSIFICATION:
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Koziel, Michael
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                                                                                                                                              Sequence 39,
Patent No. 5
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Best Local Similarity
Matches 215; Conserv
                                                                                                                                GENERAL INFORMATION:
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                              APPLICANT:
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APPLICANT:
                 APPLICANT
                                                                 APPLICANT:
                                                                                                               APPLICANT:
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LOCATION: 9..1238
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                                                                                                                                                                                                                                                                                                                                           CTAAGCTCGAAGGCAAGCTGAAGGACAACCTGGACAAGAAGAAGAAGAAGCTCAGCTACC 3445
                                                                                                                                                                                                                                                                                                                                                                            GCAAGGAGCGCGTGATCCTGAAGGTGACCGTCCCCAGCGGCAAGGGCAGCACCACCCCCA 507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACACTACAAAGGCCTCGTCAAGTATTATAATGGCGAGTCTTCTCCTCTGAAGACTCTCT 3325
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                                                                             Warren, Gregory W
Koziel, Michael G
Mullins, Martha A
Duck,
            Desai, Nalini M
Kostichka, N. Kr
                             Carr, Brian
Desai, Nalin
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Nicholas
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             N. Kristy
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Pred. No.
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Best Local Similarity 44.7
Matches 215; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-1993
ATTORNBY/AGENT INFORMATION:
                                                                                                                                            3032
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3146 TCAACTCACTGAACAATCCGAAACACGTACTGCAGAACTTCTCAGTGTTCTTCAACAAGA 3205
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ADDRESSEE: NO. 5880001.
STREET: 3054 Cornwallis Road
STREET: 7056earch Triangle Park
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                     ATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAGCTTGA-----AAGCAAAC 3145
                                                                                                                                            ACAACAAGTACAAACTGAAACTGGAGAGAGACTCTTCGACAAGAAGAAGACAGTCGGCAAGT 3091
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                                   TCGAGGACGAGATCAAGGACCTGAAGGAGATCGACAAGATGTTCGACAAGACCAAGCCTGA 267
                                                                                                        ACAACAAGAACGACATCAAGACCAACTACAAGGAGATCACCTTCAGCATAGCCGGCAGCT
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/desc = "Synthetic
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sequence encoding VIP2A(a) with the Bacillus secretion
removed as contained in pCIB5527"
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Pred. No. 0.2;
0; Mismatches
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RESULT 47
US-08-471-046A-42
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FILING DATE: 06-JUN-15
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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                                                                                                         FILING DATE: 23-MAR-PRIOR APPLICATION DATA:
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TITLE OF INVENTION: Method For Isolating Vegetative Insecticidal
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                                                   ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                  FILING DATE: 09-SEP-1994
                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                  NAME: Meigs, J. Timothy RECLISTRATION NUMBER: 38
                                                                                       APPLICATION NUMBER:
                                                                                                                                            APPLICATION NUMBER:
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 REFERENCE/DOCKET NUMBER:
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Duck, Nicholas_B
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Koziel, Michael G
Mullins, Martha A
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                  38,241
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                                                                                                       Patent No. 5872212
GENERAL INFORMATION:
                                                                                                                                            Sequence 39,
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                                 APPLICANT:
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APPLICANT:
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 APPLICANT:
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215; Conserv
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                                                                                                                                            Application US/08470566B
                  Carr, Brian
                                 Mullins, Martha
Nye, Gordon J
                                                                      Warren, Gregory
Koziel, Michael
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Best Local Similarity
Matches 215; Conserv
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INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION NUMBER: US 08/218,018
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TITLE OF INVENTION: No. 5872212el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 52
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OTHER INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                ACAACAAGTACAAACTGAAACTGGAGAGAGACTCTTCGACAAGAAGAAGAAGACAGTCGGCAAGT 3091
                                                                                                                                  AGAAGGAGAAGGAGTGGAAGCTTACCGCCACCGAGAAGGGCCAAGATGAACAACTTCCTGG 147
TCGAGGACGAGATCAAGGACCTGAAGGAGATCGACAAGATGTTCGACAAGACCAACCTGA 267
                                                                 ACAACAAGAACGACATCAAGACCAACTACAAGGAGATCACCTTCAGCATAGCCGGCAGCT
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F: 3054 Cornwallis Road
Research Triangle Park
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sequence encoding VIP2A(a) with the Bacillus
removed as contained in pCIB5527"
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                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 25-MAR-1993
                                                                                                                                                                FILING DATE: 09-SEP-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Estruch, Juan J
TITLE OF INVENTION: NO. 5872212el Pesticidal Proteins
NUMBER OF SEQUENCES: 52
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                                                                                                                                                                                                                  FILING DATE: 05-JUN-
PRIOR APPLICATION DATA:
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                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
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                                                                                                                             FILING DATE:
                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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ZIP: 27709
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                                    NAME:
 REFERENCE/DOCKET NUMBER:
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Kostichka, N. Kristy
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Koziel, Michael
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                                  J. Timothy
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CGC1695/CIP3/DIV4 - SQLv4
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                                                                                       Sequence 39, Application US/08469334 Patent No. 5990383 GENERAL INFORMATION:
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APPLICANT:
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                             APPLICANT:
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LOCATION: 9..1238
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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 APPLICANT:
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                                        Warren, Gregory
Koziel, Michael
Mullins, Martha
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Nalini M
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Pred. No.
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US-08-469-334-39
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Best Local S
Matches 215
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APPLICANT:
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APPLICATION NUMBER: US 08/037,057

FILING DATE: 25-MAR-1993
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TITLE OF INVENTION: No. 5990383el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,
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APPLICATION NUMBER: US 08/218,018
FILING DATE: 23-MAR-1994
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CURRENT APPLICATION DATA:
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OPERATING SYSTEM:
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TCAACTCACTGAACAATCCGAAACACGTACTGCAGAACTTCTCAGTGTTCTTCAACAAGA 3205
                                   TCGAGGACGAGATCAAGGACCTGAAGGAGATCGACAAGATGTTCGACAAGACCAACCTGA 267
                                                                    ATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAGCTTGA-----AAGCAAAC
                                                                                                                                                                               AGAAGGAGAAGGAGTGGAAGCTTACCGCCACCGAGAAGGGCAAGATGAACAACTTCCTGG 147
                                                                                                         ACAACAAGAACGACATCAAGACCAACTACAAGGAGATCACCTTCAGCATAGCCGGCAGCT
                                                                                                                                          ACAACAAGTACAAACTGAAACTGGAGAGAGACTCTTCGACAAGAAGAAGACAGTCGGCAAGT 3093
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                                                                                                                                                                                                                                                     Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                        sequence encoding VIP2A(a) with the Bacillus secretion sig removed as contained in pCIB5527"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                             /note= "Maize optimized DNA
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-1995
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                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                   Score 43; DB:
Pred. No. 0.2;
0; Mismatches
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                                                                                                                                                                                                                                                                                    Length 1241;
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US-08-469-334-42
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APPLICANT: Estruch, Juan J
TITLE OF INVENTION: No. 5990383el Pesticidal Proteins
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                TELECOMMUNICATION INFORMATION:
                                                            APPLICATION NUMBER: US 08
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: SPILIN, W. MULTRY
                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 1
FILING DATE: 06-JUN-
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                          APPLICATION NUMBER: US 01 FILING DATE: 23-MAR-1994
                             REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: CGC 1695/CIP3
                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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Kostichka, N. Kristy
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Koziel, Michael
Mullins, Martha
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                                                                                                     UMBER: US 08/037,057
25-MAR-1993
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Best Local Similarity
Matches 215; Conserv
                                                                                                                                                        Sequence 39, Application US/09300529 Patent No. 6066783
                                                                                                                                          GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
            APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                    3446 T
                                                                                                                                                                                                                                                                                                                                                                                                                              3326 CCGAGGAGAGCATCCAGACCGAGGGATAACTACGCCAGCCTCGAGAACTTCAAGGTCCTGT 3385
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APPLICANT
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LOCATION: 9..1238
OTHER INFORMATION:
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STRANDEDNESS: sing
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                                                                                                                                                                                                                                                                                                                                                                       CTAAGCTCGAAGGCAAGCTGAAGGACAACCTGAACCTGGAGAAGAAGAAGAAGCTCAGCTACC 3445
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                                                                                 Warren, Gregory
Koziel, Michael
Mullins, Martha
            Desai, Nalini M
Kostichka, N. Kristy
                                                                  Nye, Gordon J
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Duck,
                                               Carr, Brian
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Pred. No. 0.
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                                                                                                                                                                                Matches
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                                                                                       3032
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                            3092 ATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAGCTTGA-----AAGCAAAC 3145
                                                                                                                                                2972 AGAAGCTGGAAGAGGACATCAATAAGCTGAAGAAGACACTGCAACTGAGCTTCGACCTGT 3031
                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/218,018
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
FILING DATE: 05-JUN-
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APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Estruch, Juan J
TITLE OF INVENTION: Genes Encoding Insecticidal Proteins
                                                                                                                                                                                                                                                                                                                                    FEATURE
                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
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                                                           148
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OTHER INFORMATION:
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OPERATING SYSTEM:
                                                                                                                     88
                                                                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/037,057 FILING DATE: 25-MAR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                 DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                               Local Similarity
                                                                                      ACAACAAGTACAAACTGAAACTGGAGAGAGACTCTTCGACAAGAAGAAGACAGTCGGCAAGT 3091
 TCGAGGACGAGATCAAGGACCTGAAGGAGATCGACAAGATGTTCGACAAGACCAACCTGA 267
                                                                                                                     AGAAGGAGAAGGAGTGGAAGCTTACCGCCACCGAGAAGGGCAAGATGAACAACTTCCTGG 147
                                                        ACAACAAGAACGACATCAAGACCAACTACAAGGAGATCACCTTCAGCATAGCCGGCAGCT
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1: 3054 Cornwallis Road
Research Triangle Park
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                                                                                                                                                                                                                                                                                                                                                              other nucleic acid
/desc = "Synthetic DNA"
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06-JUN-1995
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                                                                                                                                                                                                                                                       /note= "Maize optimized DNA
sequence encoding VIP2A(a) with the Bacillus secretion
removed as contained in pCIB5527"
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Pred. No.
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US-09-300-529-42
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Patent No. 6
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                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 05-JUN-
                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
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                            PRIOR APPLICATION DATA:
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                                                                        PRIOR APPLICATION DATA:
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APPLICATION NUMBER: FILING DATE: 25-MA
                                           FILING DATE:
                                                         APPLICATION NUMBER:
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ZIP: 27709
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA;
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Koziel, Michael G
Mullins, Martha A
Nye, Gordon J
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ENTION: Genes Encoding Insecticidal Proteins
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Kostichka, N. Kristy
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05-JUN-1995
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                                                                          23-MAR-1994
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MBER: US 08/037,057
25-MAR-1993
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RESULT 54
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                                                Sequence 45, Application US/08471033 Patent No. 5770696
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                                 GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
   APPLICANT:
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NAME: Meigs, J. Timothy
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LOCATION: 9..1238
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 Warren,
Koziel,
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 325
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TCGAGGACGAGATCAAGGACCTGAAGGAGATCGACAAGATGTTCGACAAGACCAAGCCTGA 384
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US-08-471-033-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: P-40,403
REFERENCE/DOCKET NUMBER: CGC |
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,033
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DESCRIPTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 25-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 09-SEP-PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 0
FILING DATE: 09-SEP-1994
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CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 9..1355
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
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ATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAGCTTGA-----AAGCAAAC 3145
                                                                   ACAACAAGTACAAACTGAAACTGGAGAGAGTCTTTCGACAAGAAGAAGACAGTCGGCAAGT 3091
                                                                                                          AGAAGGAGAAGGAGTGGAAGCTTACCGCCACCGAGAAGGGCAAGATGAACAACTTCCTGG
                                    ACAACAAGAACGACATCAAGACCAACTACAAGGAGATCACCTTCAGCATAGCCGGCAGCT
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INVENTION: No. 5770696el Pesticidal Proteins and Strains
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Kostichka, N. Kristy
Duck, Nicholas B
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Nye, Gordon J
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SYSTEM: PC-DOS/MS-DOS
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/desc = "Synth
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25-MAR-1993
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                                                                                                                                                                                             0.98;
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                                                                                                                                                                                             Score 43;
Pred. No.
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US-08-471-044-45
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/463,483
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/471,044
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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NAME: Pace, REGISTRATION
                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 23-MA
                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: CIBA-GELGE CONTREET: 7 Skyline Drive
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                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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Kostichka, N. Kristy
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Koziel, Michael
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                                                                                                          JMBER: US 08/037,057
25-MAR-1993
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                                                                                                  Sequence 45, Application Patent No. 5849870
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                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 919-541-8689
                                 APPLICANT: APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8582
APPLICANT
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                                                                  APPLICANT:
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LOCATION: 9..1355
LOCATION: 9..1355
OTHER INFORMATION:
OTHER INFORMATION:
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les 215; Conserv
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                             Warren, Gregory
Koziel, Michael
Mullins, Martha
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 Carr, Brian
               Nye, Gordon J
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with the Bacillus secretion signal removed and the vacuola
targetting signal inserted as contained in pCIB5533"
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APPLICANT

Desai,

Nalini

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; NAME/KEY: CDS
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Best Local Similarity
Matches 215; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                     3092
                                                                                                                                                                         3032
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LENGTH: 1358 base pairs
TYPE: nucleic acid
                            3146 TCAACTCACTGAACAATCCGAAACACGTACTGCAGAACTTCTCAGTGTTCTTCAACAAGA 3205
                                                                                                                                                                                                                                         2972 AGAAGCTGGAAGAGGACATCAATAAGCTGAAGAAGACACTGCAACTGAGCTTCGACCTGT 3031
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DESCRIPTION:
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APPLICATION NUMBER:
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APPLICATION NUMBER: 1
FILING DATE: 23-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 530 PRIOR APPLICATION DATA:
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                                                                  325
                                                                                                                                                                                                        205 AGAAGGAGAAGGAGTGGAAGCTTACCGCCACCGAGAAGGGCAAGATGAACAACTTCCTGG
385 GCAACAGCATCATCACCTACAAGAACGTGGAGCCCACCACCATCGGCTTCAACAAGAGCC 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 09-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
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                                                               TCGAGGACGAGATCAAGGACCTGAAGGAGGAGCCAAGATCGACAAGATCTTCGACAAGACCAACCTGA 384
                                                                                    ATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAGCTTGA-----AAGCAAAC
                                                                                                                                                         ACAACAAGTACAAACTGGAAACTGGAGAGAGACTCTTCGACAAGAAGAAGAAGACAGTCGGCAAGT 309:
                                                                                                                                   ACAACAAGAACGACATCAAGACCAACTACAAGGAGATCACCTTCAGCATAGCCGGCAGCT
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SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                   APPLICATION NUMBER: US 01 FILING DATE: 05-JUN-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 38,241

TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                         FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 06-JUN
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Koziel, Michael
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Kostichka, N. Kristy
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Best Local Similarity 44.7%;
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Desai, Nalini M
Kostichka, N. Kristy
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with the Bacillus secretion sign
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: [38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: No. 5872212el Pesticion MUMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS: ADDRESSEE: No. 5872212artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
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FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 01
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
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MOLECULE TYPE:
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LOCATION: 9..1355
COTHER INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                               Local Similarity
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GCAACAGCATCATCACCTACAAGAACGTGGAGCCCACCACCATCGGCTTCAACAAGAGCC 444
                                                                         TCGAGGACGAGATCAAGGACCTGAAGGAGATCGACAAGATGTTCGACAAGACCAACCTGA 384
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25-MAR-1993
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with the Bacillus secretion signal removed
targetting signal inserted as contained in
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Pred. No.
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APPLICANT:
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                                  REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8615
                                                                         APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-1993
ATTORNEY_AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/CYCYETT NITUDED: 000 1007
                                                                                                                                           APPLICATION NUMBER: US 00
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 00
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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TELEFAX: 91
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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INVENTION: NO. 5990383el Pesticidal Proteins and Strains
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Kostichka, N. Kristy
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Koziel, Michael
Mullins, Martha
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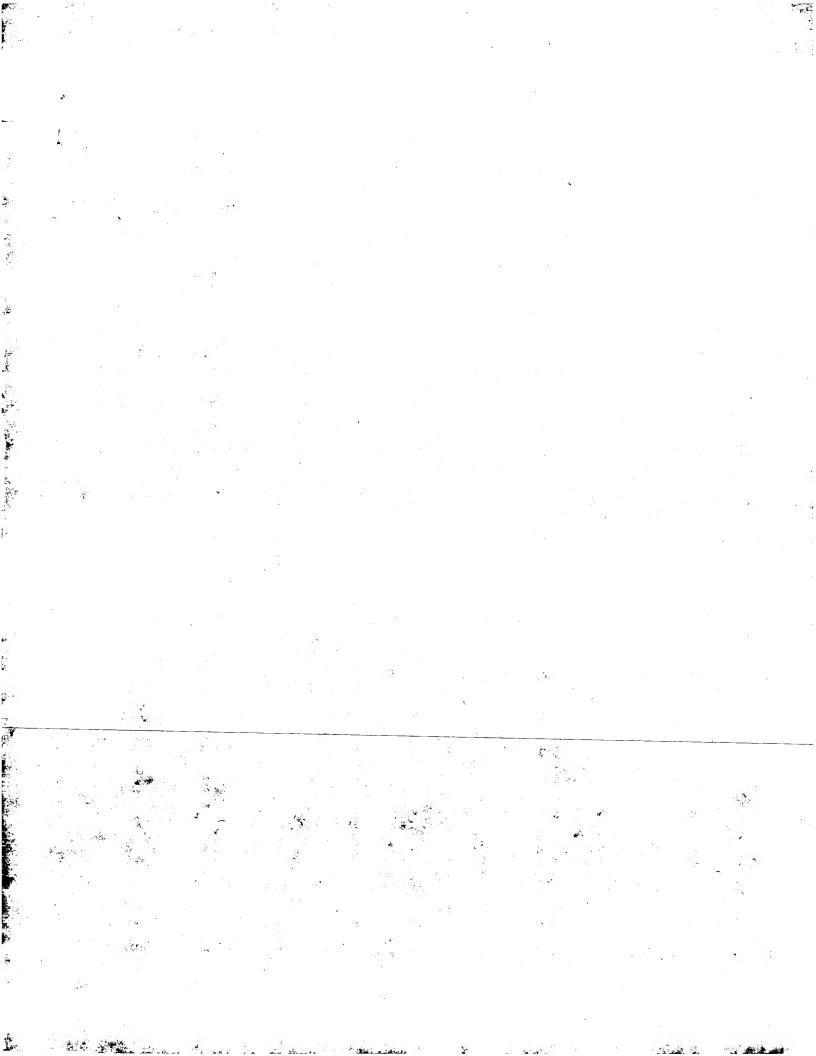
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DESCRIPTION: /desc = "Synthetic
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LENGTH: 1358 base pair
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                                                           CCAAGGCCGGCGTGATCCTGAACAACAGCGAGTACAAGATGCTGATCGACAACGGCTACA
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EATURES SOU	AUTHORS AUTHORS TITLE JOURNAL OMMENT	ACCESSION BI8157: VERSION BI8157: VERSION BI8157: KEYWORDS EST. SOURCE malaria ORGANISM Plasmoo	ON	79 57 80 57	173 57.2 174 57.2 175 57.2 176 57.2 177 57.2	168 57.6 169 57.6 170 57.6 171 57.4 172 57.4	164 57.6 165 57.6 166 57.6 167 57.6	160 57.8 161 57.8 162 57.8	154 155 155 155 156 157 157 158 157 158 157 158 157 158 157 158 157 158 157 158 157 158 157 158 157 158 157 158 157 158 158 158 158 158 158 158 158 158 158
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Fax: 314 286 181 Email: est@watsc Library was cons Washington Unive obtaining a clor obtaining a clor ostaining r: -400 seq primer: -400 High quality sec Locatic source //organi //do_xre //lab_hc	AUTHORS AUTHORS TITLE JOURNAL OMMENT	sequence. BI815756.1 BI815756.1 EST. malaria pan M Plasmodium	BI815756 ON PfESTOaa32c09.y1	79 57 1.2 80 57 1.2	173 57.2 1. 174 57.2 1. 175 57.2 1. 176 57.2 1. 177 57.2 1. 178 57.2 1.	168 57.6 1.2 169 57.6 1.2 170 57.6 1.2 171 57.4 1.2 172 57.4 1.2	164 57.6 1.2 165 57.6 1.2 166 57.6 1.2 167 57.6 1.2	160 57.8 1.2 161 57.8 1.2 162 57.8 1.2 163 57.8 1.2	154 57.8 1. 155 57.8 1. 156 57.8 1. 157 57.8 1. 158 57.8 1.
EATURES SOUICE	EFERENC AUTHOR TITLE JOURNA OMMENT	sequence. BI815756 BI815756.1 GI:15909334 EST. malaria parasite P. falciparum. Plasmodium falciparum Plasmodium falciparum	BI815756 ON PfESTOaa32c09.yl Plasmod falciparum cDNA 5' simil	79 57 1.2 645 9 A 80 57 1.2 870 17	173 57.2 1.2 571 17 174 57.2 1.2 792 17 175 57.2 1.2 796 17 176 57.2 1.2 944 17 177 57.2 1.2 1389 14	168 57.6 1.2 888 169 57.6 1.2 964 170 57.6 1.2 1215 171 57.4 1.2 739 172 57.4 1.2 829	164 57.6 1.2 297 13 165 57.6 1.2 608 13 166 57.6 1.2 617 17 167 57.6 1.2 735 17	160 57.8 1.2 1042 17 161 57.8 1.2 1042 17 161 57.8 1.2 1059 17 162 57.8 1.2 1079 17 163 57.8 1.2 1101 17	154 57.8 1.2 542 13 155 57.8 1.2 816 17 155 57.8 1.2 878 17 156 57.8 1.2 878 17 157 57.8 1.2 886 17 158 57.8 1.2 931 17

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RESULT 2
BQ452315
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                                                ORGANISM
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                                                                                                                                                                                                                                                                                                                                                             CATCTCCTTCCTGCTGATCCTCATGCTGATCCTGTACAGCTTCATCTAATAGATCGATG 4939
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                                                                                                                                                                                   BQ452315 600 bp mRNA linear EST 29-MAY-2002 PfESToaa95a12.yl Plasmodium falciparum 3D7 asexual cDNA Plasmodium falciparum cDNA 5′ similar to SW:MSP1_PLAF3 P19598 MEROZOTTE
                                           malaria parasite P. falciparum
Plasmodium falciparum
                                                                                                                    BQ452315
BQ452315.1
                 Eukaryota; Alveolata; Apicomplexa;
                                                                                                                                                                  SURFACE PROTEIN 1 PRECURSOR ;, mRNA sequence.
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(bases 1 to 600)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA isolation system (Promega, WI) using streptavidin Magnesphere particles. Directional CDNA libraries were constructed by oligo d(T) priming of poly(A)+ RNA (5mg) into EcoRI and XhoI sites of 1 ZapII vector using the Zap CDNA synthesis kit (Stragene, CA). The average size of the CDNA inserts in the library was between 1.0 and 1.5kb. Clones were mass excised using the Exassist helper phage (Stratagene), the phagemids were precitptated with PEG 8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DH10B cells."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBluescript SK plus; Site_1: EcoRI; Site_2: XhOI; Library was constructed by Debopam Chakrabarti.
                                                                                                                    GI:21255427
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Pred. No. 9.3e-43;
0; Mismatches 180;
                    Haemosporida;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       3124 AAGGAGCAGCTTGAAAGCAAACTCAACTCACTGAACAATCCGAAAACACGTACTGCAGAAAC 3183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3064 TTCGACAAGAAGAAGACAGTCGGCAAGTATAAGATGCAGATCAAGAAGTTGACTCTGCTC 3123
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                                                                                                                                                                                       GAAAACACAAAAATATTATTGAAACATTATAAAAGGACTTGTTAAATATTATAATGGTGAA 240
                                                                             TCATCTCCATTAAAAACTTTAAGTGAAGTATCAATTCAAACAGAAGATAATTATGCCAAT 300
                                                                                                                           TCTTCTCCTCTGAAGACTCTCTCCGAGGAGGAGCATCCAGACCGAGGATAACTACGCCAGC 3363
                                                                                                                                                                                                                                                                                                   TTTTCTGTTTTCTTTAACAAAAAAAAAAGAAGCTGAAATAGCAGAAACTGAAAAACACATTA 180
                                                                                                                                                                                                                                                                                                                                                    TTCTCAGTGTTCTTCAACAAGAAGAAGGAAGCCGAGATCGCCGAGACAGAGAACACTCTG 3243
                                                                                                                                                                                                                                                                                                                                                                                                           AAAGAACAATTAGAATCAAAATTGAATTCACTTAATAACCCACATAATGTATTACAAAAC
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Email: est@watson.wustl.edu
Library was constructed by Debopam Chakrabarti DNA
Washington University Genome Sequencing Center For
obtaining a clone please contact: L. David Sibley
obtaining a clone please contact: Mashington University
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WashU Plasmodium EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
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Marra,M., Hillier,L., Martin,J., Wylle,T., Dante,M., Thelsing,B.
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Jentes,E., Ronko,I
Tsagareishvili,R., Belaygorod,L., Franklin,C., Carr,L., Grow,A.,
Maguire,L., Richey,J., Wadkins,J., Kennedy,S., Levinso,D.,
Waterston,R., Wilson,R. and Sibley,D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_inst="DHIOB (GeneBlog, Invitrogen, Inc.)"
/note="Vector: pBluescript SK plus; Site_1: EcoRI; Site_2:
XhoI; Library was constructed by Debopam Chakrabarti.
Total RNA samples were isolated from mixed stage
saponin(0.1%)-1ysed P. falciparum 3D7 infected
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method. The poly A+ RNA was isolated by the polyAT-Tract
mRNA isolation system (Promega, WI) using streptavidin
Magnesphere particles. Directional cDNA libraries were
constructed by oligo d(T) priming of poly(A)+ RNA (5mg)
into EcoRI and XhoI sites of 1 ZapII vector using the Zap
cDNA synthesis kit (Stragene, CA). The average size of the
cDNA inserts in the library was between 1.0 and 1.5kb.
Clones were mass excised using the Exassist helper phage
(Stratagene), the phagemids were precitptated with PEG
8000 and extracted with phenol/chloroform. Phagemid DNA
was electroporated into DHIOB cells."
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/clone_lib="Plasmodium falciparum 3D7 asexual cDNA"
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Suzukl,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
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The University of Tokyo, Department of Parasitology
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
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Contact: L. David Sibley
WashU Plasmodium EST Project
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Library was constructed by Debopam Chakrabarti DNA sequencing labrary was constructed by Debopam Chakrabarti DNA sequencing labrary was constructed by Debopam Chakrabarti DNA sequencing labrary and Sibley obtaining a clone please contact: L. David Sibley
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                                                               Total RNA samples were isolated from mixed stage saponin(0.1%)-lysed P. falciparum 3D7 infected erythrocytes by the accidic guanidinium-phenol chloroform method. The poly A+ RNA was isolated by the polyAT-Tract mRNA isolation system (Promega, WI) using streptavidin Magnesphere particles. Directional cDNA libraries were constructed by oligo d(T) priming of poly(A)+ RNA (5mg) into EcoRI and XhoI sites of 1 ZapII vector using the Zap cDNA synthesis kit (Stragene, CA). The average size of the CDNA inserts in the library was between 1.0 and 1.5kb cDNA inserts in the library was between 1.0 and 1.5kb clones were mass excised using the Exassist helper phage (Stratagene), the phagemids were preciptated with PEG (Stratagene), the phagemids were preciptated with PEG
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
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1 (bases 1 to 432)
                                                                                                                                                                                                                       Contact: L. David Sibley
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                                   est@watson.wustl
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vatson.wustl.edu
constructed by Debopam Chakrabarti DNA sequencing
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RESULT 6 AU086832 LOCUS

DEFINITION

AU086832 Sugano Malaria cDNA library Plasmodium falciparum clone xPFn3463 similar to Plasmodium falciparum train HNS merozoite surface protein 1 precursor (msp1) gene, mRNA seg

EST 27-JAN-2001

sequence.

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KEYWORDS SOURCE

EST.
Plasmodium falciparum
Plasmodium falciparum

falciparum 3D7 falciparum 3D7 GI:12388973

ORGANISM

VERSION ACCESSION

AU086832 AU086832.1

REFERENCE

TITLE AUTHORS

Watanabe, J., Sasaki, M., Suzuki, Y. and Sugano, S. FULL-malaria: a database for a full-length enriched cDNA library

Eukaryota; Alveolata; Apicomplexa; Haemosporida; 1 (bases 1 to 500)

Plasmodium

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PfESToaa40c07.y1
falciparum cDNA :
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                                                   EST.
                                                         BI814631.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The University of Tokyo, Department of Parasitology 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Tel: 81-3-5449-5378
Plasmodium
Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library Gene 200 (1-2), 149-156 (1997).
                                 malaria parasite P. falciparum
                                                                                     BI814631
                                                                                                       mRNA
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                                                                                                     sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="3D7"
/db_xref="taxon:36329"
/clone="xppp3463"
/clone_lib="Sugano Malaria cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="erythrocytic stage"
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                                                                                                   Plasmodium falciparum 3D7 asexual CDMA Plasmodium falciparum 3D7 asexual CDMA Plasmodium 5' similar to TR:Q9UAI8 Q9UAI8 SURFACE PROTEIN-1;
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Pred. No. 1.2e
0; Mismatches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                  4714
                                                                                                                                                                                                                                                                                                                                                                                    4654 GAGCGCGAAGAGTGCAAGTGTCTCCTGAACTACAAACAAGAAGGAGATAAGTGCGTGGAG 4713
                                          4894
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                                                                                                                                                                                                        GAGGAAGACAGCGGCTCTAACGGAAAGAAAATCACATGCGAGTGTACTAAGCCCGACTCC
                                                                                                                                                                                                                                                                     TTAATACTCATGTTAATATTATACAGTTTCATTTAAAAAATGTAGG
                         CTGATCCTCATGCTGATCCTGTACAGCTTCATCTAATAGATCGATG
                                                                                                            TATCCACTCTTCGACGGGĂTTTTTTGCTCCAGCTCTAATTTCCTGGGCATCTCCTG
                                                                                                                                                                              GAAGAAGATTCAGGTAGCAGCAGAAAGAAAATCACATGTGAATGTACTAAACCTGATTCT 322
                                                                                                                                                                                                                                                                                                                AACCCAAACCCTACCTGCAATGAAAAACAATGGCGGGTGTGACGCCGATGCTAAATGCACC 4773
                                                                                                                                                                                                                                                                                                                                                                                                                                                        208;
                                                                                       TATCCACTTTTCGATGGTATTTTCTGCAGTTCCTCTAACTTCTTAGGAATATCATTCTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Library was constructed by Debopam Chakrabarti DNA Washington University Genome Sequencing Center For obtaining a clone please contact: L. David Sibley (sibley@borcim.wustl.edu), Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WashU Plasmodium EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 261.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001) Contact: L. David Sibley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Possible reversed clone: similarity on wrong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clones were mass excised using the ExAssist helper phage (Stratagene), the phagemids were precitptated with PEG 8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DH10B cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA isolation system (Promega, WI) using streptavidin Magnesphere particles. Directional CDNA libraries were constructed by oligo d(T) priming of poly(A)+ RNA (5mg) into EcoRI and XhoI sites of 1 ZapII vector using the Zap CDNA synthesis kit (Stragene, CA). The average size of the CDNA inserts in the library was between 1.0 and 1.5kb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total RNA samples were isolated from mixed stage saponin(0.1%)-lysed P. falciparum 3D7 infected erythrocytes by the acidic guanidinium-phenol chloroform method. The poly A+ RNA was isolated by the polyAT-Tract
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/note="Vector: pBluescript SK plus; Site_1
XhoI; Library was constructed by Debopam C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Plasmodium falciparum 3D7 asexual cDNA"
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/db_xref="taxon:5833"
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72.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                           4778 AAGACAGCGGCTCTAACGGAAAAGAAATCACATGCGAGTGTACTAAGCCCGACTCCTATC 4837
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                                                                                                                                                                                                                                     CAAACCCTACCTGCAATGAAAACAATGGCGGGTGTGACGCCGATGCTAAATGCACCGAGG 4777
                                                                                                                                                                                CAAATCCTACTTGTAACGAAAATAATGGTGGATGTGATGCAGATGCCACATGTACCGAAG 123
AAGATTCAGGTAGCAGCAGAAAAGAAAATCACATGTGAATGTACTAAAACCTGATTCTTATC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206;
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Contact: L. David Sibley
WashU Plasmodium EST Project
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Library was constructed by Debopam Chakrabarti DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: L. David Sibley
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/db_xref="taxon:5833"
/clone_lib="Plasmodium falciparum 3D7 asexual cDNA"
/clone_lib="Plasmodium falciparum 3D7 asexual cDNA"
/lab host="DH10B (GeneHog, Invitrogen, Inc.)"
/note="Vector: pBluescript SK plus; Site_1: EcoRI; Site_2:
XhoI; Library was constructed by Debopam Chakrabarti.
Total RNA samples were isolated from mixed stage
saponin(0.1%)-lysed P. falciparum 3D7 infected
erythrocytes by the acidic guanidinium-phenol chloroform
method. The poly A+ RNA was isolated by the polyAT-Tract
method. The poly A+ RNA was isolated by the polyAT-Tract
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Library was constructed by Debopam Chakrabarti DNA Washington University Genome Sequencing Center For obtaining a clone please contact: L. David Sibley
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
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Marra,M., Hillier,L., Martin,J., Wylle,T., Dante,M., Theising,B.,
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Jentes,E., Ronko,I.,
Tsagareishvili,R., Belaygorod,L., Franklin,C., Carr,L., Grow,A.,
Maguire,L., Richey,J., Wadkins,J., Kennedy,S., Levinso,D.,
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1 (bases 1 to 522)
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BQ452445.1 GI:21255557
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522 bp mRNA linear EST 29-MAY-2002 PfESToaa96g05.yl Plasmodium falciparum 3D7 asexual cDNA Plasmodium falciparum cDNA 5' similar to TR:Q9UAI8 Q9UAI8 SURFACE PROTEIN-1;
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Fax: 314 286 1810
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Seq primer: -40UP from Gibco
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                                                     mRNA isolation system (Promega, WI) using streptavidin Magnesphere particles. Directional CDNA libraries were constructed by oligo d(T) priming of poly(A)+ RNA (5mg) into EcoRI and XhoI sites of 1 ZapII vector using the Zap CDNA synthesis kit (Stragene, CA). The average size of the cDNA inserts in the library was between 1.0 and 1.5kb. Clones were mass excised using the Exassist helper phage (Stratagene), the phagemids were precitptated with PEG 8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DH10B cells."
                                                                                                                                                                                                                                                                                                                                                        /clone_jib="Plasmodium falciparum 3D7 asexual cDNA"
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/note="Vector: pBluescript SK plus; Site_1: EcoR; Site_2:
KhoI; Library was constructed by Debopam Chakrabarti.
Total RNA samples were isolated from mixed stage
saponin(0.1%)-lysed P. falciparum 3D7 infected
erythrocytes by the acidic guanidinium-phenol chloroform
method. The poly A+ RNA was isolated by the polyAT-Tract
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Query Match
Best Local Similarity 73...
Matches 205; Conservative

3.2%;

Score 160; DB 14; Pred. No. 1.2e-25; 0; Mismatches 75

DB 14;

Length 522; Indels

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Contact: L. David Sibley
WashU Plasmodium EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marra,M., Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B. Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Jentes,E., Ronko,I Tsagareishvili,R., Belaygorod,L., Fanklin,C., Carr,L., Grow,A., Maguire,L., Richey,J., Wadkins,J., Kennedy,S., Levinso,D., Waterston,R., Wilson,R. and Sibley,D.
WashU Plasmodium EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Library was constructed by Debopam Chakrabarti DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: L. David Sibley (sibley@borcim.wustl.edu), Washington University Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BQ451036 455 bp mRNA linear EST 29-MAY-2002 PfESToab03a10.yl Plasmodium falciparum 3D7 asexual cDNA Plasmodium falciparum cDNA 5' similar to TR:Q9UAI8 Q9UAI8 SURFACE PROTEIN-1;,
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Plasmodium falciparum
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4721 ACCCTACCTGCAATGAAAACAATGGCGGGTGTGACGCCGATGCTAAATGCACCGAGGAAG 4780
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                                                                                                                                                                                                                                                                                                Email: jwatanab@manage.ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction land characterization of a full length-enriched and
a 5'-end-enriched cDNA library Gene 200 (1-2), 149-156 (1997).
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Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                                                             Fax: 81-3-5449-5410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Junichi Watanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Institute of Medical Science
The University of Tokyo, Department of Parasitology
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81-3-5449-5378
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52 c 58 g 153 t
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                                                                                                                                                             /clone="XPFn5232"
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                                                                                     Email: jwatanab@manage.ims.u-tokyo.ac.jp
Suzukl,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
                                                                                                                                                                               Institute of Medical Science
The University of Tokyo, Department of 4-6-1, Shirokanedai, Minatoku, Tokyo
Tel: 81-3-5449-5378
Fax: 81-3-5449-5410
                                                                                                                                                                                                                                                                                                         FULL-malaria: a database for a full-length enriched from human malaria parasite, Plasmodium falciparum Nucleic Acids Res. 29 (1), 70-71 (2001)
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Library was constructed by Debopam Chakrabarti DNA Washington University Genome Sequencing Center For obtaining a clone please contact: L. David Sibley
                                                                      Unpublished (2001)
Contact: L. David Sibley
WashU Plasmodium EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                              Maguire,L., Richey,J., Wadkins,J., Kennedy,S., Levinso,D., Waterston,R., Wilson,R. and Sibley,D. WashU Plasmodium EST Project
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                                                     Email: est@watson.wustl.edu
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                                                                   Tang,K., Cole,R., Chakrabarti,D., Haywood,R., Clifton,S., Pape,D Marra,M., Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B. Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Jentes,E., Ronko,I Tsagareishvili,R., Belaygorod,L., Franklin,C., Carr,L., Grow,A., Maguire,L., Richey,J., Wadkins,J., Kennedy,S., Levinso,D., Waterston,R., Wilson,R. and Sibley,D.
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Unpublished Contact: L.
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                                              WashU Plasmodium EST Project
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h quality sequence stop: 257.
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Total RNA samples were isolated from mixed stage saponin(0.1%)-lysed P. falciparum 3D7 infected erythrocytes by the acidic guanidinium-phenol chloroform method. The poly A+ RNA was isolated by the polyAT-Tract mRNA isolation system (Promega, WI) using streptavidin Magnesphere particles. Directional cDNA libraries were constructed by oligo d(T) priming of poly(A)+ RNA (5mg) into EconI and KhoI sites of 1 2pII vector using the Zap cDNA synthesis kit (Stragene, CA). The average size of the CDNA inserts in the library was between 1.0 and 1.5kb. Clones were mass excised using the Exassist helper phage (Stratagene), the phagemids were preciptated with PEG 8000 and extracted with phenol/chloroform. Phagemid DNA as electroporated into DH10B cells."
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/db_xref="taxon:5833"
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  David Sibley
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                                                                                                                          TATGTTAAACATTTCACAACACCAATGCGTAAAAAAAACAATGTCCAGAAAATTCTGGATG
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Washington University School of Medicine
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Waterston, R., Wilson, R. and Sibley, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BI814931 408 bp mRNA linear EST 03-OCT-2001 PfESToaa08b05.yl Plasmodium falciparum 3D7 asexual cDNA Plasmodium falciparum cDNA 5' similar to TR:Q9UAI8 Q9UAI8 SURFACE PROTEIN-1;
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Putative full length read
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Library was constructed by Debopam Chakrabarti DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: L. David Sibley
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Contact: L. David Sibley
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314 286 1810
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XhoI; Library was constructed by Debopam Chakrabarti.
Total RNA samples were isolated from mixed stage
saponin(0.1%)-lysed P. falciparum 3D7 infected
erythrocytes by the acidic guanidinium-phenol chloroform
method. The poly A+ RNA was isolated by the polyAT-Tract
mRNA isolation system (Promega, WI) using streptavidin
Magnesphere particles. Directional cDNA libraries were
constructed by oligo d(T) priming of poly(A)+ RNA (5mg)
into EcoRI and XhoI sites of 1 ZapII vector using the Zap
cDNA synthesis kit (Stragene, CA). The average size of the
cDNA inserts in the library was between 1.0 and 1.5kb.
Clones were mass excised using the ExAssist helper phage
(Stratagene), the phagemids were precitptated with PEG
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/db_xref="taxon:5833"
/db_xref="taxon:5833"
/clone_lib="Plasmodium falciparum 3D7 asexual cDNA"
/lab_host="DH10B (GeneHog, Invitrogen, Inc.)"
/note="Yector: pBluescript SK plus; Site_1: EcoRI: Site_2:
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Library was constructed by Debopam Chakrabarti DNA
Washington University Genome Sequencing Center For
obtaining a clone please contact: L. David Sibley
(sibley@borcim.wustl.edu), Washington University
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
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Contact: L. David Sibley
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UL Unpublished (2001)
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
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Seq primer: -40UP from Gibco.
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                                                                                                                                                                                                                                                                                                                                                               /Organism="Plasmodium falciparum"
/db_xref="taxon:5833"
/clone_lib="Plasmodium falciparum 3D7 asexual cDNA"
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xhoI; Library was constructed by Debopam Chakrabarti.
Total RNA samples were isolated from mixed stage
saponin(0.1%)-1ysed P. falciparum 3D7 infected
erythrocytes by the acidic guanidinium-phenol chloroform
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Orlando, FL 32816-2360
Tel: 407 384 2061
Fax: 407 384 3095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Debopam Chakrabarti
Department of Molecular Biology and Microbiology
University of Central Florida
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1183C3 czapPFDd2.1,
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                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: dchak@pegasus.cc.ucf.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer: T3
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                                                            Conservative
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                                                                                                                                                        /note="Vector: Lambda ZAP II; Site_1: EcoR I; Site_2: Xho I: PolyA+ RNA, from asynchronous blood stage parasites of the Dd2 isolate cultured in vitro, was reverse transcribed using an oligo dT Xho I primer. Second strand was prepared using RNase H and DNA polymerase I. EcoR I adapters were ligated to the cDNA, and it was digested with Xho I. Prepared fragments were ligated into EcoR I + Xho I digested lambda ZAP II vector. "
                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:5833"
/clone="PF1183C"
                                                                                                                                                                                                                                                                                                                                      /clone_lib="czapPFDd2.1, Debopam Chakrabarti"
/lab_host="E. coli XL-1 blue"
                                                                                                                                                                                                                                                                                                                                                                                                                     /strain=|"Dd2"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Plasmodium falciparum"
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Pred. No. 1.7e-:
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0; Mismatches 61;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 301-856 veri
Email: carlton@tigr.org
For clone info, please contact the
For clone info, please contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Fraser, C.M. and Carucci, D.J.
Plasmodium yoelli EST project at TIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2001)
Contact: Jane Carlton
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Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 597)
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
Tel: 301-530-9319
Fax: 301-838-0208
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Seg primer: ADF.
/dev_stage="Asexual blood stages"
//dev_stage="Asexual blood stages"
//lab_host="E. coli XL-1 Blue"
//lab_host="E. coli XL-1 Blue"
//note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/CByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms.
                                                                                                                                                                                                                                                                                                                          /organism="Plasmodium yoelii
/strain="17XL"
                                                                                                                                                                                                                                                                           /clone_lib="PyBS"
                                                                                                                                                                                                                                                                                            /clone="PYCJG14"
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AU086246 Sugano Malaria cDNA library Plasmodium falciparum 3D7 cDNA clone xPFn2175 similar to P.falciparum gp190 (MSA1, MSP1, PMMSA) for precursor of major merozoite surface antigens, mRNA sequence.

SION AU086246

SION AU086246.1 GI:12388387

RDS EXT.

E Plasmodium falciparum 3D7.

E Plasmodium falciparum 3D7.

E Plasmodium falciparum 3D7

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

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RESULT 21
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                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                    AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCAGAAGGTGCTCCTCATGAACAAGATTGATGAACTCAAGAAGACTCAACTCATTCTGA 1924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGGACTAACACATTCAGCAAATGGTTCCTTAGAAAGTATCTGATATTGTAAAATTACAAG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATACAATAATTAACAGAAGAAATAAAGAGTAGTGAAAAACAAAATTCTAGAAAAAATTTA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAAAGTAAAAGACATGTTAAAGAAAGA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGAACCATATTAATTGTATTAAAAAAAAAAGAAGTAGATAAATTAAAAGAATTTATAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: jwatanab@manage.ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library Gene 200 (1-2), 149-156 (1997).
                                                                                                                                                                                                                                                                                                                   Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
I (bases 1 to 755)
                                       Email: carlton@tigr.org
For clone info, please contact the Malaria Research and
Reagent Resource Center, ATCC
                                                                                                                        Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
Tel: 301-530-9319
                                                                                                                                                                                                                                    Plasmodium yoelii EST project at Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BM159731 FST562254 PyBS Plasmodium
                   http://www.malaria.mr4.org/mr4pages/index.htm
                                                                                                                                                                                                                Contact: Jane Carlton
                                                                                                                                                                                                                                                                              Fraser, C.M. and Carucci, D.J.
                                                                                                                                                                                                                                                                                               Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W.,
                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium yoelii yoelii.
                                                                                                                                                                                                                                                                                                                                                                                                                               BM159731.1 GI:17305412
                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
BM159731
primer:
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81-3-5449-5410
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/clone_lib="Sugano Malaria cDNA library"
/dev_stage="erythrocytic stage"
/dev_stage="erythrocytic stage"
/dev_stage="72g" 115 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Plasmodium falciparum 3D7"
/strain="3D7"
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Pred. No. 6e-14;
0; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      755 bp
m yoelii
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yoelii cDNA clone
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PYCJH95 5' end,
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                                             1000 GCCA 1003
                                                                                                                                                                                    459
                                                                                                                                                                                                                                                                                                                           820
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                                                                                          519
                                                                                                                                    940 AAGAATGAAAATATCAAAGAACTGCTCGACAAGATTAATGAAATTAAGAATCCTCCGCCA 999
                                                                                                                                                                                                                            880 CAGCTTGAAGAAGCCCATAACCTCATCAGCGTACTGGAGAAGCGCATAGACACCCCTCAAG 939
                                                                                                                                                                                                                                                                           399 AAATATAATAAAAAAAAACCAATATACCAAGCTATGTACAATGTTATATTTTTACAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             279 ATTTACATAGAAAGAAATAAAGAAACTGTTGCAGCTTTAAACGCTCTTATTGCTGAAGAA 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           607
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                                                                                                                                                                                                                                                                                                                                                                                                                  AAAAAGACCATA-----
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                                                                                          AAAAATGATGCCATCAAACCATTATGGCAACAAATTGAAGTTCTCAATGCTGCCCCCGTC 578
                                                                                                                                                                                    CAATTAGCTGAAATACAAAAGGTTGTCGAAGTCTTAGAAAAACGAGTTTCTACATTAAAG
                                                                                                                                                                                                                                                                                                                        AAGGAGGAAGAAAGAAGAAGTTGTACCAGGCCCAGTACGACCTGTCCATCTATAACAAA 879
                                                                                                                                                                                                                                                                                                                                                                     ACAAAAAAATACAACCTGAAGGTAACGAAGATTGCAATGACGCTAGTTGTGATAGCGAT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATTATATAAAAAAGAATAAGAAGACCATCGAGAACATTAACGAGCTGATCGAAGAATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAATAAATTTTTATTATGATGTACTTAGAGATAAATTAAATGATATGTGTGCAAATAAT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors, ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacry 1 s-500 column.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
/note="Vector: pADD-GAL4; At 20-25% parasitemia, blc
collected from BALB/CByJ mice infected with Py17XL
parasites, and leukocytes removed by passage over
microcrystalline cellulose collumns. Total RNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Size-fractionated cDNA was precipitated and ligated to HybriJAP arms directionally using EcoRT-XhoI cleaved at After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isolated
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/clone="pYCJH95"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="17XL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                       607 TATTGTCAAATTCCATTCAATTTGAAGATCAGAGCCAACGAGTTGGACGTATTGAAGAAG 666
                                                                                                                                                547
                                                                                                                                                                                        232 GCAATAAATTTTTATTATGATGTACTTAGAGATAAATTAAATGATATGTGTGCAAATAAT 291
TATTGTGAAATTCCTGAACATCTTAAAATTAGTGAAGAAGAAACAGAAATGCTTAAAAAA 351
                                                                                                                       AAGTTGAATTTCTACTTCGACTTGCTAAGGGCCAAACTGAATGACGTTTGCGCCAATGAC 606
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BM160423.1 GI:17306104
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The Institute for Genomic Research
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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EST562946 PyBS Plasmodium yoelii yoelii cDNA clone PYCJR11 5' end,
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                                                                                                                                                                                                                                                                                         Conservative
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//dev_stage="Asexual blood stages"
//lab_host="E. coli XL-1 Blue"
//note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BAIB/cByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was escised from the HybriZAP vector and plasmid DNA
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Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
Fax: 301-838-0208
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Fraser,C.M. and Carucci,D.J.
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For clone info, please contact the Malaria Research and Reference
Reagent Resource Center, ATCC
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/lab_host="E. coli XL-1 Blue"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/CByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was
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Conservative

Score 105; DB 13; Pred. No. 4.7e-13; 0; Mismatches 225

DB 13;

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                                                                                                                                                                                        Unpublished (2001)
Contact: L. David Sibley
WashU Plasmodium EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                 malaria parasite P. falciparum.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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402 bp mRNA linear EST 12-SEP-2001 PfESToaa02ell.yl Plasmodium falciparum 3D7 asexual cDNA Plasmodium falciparum 3D7 asexual cDNA Plasmodium falciparum cDNA 5', similar to TR:043995 043995 MEROZOITE SURFACE
                                                                           Library was constructed by Debopam Chakrabarti DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: L. David Sibley
              High quality sequence stop: 352
Location/Qualifiers
                                                                                                                            Email: est@watson.wustl.edu
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                                               primer: -40UP from Gibco
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314 286 1810
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                                                           Washington University
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                                                Coppel,R., Cowman,A., Craig,A., Fischer,K., Foster,J., Good Hinterberg,K., Holder,A.A., Holt,D., Kemp,D., Lanzer,M., Li. Newbold,C., Ravetch,J.V., Mbio,J., Schuster,S., X.-Z., Thompson,J.K., Vital,F., Wellems,T.E. and Werner,E. Current status of the Plasmodium falciparum genome project Mol. Biochem. Parasitol. 79, 1-12 (1996)
                                                                                                                                                                                                                                      Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                               Dame, J.B., Arnot, D.E., Bourke, P., Chakrabarti, D., Christodoulou, 2.,
Contact: Debopam Chakrabarti
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Total RNA samples were isolated from mixed stage
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/note="Vector: pBluescript SK plus; Site_1:
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                                                                                                                                                                                                           malaria parasite P. falciparum.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
1 (bases 1 to 354)
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Orlando, FL 32816-2360
Tel: 407 384 2061
Fax: 407 384 3095
Contact: Debopam Chakrabarti
Department of Molecular Biology and Microbiology
                                                             Dame, J.B., Arnot, D.E., Bourke, P., Chakrabarti, D., Christodoulou, Z., Coppel, R., Cowman, A., Craig, A., Fischer, K., Foster, J., Goodman, N., Hinterberg, K., Holder, A.A., Holt, D., Kemp, D., Lanzer, M., Lim, A., Newbold, C., Ravetch, J.V., Reddy, G.R., Rubio, J., Schuster, S.M., Su, X.-Z., Thompson, J.K., Vital, F., Wellems, T.E. and Werner, E. Current status of the plasmodium falciparum genome project Current scatus of the plasmodium falciparum genome project Mol. Biochem. Parasitol. 79, 1-12 (1996)
                                                                                                                                                                                                                                                                                                                                                             1039C3 czapPFDd2.1, clone PF1039C, mRNA
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N97605.1 GI:1674623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"Vector: Lambda ZAP II; Site_1: EcoR I; Site_2: Xho I: PolyA+ RNA, from asynchronous blood stage parasites of the Dd2 isolate cultured in vitro, was reverse transcribed using an oligo dT-Xho I primer. Second strand was prepared using RNase H and DNA polymerase I. EcoR I adapters were ligated to the cDNA, and it was digested with Xho I. Prepared fragments were ligated into EcoR I + Xho I digested lambda ZAP II vector. "
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/lab_host="E. coli XL-1 blue"
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/clone="PF1114C"
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Debopam Chakrabarti Plasmodium
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Pred. No. 2.5e-12;
0; Mismatches 109;
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                                                                                                                                                                                  TITLE
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261PbC05 Pb
AZ526918
                                                                                                                     Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 647)
Carlton,J.M.-R. and Dame,J.B.
The Plasmodium vivax and P. berghei gene sequence tag projects Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)
Contact: Dame JB
Dept. of Patholology, College of Veterinary Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University of Central Florida orlando, FL 32816-2360 Tel: 407 384 2061 Fax: 407 384 3095 Email: dchak@pegasus.cc.ucf.eq
                                                   University of Florida
2015 SW 23rd Avenue, Bldg
Tel: 352 392 4700
Fax: 352 392 9704
                                                                                                                                                                                                                                                                                               GSS
                                                                                                                                                                                                                                                                                                               AZ526918.1
             Email: damej@mail.vetmed.ufl.edu
Seq primer: M13(-20) forward
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                                                                                                                                                                                                                                                                          Plasmodium berghei.
Class: shotgun.
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primer: T3.
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/(lone_lib="czappFDd2.1, Debopam Chakrabart1"
/(lone_lib="czappFDd2.1, Debopam Chakrabart1"
/(lone_lib="czappFDd2.1, Debopam Chakrabart1"
/(lone_lib="czappFDd2.1, Debopam Chakrabart1"
/(note="vector: Lambda Zap II; Site_1: EcoR I; Site_2: Xho
I; PolyA+ RNA, from asynchronous blood stage parasites of
the Dd2 isolate cultured in vitro, was reverse transcribed
using an oligo dT-Xho I primer. Second strand was
prepared using RNase H and DNA polymerase I. EcoR I
adapters were ligated to the cDNA, and it was digested
with Xho I. Prepared fragments were ligated into EcoR I +
Xho I digested lambda Zap II vector. "
Xho I digested lambda Zap II vector."
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/db_xref="taxon:5833"
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ש berghei
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DNA sequence
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JOURNAL COMMENT
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AUTHORS
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ORGANISM
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Best Local Similarity
Matches 177; Conserv
                                       TITLE
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           Plasmodium yoelii yoelii.
Plasmodium yoelii yoelii
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 660)
1 (carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B.
Fraser,C.M. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
Unpublished (2001)
                                                                                                                                                                                                             mRNA sequence.
BM159472
                                                                                                                                                                                                                                               BM159472 660 bp mRNA linear EST 04-DEC-200 EST561995 PyBS Plasmodium yoelii yoelii cDNA clone PYCJE56 5' end,
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10 c 92 g 202 t 1 others
 Jane Carlton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pBluescript SK(+) vector DNA, phagemid excised from lambda ZAP; Site_1: ECORV; Site_2: ECORV; Genomic DNA was prepared from asynchronous blood stage forms of the cloned ANKA isolate of P. berghei grown in laboratory Swiss white mice. The DNA was purified from contaminating host DNA by Hoechst Dye 33258-CsCl
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/db_xref="taxon:5821"
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/note="Vector: pBluescri
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The Institute for Genomic Research
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//dev_stage="Asexual blood stages"
//dev_stage="Asexual blood stages"
//lab_host="E. coli XL-1 Blue"
//note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was
collected from BALB/CByJ mice infected with Pyl7XL
parasites, and leukocytes removed by passage over
microcrystalline cellulose collumns. Total RNA was
isolated using the guanidinium isothiocyanate method, and
mRNA isolated using oligo(dT)-cellulose chromatography.
First strand cDNA synthesis was completed using a 50-base
primer and reverse transcriptase in the presence of
5-methyl dCTP. After second strand synthesis, uneven
termini were treated with Pfu DNA polymerase and EcoRI
adaptors ligated to the blunt ends. The sample was cleaved
with XhoI and separated on a Sephacryl S-500 column.
Size-fractionated cDNA was precipitated and ligated to
HybrlZAP arms directionally using EcoRI-XhoI cleaved arms.
After packaging, the phagemid vector (pAD-GAL4) was
excised from the HybrlZAP vector and plasmid DNA
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/strain="17xL"
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                                                                AGAAGAGAAGCTGAAAAAACAATATGTAGATAATGCATTAAAAAAATACTGATATGTTATTA 302
                                                                                                              AAGAAGGAAGCCGAGATCGCCGAGACAGAGAACACTCTGGAGAACACCAAGATTCTTCTC 3264
                                                                                                                                                            AAACAAACTCTTAATGGCGTATTTTATATATTAAATGGTTATGTAAATTTCTTTAACAAG
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                                                                                                                                                                                                                                                                                                GGCAAGTATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAGCTTGAAAGCAAA 3144
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
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Seq primer: ADF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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For clone info, please contact the Malaria Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pAD-GAL4; At 20-25% parasitemia, blood well-collected from BALB/CByJ mice infected with Py17XL parasites, and leukocytes remove by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method, a mRNA isolated using oligo(dT) cellulose chromatography.
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The Institute for Genomic Re
9712 Medical Center Drive, F
Tel: 301-530-9319
Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: carlton@tigr.org
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                                                                                       //dev_stage="Rsexual blood stages"
//dev_stage="Rsexual blood stages"
//lab_host="E. coli XL-1 Blue"
//note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/cByJ mice infected with Py17XL collected from BALB/cByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with the presence of sample was contacted to the blunt ends. The sample was cleaved to the blunt ends. The sample was cleaved to the blunt ends. The sample was cleaved to the blunt ends. The sample was cleaved to the blunt ends. The sample was cleaved to the blunt ends. The sample was cleaved to the blunt ends. The sample was cleaved to the blunt ends. The sample was cleaved to the blunt ends. The sample was cleaved to the blunt ends. The sample was cleaved the presence of the blunt ends. The sample was cleaved the presence of the blunt ends. The sample was cleaved the presence of the blunt ends. The sample was cleaved the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the presence of the prese
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                                                                                                                                                                                                                     Contact: Debopam Chakrabarti
Department of Molecular Biolo
University of Central Florida
Orlando, FL 32816-2360
Tel: 407 384 2061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T18122 313 bp mRNA linear 0676c3 zcapPFDd2.1, Debopam Chakrabarti Plasmodium clone 0676c 5', mRNA sequence.
T18122 T18122.1 GI:462908
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                             malaria parasite P. falciparum.
                                                                                                                                                                                                          Fax: 407 384 3095
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                                                                                                                                                                    primer:
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                                                                                                                                                                                     dchak@pegasus.cc.ucf.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA isolated."
/clone_lib="czapPFDd2.1, Debopam Chakrabarti"
/lab_host="E. coli XL-1 blue"
/note="Vector: Lambda ZAP II; Site_1: EcoR I;
                                                        /clone="0676c"
                                                                          /strain="Dd2"
/db_xref="taxon:5833"
                                                                                                              /organism="Plasmodium falciparum"
                                                                                                                                                  Location/Qualifiers
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No. 1.6e-09;
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Site_1: EcoR I; Site_2:
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RESULT 32
BQ451205
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Matches 180
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                                                           Library was constructed by Debopam Chakrabarti DNA Washington University Genome Sequencing Center For obtaining a clone please contact: L. David Sibley
                                                                                                                                                                                        Contact: L. David Sibley
Washington University School o
4444 Forest Park Parkway, Box
                 (sibley@borcim.wustl.edu), Washington University Seq primer: -40UP from Gibco.
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Plasmodium falciparum
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BQ451205.1 GI:21254317
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                                                                                                                             Email: est@watson,wustl.edu
                                                                                                                                                                                                                                                                            Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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35 c 35 g 98 t l others
Location/Qualifiers
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCACTTTTCGATGGTATTTTCTGCAGTTCCTCTAACTTCTTAGGAATATCATTCTTATTA 121
                                                                                                                                                                                                                                                                                                Tang, K., Cole, R., Chakrabarti, D., Haywood, R., Clifton, S., Pape, D., Marran, M., Hiller, L., Martin, J., Wylle, T., Dante, M., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Jentes, E., Ronko, I., Tsagareishvili, R., Belaygorod, L., Franklin, C., Carr, L., Grow, A., Maguire, L., Richey, J., Wadkins, J., Kennedy, S., Levinso, D., Waterston, R., Wilson, R. and Sibley, D. Washu Plasmodium EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BUD//302 352 bp mRNA linear EST 19-JUN-2002 PESTGOBLI7C05.yl plasmodium talciparum 3D7 asexual cDNA plasmodium
                    Email: est@watson.wustl.edu
Library was constructed by Debopam Chakrabarti DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: L. David Sibley
                                                                                                                                                                      Washington University School of Medicine
                                                                                                                                                                                                                        Contact: L. David Sibley
WashU Plasmodium EST Project
                                                                                                                                                                                                                                                                         Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence
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(sibley@borcim.wustl.edu), Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 352)
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314 286 1810
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/note="Vector: pBluescript SK plus; Site_1: EcoRI; Site_2:
XhoI; Library was constructed by Debopam Chakrabarti.
Total RNA samples were isolated from mixed stage
saponin(0.1%)-lysed P. falciparum 3D7 infected
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/db_xref="taxon:5833"
/clone_11b="Plasmodium falciparum 3D7 asexual cDNA"
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                                                                                                                                                                      St. Louis, MO 63108, USA
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCTCATGCTGATCCTGTACAGCTTCATCTAATAGATCGATG 4939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Molecular Biology and Microbiology University of Central Florida Collando, FL 32816-2360
                                                                                                                                                                                                                                                                                                                                                           Chakrabarti,D., Reddy,G.R., Dame,J.B., Almira,E.C., Laipis,P.J., Ferl,R.J., Yang,T.P., Rowe,T.C. and Schuster,S.M. Ferl,R.J., Yang,T.P., Rowe,T.G. and Schuster,S.M. Analysis of Expressed Sequence Tags from Plasmodium Falciparum Mol. Biochem. Parasitol. 66, 97-104 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        718003 282 bp mRNA linear EST 30-AU 0325c 365eFfHB3.1, Debopam Chakrabarti Plasmodium falciparum clone 0325c 5', mRNA sequence.
T18003
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                          Contact: Debopam Chakrabarti
                                                                                                                                                                                                                                                                                                                                         95075403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       malaria parasite P. falciparum.
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                                                                                                                                                                    Fax: 407 384 3095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 282)
                                                                                                        il: dchak@pegasus.cc.ucf.edu
primer: T3.
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/note="vector: pBluescript SK plus; Site_1: EcoRI; Site_2:
XhoI; Library was constructed by Debopam Chakrabarti.
Total RNA samples were isolated from mixed stage
saponin(0.1%)-lysed P. falciparum 3D7 infected
erythrocytes by the acidic quanidatinum-phenol chloroform
method. The poly A+ RNA was isolated by the polyAT-Tract
mRNA isolation system (Promega, WI) using streptavidin
Magnesphere particles. Directional cDNA libraries were
constructed by oligo d(T) priming of poly(A)+ RNA (5mg)
into EcoRI and XhoI sites of 1 ZapII vector using the Zap
cDNA synthesis kit (Stragene, CA). The average size of the
cDNA inserts in the library was between 1.0 and 1.5kb.
Clones were mass excised using the Exassist helper phage
(Stratagene), the phagemids were precitptated with PEG
8000 and extracted with phenol/chloroform. Phagemid DNA
was electroporated into DH10B cells."
/organism="Plasmodium falciparum"
/db_xref="taxon:5833"
                                                                                 Location/Qualifiers
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/db_xref="taxon:5833"
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70.48;
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RESULT 35
BH153470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTTCCAGAAGGAGAAGATGGTGCTGAATGAAGGGACGACGGCCGTTACAACCA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGTAATTCAAGACGTACAAATCCTTCAGNTAATTCAAGTGATTCAGATGCTAAATCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGGTTCCGTCGCCTCCGGCGGCAGCGTGGCATCAGGTGGCTCAGTGGCAAGCGGCGGTT 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Entamoeba histolytica.
Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BH153470 878 bp DNA linear GSS 24-SEP-20 ENTRE19TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
                                                                                                                                                 Class: shotgun
                                                                                                                                                                                           DNA library
                                                                                                                                                                                                            Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                  Department of Eukaryotic Genomics
The Institute for Genomic Researc
                                                                                                                                                                                                                                                                                                                                                                Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                       HM1: IMSS sheared DNA library (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 878)
Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Entamoebidae; Entamoeba.
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BH153470
                                                                                                                                                                     primer: M13-Forward
                                                                                                                                                                                                                                                                                       Medical Center Dr., Rockville,
                                                                                                     quality sequence stop: 840
                                                                                                                         quality sequence start: 16
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301 838 3543
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/lab_host="E. coli XL1-Blue"
/note="Vector: pBlueScript SK(+); PolyA+ RNA, from
/note="Vector: pBlueScript SK(+); PolyA+ RNA, from
asynchronous blood stage parasites of the cloned Honduran
HB3 isolate cultured in vitro, was reverse transcribed
using an oligo d".Yho I primer. Second strand was prepared
using RNase H and DNA polymerase I. EcoR I adapters were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ligated to the cDNA, and it was cleaved with Xho I. Prepared fragments were ligated into EcoR I + Xho I double-digested pBlueScript SK(+), and transformed E. XL1-Rlue
                                                                                   Location/Qualifiers
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/organism="Entamoeba histolytica"
/strain="HM1:IMSS"
/db_xref="taxon:5759"
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Pred. No. 4.5e-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    486 AAGAACAACCAAAACAAGAAGAAGAAACTCCTCGTTGAAGAAGTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234;
                                                                                                                                                Plasmodium yoelii yoelii.
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 483)
                                                            Plasmodium yoelii EST project at TIGR Unpublished (2001)
                                                                                                          Carlton, J.M., Dally, T.M., Long, C.A., Bergman, L.W., Fraser, C.M. and Carucci, D.J.
                                                                                                                                                                                                                                                      BM165179.1 GI:17310860
EST.
                                                                                                                                                                                                                                                                                                                  mRNA sequence.
                                                                                                                                                                                                                                                                                                                                               BM165179 4
EST567702 PyBS Plasmodium
Parasite Genomics
The Institute for
                                           Contact: Jane Carlton
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/note="Vector: pHOS1; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.) The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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Pred. No. 1.9e
0; Mismatches
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Research
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1.9e-07;
nes 229;
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REFERENCE
AUTHORS
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Best Local Similarity
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Cariton,J.M., Daly,T.M., Long,C.A., Bergman,L.W.,
Fraser,C.M. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
                                                                                                                                                                             mRNA sequence.
BM167609
BM167609.1 GI:17300841
                                                                                                                                                                                                                                             BM167609 Test Plasmodium
                                                                                   Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                           EST
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                                                                                                                                     Plasmodium yoelii yoelii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 301-838-0208
                                                                 (bases 1 to 703)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. coli XL-1 Blue"
/note="Vector: pAD-GAL4; At 20-28 parasitemia, blood was collected from BALB/CByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography.
First strand cDNA synthesis was completed using a 50-base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA
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Pred. No. 3.8e-07;
0; Mismatches 100; Indels
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361 TACAAAAGGTTGTCGAAGTCTTAGAAAAACGAGTTTCTACATTAAAGAAAAATGATGCCA 420
                                                893 CCCATAACCTCATCAGCGTACTGGAGAAGCGCATAGACACCCTCAAGAAGAATGAAAATA 952
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                                                                                                                                                                                                                                                                                                                                                                                                                   ATAGAAAACCAATAGAAAATATTCAAGACGATATTGAAAAGTTAGAAATTTACATAGAAA 180
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The Institute for Genomic Research
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First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA isolated."
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/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/CByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method, and
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Pred. No. 4.1e-07;
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                                                                                                                                         285;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida;
1 (bases 1 to 769)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockvill
Tel: 301-530-9319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium yoelii EST project at TIGR Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM166688 769 bp mRNA linear EST 04-DEC-2001 EST569211 PyBS Plasmodium yoelii yoelii cDNA clone PYCNV80 5' end,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: carlton@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Jane Carlton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fraser, C.M. and Carucci, D.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Vaidya, A.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium yoelii yoelii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reagent Resource Center, ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   For clone info, please contact the Malaria Research
                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="Asexual blood stages"
/lab_host="E. coli xL-1 Blue"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blocollected from BALB/CByJ mice infected with py17xL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was
                                                                                                                                                                                                                                                                             Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms After packaging, the phagemid vector (pAD-GAL4) was
                                                                                                                                                                                                                                                                                                                                5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EccRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column.
                                                                                                                                                                                                                                             isolated."
                                                                                                                                                                                                                                                             excised from the HybriZAP vector and plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                     primer and reverse transcriptase in the presence of
                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA isolated using oligo(dT)-cellulose chromatography First strand cDNA synthesis was completed using a 50-ba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="17XL"
/db_xref="taxon:73239"
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High quality sequence stop: 2
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                                                                                                                                                                                                                                                                             Tel: 215-898-9384
Fax: 215-898-8780
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1 (bases 1 to 1147)
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Arabidopsis thaliana
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University of Pennsylvania
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                                                                                                                                                                                                                                                                                                                                                               . of Biology, | University of Pennsylvania, Philadelphia, PA
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
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/sex="hermaphrodite"
/note="Vector: BeloBACII; Site_1: HindIII; Site_2: HindIII
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CAAGAACAAGAACAAGAACAAGAACAAGAACAAGAACAAGAACAAGAACAAGAACAA
                                                                                      CATCGAGAACATTAACGAGCTGATCGAAGAATCCAAAAAAGACCATAGACAAAAATAAGAA 812
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45 w. Gude Dr.,
Tel: 2404533151
Fax: 2404534580
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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170000887387385 A.Gam.ad.cDNA1 Anopheles
19600449658190 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2002)
Contact: Holt R.A.
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                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                     /note="Vector: pSport1; Site_1: Sal1; Site_2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)." 7 t
                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome)
                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="RSP-ST (Reduced
                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10b"
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/dev_stage="Adult"
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Pred. No. 9.9e-07;
0; Mismatches 198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAGCACGAGAAAGAGATCAAAGAGAGATCGCCAAAAACCATTAAGTTCAACA 1102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2001)
Contact: Jane Carlton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 344)
Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Vaidya, A.B.,
Fraser, C.M. and Carucci, D.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium yoelii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST561889 PyBS Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                For clone info, please contact the Malaria Research and Reference Reagent Resource Center, \mathtt{ATCC}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium yoelii EST project at TIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.malaria.mr4.org/mr4pages/index.html
Seg primer: ADF.
                            145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carlton@tigr.org
                            þ
                                                                                                                           mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to hybrizAP arms directionally using EcoRI-xhoI cleaved arms.
                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pAD-GAL4; At 20-25% parasitemia, blood collected from BALB/CByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method,
                            isolated."
1 65 c
                                                                           After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="17XL"
/db_xref="taxon:73239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="PyBS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Plasmodium yoelii yoelii"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="PYCJD17"
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m yoelii
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RESULT 42
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1921 CTGAAGAACGTGGAGTTAAÀACATAATATACATGTGCCGAATAGTTATAAGCAGGAGAAT 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1861 CAAGTGCAGAAGGTGCTCCTCATGAACAAGATTGATGAACTCAAGAAGACTCAACTCATT 1920
                                                                                                                                                                                                                                                                                                                                                                          source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGCAGGAACCATACCTCCTCATCGTACTCAAGAAAGAGATAGACAAACTGAAAGTGTTC 2040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGCCCAAAGTCGAGGCCTGATCAACGAAGAAGAAGAAGAACATTAAA 2088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAACCAGAACCATACTATTTAATAGCTGTAAAAAAAGAAGTTGACAGACTTGCCCAATTT 181
                                                                                                                                                                                                                                                                                                                                                                                                            seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reil,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern, and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2M0080C24F Mouse 104
clone UUGC2M0080C24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
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GSS.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                          Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 was blunt end-repaired with T4 DNA polymerase and T4
                                                                                                                                                                        /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biomedical Polymers Research Bldg.,
                    polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
adaptored DNA was
                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                            /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                /clone_1|ib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                  /clone="UUGC2M0080C24"
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24 F, DNA sequence.
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Pred. No. 3
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dand size-selected
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGAAGACTGAGAAGAAGAAGAACTGAGAAGAAGAAGAAGAACAACAACAAGAACA 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186;
                                              Tel: 919.515.6699
Fax: 919.515.9500
Email: warthog@unity.ncsu.edu
GT11-4PCN F H07 PCN 4 F 060.ab1
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       Globodera pallida.
Globodera pallida
Eukaryota, Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BM415494 948 bp mRNA linear ES OP20570 Mixed Stage EST's from Globodera pallida, the
                                                                                                                                                        Center for the Biology of Nematode Parasitism NC State University; IACR-Rothamsted Campus Box 7616; Raleigh, NC 27695, USA
                                                                                                                                                                                                                                           Heer,J., Sosinski,B., Pokrzywa,R.M., Warry,A. Mixed Stage EST's from Globodera pallida, the Unpublished (2001)
                                                                                                                                                                                                                      Contact: Opperman, C
                                                                                                                                                                                                                                                                                                                                                                                                            EST
                                                                                                                                                                                                                                                                                                                                                                                                                               BM415494.1 GI:18382210
                                                                                                                                                                                                                                                                                                                                                                                                                                                    BM415494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gli4732114) gbjaFr129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for ampicallin resistance."
/organism="Globodera pallida'
/db_xref="taxon:36090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pallida cDNA, mRNA sequence.
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/note="Vector: lambda GT11; This is a collaborative effort between IACR-Rothamsted and North Carolina State University. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs, IACR-Rothamsted."

1 ACR-Rothamsted. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs, IACR-Rothamsted. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs, IACR-Rothamsted. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs, IACR-Rothamsted. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs, IACR-Rothamsted. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs, IACR-Rothamsted. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs, IACR-Rothamsted. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs, IACR-Rothamsted. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs, IACR-Rothamsted. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs, IACR-Rothamsted. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs, IACR-Rothamsted. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs, IACR-Rothamsted. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs, IACR-Rothamsted. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs, IACR-Rothamsted. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs, IACR-Rothamsted from mixed stage G. pallida in lambda GT11 by Paul Burroughs, IACR-Rothamsted from mixed stage G. pallida in lambda GT11 by Paul Burroughs, IACR-Rothamsted from mixed stage G. pallida in lambda GT11 by Paul Burroughs, IACR
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
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International Triticeae EST Cooperative (ITEC)
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Menzinger Str. 67, D-80638 Munchen GERMANY
Fax: 49 30 171683
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                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="HWM002.B02"
/clone=lib="ITEC HWM Barley Leaf Library"
/tlssue_type="leaf"
/dev_stage="14 day old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Hordeum vulgare"
/cultivar="Barke"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBluescriptSK(~); 850 bp average insert
size."
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Pred. No. 2.6e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTCCGCCAGCCAACTCTGGGAACACCCCCTAACACGCTGCTGGACAAGAACAAGAAGATA 1050
                                                                                Zhao, S., Nierman, W., Malek, J., Shatsman, S., Ak
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A.,
Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
                         Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                          GSS.
                                                                                                                                                                                                                                     DNA sequence.
BH040136
                                                       Unpublished (1999)
Other_GSSs: RPCI=24-255A23.TJ
                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                       вн040136.1
                                                                                                                                                                                                                                                              RPCI-24-255A23.TV
                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                             house mouse
                                                                                                                                                                                                                                                                            вн040136
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                                                                                                                                      (bases 1 to 691)
Institute for Genomic Research 2 Medical Center Dr., Rockville,
                                                                                                                                                                                                                       GI:14818806
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e RPCI-24-255A23
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Murinae; Mus
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RESULT 46
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                                                                                                                                                                                                                                                                                               AATGAAAATATCAAAGAACTGCTCGACAAGATTAATGAAATTAAGAATCCTCCGCCAGCC
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             Plasmodium yoelii yoelii.
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                 mRNA sequence.
BM170771
BM170771.1 GI:17304003
                                                               EST
                                                                                                                                 EST573294 PyBS Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: T7
Class: BAC ends.
                                                                                                                                                  BM170771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 255 row: A column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC
 (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1; RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-255A23"
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to 682)
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                                                                                                                                      CGGCAATAGCCCAAGCGAGAATAATACAGACGTGAATAACGCACTGGAATCTTACAAGAA 3569
                                                                                                                                                                                     AGGAGGTTTACACCACGTATTTGAAGAATTTAAAGAACTTATAAAAGATAAAGACTATAC
                                                                                                                                                                                                                                  TAGCGGACTGCATCACCTGATCGCCGAGCTCAAGGAAGTCATTAAGAACAAGAACTACAC 3509
                                                                                                                                                                                                                                                                                    ATTAGAATTAAGATTAAAAAAAAATATTAATTTAGGAAAGGAAAGAATTTCATATGTATC
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                                                                                            CGGAAAAAAAACCCTGATAATGCCCCTGAAGTTACCAATGCATTCGAACAATATAAAAGA
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167; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Jane Carlton
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          For clone info, please contact the Malaria Research Reagent Resource Center, ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: carlton@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 301-838-0208
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/lab_host=E. coli XL-1 Blue"

/note="vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/cByJ mice infected with Py17XL collected from BALB/cByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothicyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dcTp. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with NhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to Hybrilap arms directionally using EcoRI XhoI cleaved arms.
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Pred. No. 9.7e-05;
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                                                     GATGATGATGATGAAGAAGAAGAAGATGATGATGAAGATGAAGACGATGAAGACGAC 246
                                                                                       CATCGACCTGACCAACTTCGAGAAAATGATGGGAAAACGGT---ACTCTTACAAAGTGGA 1574
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                                                                                                                                                                                                       GAAGAAGAAATTGAGAGTGACAAGAAAAGTTACGAAGACCGCAGCAAAAGTCTAAACGA 1457
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High quality sequence stop: E
Location/Qualifiers
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ENTEK30TR Entamoeba histolytica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: bjloftus@tigr.org
Clones are derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Eukaryotic Genomics
The Institute for Genomic Research
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Loftus, B., Van Aken, S. and Fraser, C.

Determination of clone end sequences from

HM1:IMSS sheared DNA library
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301 838 0208
301 838 3543
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/note="Vector: pHOS1; Site_l: Bat I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (193) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole general recommendation projects.
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Barell, c
16 c
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16 c 289 g 169 t
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/db_xref="taxon:5759"
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                                                                                                                                                                                                                                                                                                                          Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
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BJ420171 Dictyostelium discoideum cDNA library,
discoideum cDNA clone ddv38p08 5', mRNA sequence
BJ420171
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EST.
                                                                                                                                                                                                                              Email: tshini@genes.nig.ac.jp
Location/Qualifiers
                                                                                                                                                                                                                                                                             Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                              National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                               stage
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 Conservative
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                                                                                                                                               /organism="Dictyostelium discoideum"
|strain="AX4"
|/db_xref="raxon:44689"
|/clone="ddv38p08"
                                                                               /dev_stage="Growth phase"
39 c 94 g 47
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/sex="mat A"
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                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0265 row: I column: 2
                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                              University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                    Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
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AZ460541.1 GI:10618666
                                                                                                                                                                                                                                                                                                                                                                         plasmid inserts
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Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
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                                                                                                                                                   Seq primer: CACACAGGAAACAGCTATGACC
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                                                                                                           quality sequence stop: 596
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0265124"
                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATGAAATTAAGAATCCTCCGCCAGCCAACTCTGGGAACACCCCTAACACGCTGCTGGAC
                                                                                                                                                                                                    sequence.
AL176953
AL176953.1
Tetraodontidae: Tetraodon.

1 (bases 1 to 907)
Roest-Crollius,H., Jaillon,O., Dasi
Bernot,A., Fizames,C., Wincker,P.,
Saurin,W. and Weissenbach,J.
                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                               Tetraodon nigroviridis
                                                                                                                                                                  GSS; genome survey sequence. Tetraodon nigroviridis.
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genomic survey

GSS 12-MAY-2000

1035

268

208

328

of clone

GI:7815010

Dasilva, C., Bouneau, L., Fisher, C.

Brottier, P.,

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736 AAAAAGAATAAGAAGACCATCGAGAACATTAACGAGCTGATCGAAGAATCCAAAAAGACC 795
                                                                                                                                                                                                                                                                                             Local Similarity
TACGACCTGTCCATCTATAACAAACAGCTTGAAGAAGCCCATAACCTCATCAGCGTACTG
                                                     ATAGACAAAAATAAGAATGCAACCAAGGAGGAAGAAAAAGAAGAAGTTGTACCAGGCCCAG
                                                                                                                                                               315
                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                purified. The sheared, agaptored into adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

a 59 c 145 g 77 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil473214)gblafr129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarness and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: PWD42nv; Purified genomic DNA fromusculus C57BL/6J (male) was obtained from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                          50.3%;
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                                                                                                                                                                                                                                                                                             Score 68.4;
Pred. No. 0.
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                                                                                                                                                         TTACTGATCCCCTTGAGCTGGAGTACTACTTGAGAGAGAAGAATAAGAATATAGACATCT 1174
                                                                                                                                                                                                                     AGCACGAGAAAGAGATCAAAGAGATCGCCAAAACCATTAAGTTCAACATAGATTCTCTCT 1114
                                                                                                                                                                                                                                                                        ARAAAAACACSGAKAAAAKGAAAAAAAAAAAAAAYTCAGHAGAAAAAAAAAAATAAAAA
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ACCCTCTGTCTTATAACGATATCAACAACGCTCTCAACGAGCTCAATAGCTTCGGTGACT 1294
                                                             AAARAGAAAGGGAGNADDAGAAAAAAAAAATACTAYTAYGABAHCAATDAAAAAAAAAAAA
                                                                                          CCGCCAAAGTCGAGACAAAGGAATCAACCGAACCTAATGAATATCCCAATGGTGTGACGT 1234
                                                                                                                            MSMACYAASAAWASCAAAAABACATAAAAAAAAAAAAAAAWBKAAAAAAAAAAATHTYA 449
                                                                                                                                                                                                                                                        337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 907)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (12-APR-2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human gene number estimate provided by genome
Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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/db_xref="taxon:99883"
/clone="225N09"
/clone_lib="G"
/clone_lib="G"
/note="Genoscope sequence ID : COAPUC-Ori"
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t; Pred. No. 0.00014;
41; Mismatches 482
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RESULT 51
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AGAAAATTGAGAGTGACAAGAAAAGTTACGAAGACCGCAGCAAAAGTCTAAACGATATCA 1462
                                                           CAGACAATGAGAGAAGAAGTTTATCAACGAAATCAAGGAGAAGATCAAAATTGAGAAGA 1402
                                                                                                                    GCTTCGGTGACTTGATTAACCCCCTTCGATTATACGAAAGAACCCCTCTAAGAATATCTACA 1342
                                                                                                                                                    ATGTTGTAACGAACAAATTCAACAACAACAAGAACAAGAACAACAACTACAACAACAACT 187
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                                                                                                                                                                                                                  162;
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1 (bases 1 to 494)

Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.

Full length cDNA of Dictyostelium discoideum at the
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BJ360881 Dictyostelium discoideum
discoideum cDNA clone ddc8k12 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2002)
Contact: Tadasu Sh
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Dictyostelium discoideum
                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                  Conservative
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Location/Qualifiers
                                                                                                                                                                                                                                                                                          /dev_stage="Culmination stage" 129 c 34 g 48 t
                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:44689"
/clone="ddc8k12"
                                                                                                                                                                                                                                                                                                                                                                                  /organism="Dictyostelium
/strain="AX4"
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Pred. No. 0.00019;
0; Mismatches 159;
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                                             TCCTTTACCACTCACTGATATTCATAATTCATTAGCTGCAGATAATGATAAAAATTCATA 278
                                                                          CCCTCTGTCTTATAACGATATCAACAA---
                                                                                                     ACAAGATCCTACGAAATCTGTTCAAATACCAAAAGTTCCTTATCCAAATGGTATTGTATA
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                                                                                                                                                                                                                                                                                   238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: jwatanab@manage.ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library Gene 200 (1-2), 149-156 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Junichi Watanabe
Institute of Medical Science
The University of Tokyo, Department of Parasitology
4-6-1, Shirokanedal, Minatoku, Tokyo 108-8639, Japan
Tel: 81-3-5449-5378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Watanabe, J., Sasaki, M., Suzuki, Y. and Sugano, S.
FULL-malaria: a database for a full-length enriched cDNA library
from human malaria parasite, plasmodium falciparum
Nucleic Acids Res. 29 (1), 70-71 (2001)
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Plasmodium falciparum 3D7
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                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                   /clone="XPFn5428"
/clone_lib="Sugano Malaria cDNA library"
/dev_stage="erythrocytic stage"
/dev_51 c 55 g 148 t 10 other
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Plasmodium falciparum
                                                                                                                      -GACAAAGGAATCAACCGAACCTAATGAATATCCCAATGGTGTGACGTA 1235
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Pred. No. 0.00019;
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AACGATATCAACAACGCTCTCAACGAGCTCAATAGCTTCGGTGACTTGATTAACCCCTTC
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                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-APR-2000)
This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNS02156 827 bp DNA linear GSS 12-MAY:
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clc
224F10 of library G from Tetraodon nigroviridis, genomic survey
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Human gene number estimate provided by genome wide anal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS; genome survey sequence. Tetraodon nigroviridis.
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Direct Submission
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Bouneau, L., Billault, A.,
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                                                                Conservative
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/clone_lib="G"
/note="Genoscope sequence
                                                                                                                                                                                                                                                                                                  /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
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Quetier,F.,
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AGENCOURT_8929072 NIH_MGC_40
5', mRNA sequence.
BQ931326
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
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                                                                                                                                                                                                                                                                                  quality sequence stop:
Location/Qualifiers
/clone_lib="NIH_MGC_40"
/clone_lib="NIH_MGC_40"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage=resistant)"
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                            /clone="IMAGE:6484392"
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                                                                                                  NNNAAAGNNNGATGAAGAAGACACCCAGGAACACAGC
                                                                                                                                 GTACTCTTACAAAGTGGAGAAACTGACACCACCATAATACC
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AZ191902
SP_1020_A2_D08_SP6E
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731 bp DNA
Strongylocentrotus
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Pred. No. 0.00043;
0; Mismatches 673;
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74 g 503 t 444 others
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GSS 30-AUG-2000 purple sea
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                                                                                               TCTAAGCATAATCTTGAGAAGCTCACCAAAGCTCTTAAGTATATGGAGGACTATTCTCTG
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Class: BAC ends
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Tel: (626) 395-8421
Fax: (626) 793-3047
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California Institute of Technology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BAGS. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
AAGCCCATAACCTCATCAGCGTACTGGAGAAGCGCCCATAGACACCCTCAAGAAGAATGAAA
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Determination of this BAC-end sequence was
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                                                                                                                Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
                                                                                                                                                                                                                   Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
1 (bases 1 to 626)
Urushihara, H., Tanaka, Y., Kohara, Y., and Shin-i, T.
                                                                                                                                                                                                                                                                                                                                                            BJ426817 626 bp mRNA linear EST 11-MAR-2 BJ426817 Dictyostelium discoideum cDNA library, VF Dictyostelium discoideum cDNA clone ddv60i07 5', mRNA sequence.
                                                                                                                                                                                        stage
                                                                                                                                                                                                                                                                        Dictyostelium discoideum
                                                                                                                                                                     Unpublished (2002)
                                                                                                                                                                                                      Full length cDNA of Dictyostelium
                                                                                                                                                                                                                                                                                             Dictyostelium
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                                                                                  Yata, Mishima,
81-559-81-6856
                                                                  81-559-81-6855
                             tshini@genes.nig.ac.jp.
Location/Qualifiers
/organism="Dictyostelium
                                                                                                                                                                                                                                                                                                                              GI:19344253
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                                                                                                    Shizuoka
                                                                                                    411-8540,
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discoideum'
                                                                                                  Japan
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TITLE
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Best Local Similarity
Matches 242; Conserv
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                                                                                                                                                                                                                                                                                                                                                          GAAAACGAGATCGAGACGCTTGTTGAGAACATTAAGAAGGATGAAGAACAGTTGTTTGAG
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Eukaryota; Metazóa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neopteza; Endoptérygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                  CNSO11L2 . 783 bp
Drosophila melanogaster genome sur
BACN06P17 of DrosBAC library from
fly), genomic survey sequence.
AL100400
AL100400.1 GI:5612011
GSS
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/db_xref="taxon:44689"
/clone="ddv60107"
/clone_lib="Dictyostelium"
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38 c 104 g 42
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Pred. No. 0.00051;
0; Mismatches 277;
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survey sequence SP6 end
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segref@genoscope.cns
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                                                                                                                                                                                                                                                                                                                                   TGGGAACACCCCTAACACGCTGCTGGACAAGAACAAGAAGATAGAGGAGCACGAGAAAGA 1067
                                                                                                                                                                                                                                                                                                                CMMCAGMCAAAMAAACCGAGACCAAAAAAAATCAAAAAAGTGCCCCGMAAAGNAAANAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.
                                                                                    Debaryomyces hansenii.
Debaryomyces hansenii
                                                                                                                   GSS.
                                                                                                                                             Debaryomyces hansenii, genomic survey sequence. AL436389
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Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
                             Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G
                                                                     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                              AL436389.1 GI:12219802
                                                         Saccharomycetales; Saccharomycetaceae;
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/plasmid="pBeloBAC11"
/note="end : SP6"
a 58 c 155 g
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41.7%; Pred. No. 0.00054;
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library BCOAA from strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                             1453
                                                                                                                                                                                                                                                                                                                                         1333 AATATCTACACAGACAATGAGAAGAAGAAGTTTATCAACGAAATCAAGGAGAAGATCAAA 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
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                                                                                                                                          462
                                                                                                                                                                                                                                                                                                                642
                                                                                                                                                                                                                                                                                                                                                                                  Local
 AAAGAACTAAAGTATTACAAGAATCTCATAAGTAAGATCGAAAACGAGATCGAGACGCTT 1752
                                                        AAGCTCACCAAAGCTCTTAAGTATATGGAGGACTATTCTCTGCGGAACATTGTTGTGGAG 1692
                                                                                                              GAGAAACTGACACCATAATACCTTTGCATCCTATGAGAATTCTAAGCATAATCTTGAG 1632
                                                                                                                                                                   AATAACATCGACCTGACCAACTTCGAGAAAATGATGGGAAAACGGTACTCTTACAAAGTG 1572
                                                                                                                                                                                                                                                       AACGATATCACTAAAGAGTATGAAAAGCTGCTGAACGAGATCTATGATTCCAAATTCAAC 1512
                                                                                                                                                                                                                                                                                   ATTGAGAAGAAGAAATTGAGAGTGACAAGAAAAGTTACGAAGACCGCAGCAAAAGTCTA 1452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                           148
                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="CBS 767"
/varlety="hanseni1"
/db_xref="taxon:4959"
/clone="BCOAA003A12"
/clone_lib="BCOAA"
/note="end: T7"
                                                                                                                                                                                                                                                                                                                                                                                  1.3%; Score 65.4;
42.1%; Pred. No. 0.
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Mismatches

0.00056;

DB 17;

Length 897; Indels

0,

Gaps

0

343

47 g

590 t.

42

others

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Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

1 807
                                                                                                                                                                                                                                                                       2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex - FRANCE (E-mail: segref@genoscope.cns.fr) Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lepingle,A., Casaregola,S., Neuveglise,C., Bon,E., Artiguenave,F., Wincker,P. and Gaillardin,C. Genomic exploration of the hemiascomycetous yeasts: Debaryomyces hansenii var. hansenii FEBS Lett. 487 (1), 82-86 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M. Wincker, P. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomic exploration of the hemiascomycetous yeasts: yeast species for molecular evolution studies
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′organism="Debaryomyces
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hansenii"
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    A set of

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